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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 15:32:30 ; Search time 215.959 Seconds
(without alignments)
317.043 Million cell updates/sec

Title: US-10-757-745-2_COPY_54_273

Perfect score: 1131

Sequence: 1 MERALNSYFPPVBSALER.....SATVIFAGDTNLRDREVTTC 220

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3289935 segs, 155610033 residues

Total number of hits satisfying chosen parameters: 6579870

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Command line parameters:

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Database : Published Applications NA New:

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7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	85.5	7.6	165883	7	US-11-112-908-18
5	85	7.5	207908	7	US-11-112-908-21
6	81.5	7.2	172147	7	US-11-112-908-22
7	81.5	7.2	207908	7	US-11-112-908-21
8	81.5	7.2	212805	7	US-11-112-908-19
C 1	196	17.3	952	6	US-10-750-185-25698
2	88.5	7.8	3828	6	US-10-821-234-746
3	87.5	7.7	212805	7	US-11-112-908-19
4	85.5	7.6	165883	7	US-11-112-908-18
5	85	7.5	207908	7	US-11-112-908-21
6	81.5	7.2	172147	7	US-11-112-908-22
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7	US-11-112-908-53	6.9	191343	78.5	Sequence 53, Appl
6	US-10-821-234-301	6.9	3672	78	Sequence 301, Appl
6	US-10-510-386-71	6.8	1621	77	Sequence 71, Appl
7	US-11-112-908-22	6.8	172147	77	Sequence 22, Appl
7	US-11-112-908-23	6.8	186682	77	Sequence 23, Appl
6	US-10-750-185-41248	6.8	1673	76.5	Sequence 41248, A
6	US-10-909-125-801	6.5	4339	74	Sequence 801, Appl
6	US-10-645-441-11	6.5	2532	73.5	Sequence 11, Appl
6	US-10-485-517-118	6.5	2361	73	Sequence 118, Appl
6	US-10-821-234-606	6.4	1503	72.5	Sequence 606, Appl
6	US-10-793-626-1499	6.4	2238	72.5	Sequence 1499, Ap
6	US-10-793-626-3413	6.4	3207	72.5	Sequence 3413, Ap
6	US-10-793-626-3737	6.4	4434	72	Sequence 3737, Ap
6	US-10-750-185-50641	6.3	1611	71.5	Sequence 50641, A
6	US-10-750-185-63174	6.3	3396	71.5	Sequence 63174, A
6	US-10-793-626-3009	6.3	720	71	Sequence 3009, Ap
6	US-10-467-657-47	6.3	1500	71	Sequence 47, Appl
6	US-10-467-657-7735	6.3	1617	71	Sequence 7735, Ap
6	US-10-750-185-61286	6.3	1711	71	Sequence 61286, A
6	US-10-750-185-50529	6.3	1796	71	Sequence 50529, A
6	US-10-793-626-2097	6.3	2055	71	Sequence 2097, Ap
6	US-10-793-626-3580	6.3	2999	71	Sequence 3580, Ap
6	US-10-793-626-3527	6.3	3572	71	Sequence 3527, Ap
6	US-10-793-626-4046	6.3	3668	71	Sequence 4046, Ap
6	US-10-793-626-3619	6.3	4015	71	Sequence 3619, Ap
6	US-10-793-626-3631	6.3	4207	71	Sequence 81, Appl
6	US-10-401-386B-81	6.3	5302	71	Sequence 50173, A
6	US-10-750-185-50173	6.2	1425	70.5	Sequence 50173, A
6	US-10-750-185-56041	6.2	1541	70.5	Sequence 56041, A
6	US-10-750-185-50876	6.2	1624	70.5	Sequence 50876, A
6	US-10-750-185-57823	6.2	2360	70.5	Sequence 57823, A
6	US-10-467-962B-102	6.2	2361	70.5	Sequence 102, App
6	US-10-793-626-3423	6.2	3506	70.5	Sequence 3423, Ap
6	US-10-909-125-792	6.2	8096	70.5	Sequence 792, App
6	US-10-750-185-34532	6.2	2523	70	Sequence 34532, A
6	US-10-131-826A-85	6.2	2750	70	Sequence 85, Appl
6	US-10-750-185-55091	6.1	1354	69.5	Sequence 55091, A
6	US-10-750-185-63649	6.1	1643	69.5	Sequence 63649, A
6	US-10-750-185-24828	6.1	1650	69.5	Sequence 24828, A
6	US-10-750-185-36391	6.1	2034	69.5	Sequence 36391, A
6	US-10-750-185-36519	6.1	2233	69.5	Sequence 36519, A
6	US-10-623-155-119	6.1	8948	69.5	Sequence 119, App
6	US-10-401-386B-63	6.1	474	69	Sequence 63, Appl
6	US-10-750-185-35895	6.1	970	69	Sequence 35895, A
6	US-10-632-150-51	6.1	1777	69	Sequence 51, Appl
7	US-11-073-457-51	6.1	1777	69	Sequence 51, Appl
6	US-10-750-185-51119	6.1	1788	69	Sequence 51119, A
6	US-10-750-185-31052	6.1	6616	69	Sequence 31052, A
6	US-10-508-263-101	6.1	804	69	Sequence 101, App
6	US-10-793-626-1459	6.1	990	69	Sequence 45, Appl
6	US-10-689-742-45	6.1	3119	69	Sequence 2647, Ap
6	US-10-467-657-2647	6.1	3201	69	Sequence 2647, Ap
6	US-10-793-626-3832	6.1	3775	69	Sequence 3832, Ap
6	US-10-401-386B-75	6.0	471	68	Sequence 75, Appl
6	US-10-401-386B-77	6.0	471	68	Sequence 77, Appl
6	US-10-401-386B-79	6.0	471	68	Sequence 79, Appl
6	US-10-750-185-49551	6.0	634	68	Sequence 49551, A
6	US-10-750-185-58265	6.0	1053	68	Sequence 58265, A
6	US-10-750-185-39238	6.0	1167	68	Sequence 39238, A
6	US-10-793-626-483	6.0	1287	68	Sequence 483, Appl
6	US-10-750-185-38535	6.0	1731	68	Sequence 38535, A
6	US-10-793-626-3670	6.0	3683	68	Sequence 3670, Ap
6	US-10-793-626-3670	6.0	3794	68	Sequence 3670, Ap
6	US-10-793-626-1005	6.0	471	68	Sequence 1005, Ap
6	US-10-750-185-39657	6.0	906	68	Sequence 39657, A
7	US-11-074-176-121	6.0	1428	74	Sequence 121, App
6	US-10-793-626-4427	6.0	2397	74	Sequence 4427, Ap
6	US-10-750-185-52753	6.0	2453	75	Sequence 52753, A
6	US-10-793-626-3454	6.0	3196	76	Sequence 3454, Ap
6	US-10-750-185-34805	6.0	3899	77	Sequence 34805, A
6	US-10-821-234-59	6.0	4243	78	Sequence 59, Appl
7	US-11-112-908-58	6.0	168656	80	Sequence 58, Appl
7	US-11-112-908-58	6.0	170285	81	Sequence 58, Appl

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C 83	67	5.9	756	6	US-10-750-185-44698	Sequence 44698, A	C 156	64	5.7	1644	6	US-10-467-657-695	Sequence 695, App
C 84	67	5.9	955	6	US-10-750-185-47801	Sequence 47801, A	C 157	64	5.7	1674	6	US-10-467-657-693	Sequence 693, App
C 85	67	5.9	1069	6	US-10-750-185-46512	Sequence 46512, A	C 158	64	5.7	1877	6	US-10-793-626-2843	Sequence 2843, App
C 86	67	5.9	1089	6	US-10-750-185-32692	Sequence 32692, A	C 159	64	5.7	1986	6	US-10-793-626-273	Sequence 273, App
C 87	67	5.9	1152	7	US-11-102-240-153	Sequence 153, App	C 160	64	5.7	2094	6	US-10-750-185-45954	Sequence 45954, A
C 88	67	5.9	1165	6	US-10-750-185-35142	Sequence 35142, A	C 161	64	5.7	2142	6	US-10-750-185-32629	Sequence 32629, A
C 89	67	5.9	2477	6	US-10-131-826A-331	Sequence 331, App	C 162	64	5.7	2559	6	US-10-750-185-59818	Sequence 59818, A
C 90	67	5.9	3192	6	US-10-131-826A-75	Sequence 75, Appl	C 163	64	5.7	2707	6	US-10-821-234-319	Sequence 319, App
C 91	67	5.9	3569	6	US-10-415-198A-3	Sequence 3, Appl	C 164	64	5.7	2822	6	US-10-131-826A-305	Sequence 305, App
C 92	67	5.9	4033	6	US-10-750-185-56700	Sequence 56700, A	C 165	64	5.7	3155	6	US-10-793-626-3424	Sequence 3424, App
C 93	67	5.9	4265	7	US-11-044-051-74	Sequence 74, Appl	C 166	64	5.7	3175	6	US-10-750-185-48090	Sequence 48090, A
C 94	66.5	5.9	1260	6	US-10-750-185-28376	Sequence 28376, A	C 167	64	5.7	3549	6	US-10-750-185-48090	Sequence 48090, A
C 95	66.5	5.9	1530	6	US-10-750-185-50503	Sequence 50503, A	C 168	64	5.7	3636	6	US-10-793-626-3588	Sequence 3588, App
C 96	66.5	5.9	1898	6	US-10-750-185-41396	Sequence 41396, A	C 169	64	5.7	3791	6	US-10-658-986-1	Sequence 1, Appl
C 97	66.5	5.9	2158	6	US-10-750-185-33606	Sequence 33606, A	C 170	64	5.7	4055	6	US-10-793-626-3357	Sequence 3357, App
C 98	66.5	5.9	2908	6	US-10-793-626-4359	Sequence 4359, App	C 171	64	5.7	4104	6	US-10-131-826A-449	Sequence 449, App
C 99	66.5	5.9	3756	6	US-10-750-185-30101	Sequence 30101, A	C 172	64	5.7	4529	6	US-10-821-234-285	Sequence 285, App
C 100	66.5	5.9	150173	7	US-11-112-908-26	Sequence 26, Appl	C 173	64	5.7	4788	6	US-10-658-986-3	Sequence 3, Appl
C 101	66.5	5.9	171247	7	US-11-112-908-27	Sequence 27, Appl	C 174	64	5.7	5213	7	US-11-102-978-1	Sequence 1, Appl
C 102	66.5	5.9	172781	7	US-11-112-908-25	Sequence 25, Appl	C 175	64	5.7	5527	7	US-11-192-967-3	Sequence 3, Appl
C 103	66	5.8	598	6	US-10-750-185-1737	Sequence 1737, App	C 176	64	5.7	5527	7	US-11-193-715-3	Sequence 3, Appl
C 104	66	5.8	598	6	US-10-750-185-1982	Sequence 1982, App	C 177	64	5.7	125594	6	US-10-658-986-5	Sequence 5, Appl
C 105	66	5.8	600	6	US-10-750-185-1928	Sequence 1928, App	C 178	64	5.7	150450	7	US-11-112-908-54	Sequence 54, Appl
C 106	66	5.8	600	6	US-10-750-185-1934	Sequence 1934, App	C 179	64	5.7	150491	7	US-11-112-908-46	Sequence 46, Appl
C 107	66	5.8	950	6	US-10-750-185-43582	Sequence 43582, A	C 180	63.5	5.6	1100	6	US-10-742-634-1	Sequence 1, Appl
C 108	66	5.8	1818	6	US-10-750-185-49182	Sequence 49182, A	C 181	63.5	5.6	1121	6	US-10-131-826A-23	Sequence 23, Appl
C 109	66	5.8	1827	6	US-10-750-185-34154	Sequence 34154, A	C 182	63.5	5.6	1149	6	US-10-750-185-36217	Sequence 23, Appl
C 110	66	5.8	2524	6	US-10-750-185-41208	Sequence 41208, A	C 183	63.5	5.6	1377	6	US-10-750-185-37499	Sequence 37499, A
C 111	66	5.8	3511	6	US-10-793-626-3930	Sequence 3930, App	C 184	63.5	5.6	1419	6	US-10-131-826A-517	Sequence 517, App
C 112	66	5.8	5563	6	US-10-750-185-28063	Sequence 28063, A	C 185	63.5	5.6	1542	6	US-10-750-185-45928	Sequence 45928, A
C 113	65.5	5.8	471	6	US-10-401-386B-67	Sequence 67, Appl	C 186	63.5	5.6	1589	6	US-10-750-185-36365	Sequence 36365, A
C 114	65.5	5.8	1190	6	US-10-750-185-28873	Sequence 28873, A	C 187	63.5	5.6	2140	6	US-10-750-185-54276	Sequence 54276, A
C 115	65.5	5.8	1191	6	US-10-750-185-45984	Sequence 45984, A	C 188	63.5	5.6	2428	6	US-10-276-233A-23	Sequence 23, Appl
C 116	65.5	5.8	1284	7	US-11-074-176-363	Sequence 363, App	C 189	63.5	5.6	3094	6	US-10-750-185-62421	Sequence 62421, A
C 117	65.5	5.8	1545	6	US-10-821-234-659	Sequence 659, App	C 190	63.5	5.6	3415	6	US-10-750-185-31178	Sequence 31178, A
C 118	65.5	5.8	1709	6	US-10-750-185-61369	Sequence 61369, A	C 191	63.5	5.6	4775	6	US-10-750-185-29408	Sequence 29408, A
C 119	65.5	5.8	2076	6	US-10-750-185-39934	Sequence 39934, A	C 192	63.5	5.6	6160	7	US-11-060-005-3	Sequence 3, Appl
C 120	65.5	5.8	2730	6	US-10-750-185-42545	Sequence 42545, A	C 193	63.5	5.6	197781	7	US-11-112-908-34	Sequence 34, Appl
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C 124	65	5.7	785	6	US-10-750-185-41412	Sequence 41412, A	C 197	63	5.6	1227	6	US-10-750-185-34855	Sequence 34855, A
C 125	65	5.7	930	6	US-10-793-626-1607	Sequence 1607, App	C 198	63	5.6	1233	6	US-10-467-657-4443	Sequence 4443, App
C 126	65	5.7	966	6	US-10-750-185-48610	Sequence 48610, A	C 199	63	5.6	1338	6	US-10-821-234-754	Sequence 754, App
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C 128	65	5.7	1923	6	US-10-750-185-49025	Sequence 49025, A	C 201	63	5.6	1539	6	US-10-750-185-45144	Sequence 45144, A
C 129	65	5.7	3155	6	US-10-793-626-3881	Sequence 3881, App	C 202	63	5.6	1550	6	US-10-750-185-33704	Sequence 33704, A
C 130	65	5.7	3585	6	US-10-750-185-59285	Sequence 59285, A	C 203	63	5.6	1672	6	US-10-750-185-33572	Sequence 33572, A
C 131	65	5.7	3959	6	US-10-750-185-26934	Sequence 26934, A	C 204	63	5.6	1935	6	US-10-750-185-50882	Sequence 50882, A
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C 137	64.5	5.7	1222	6	US-10-750-185-51621	Sequence 51621, A	C 210	63	5.6	3232	6	US-10-750-185-62480	Sequence 62480, A
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C 140	64.5	5.7	1871	7	US-11-102-240-91	Sequence 91, Appl	C 213	63	5.6	3956	6	US-10-750-185-48696	Sequence 48696, A
C 141	64.5	5.7	1914	6	US-10-750-185-42446	Sequence 42446, A	C 214	63	5.6	4243	6	US-10-821-234-59	Sequence 59, Appl
C 142	64.5	5.7	2122	6	US-10-750-185-57886	Sequence 57886, A	C 215	63	5.6	5700	6	US-10-513-786-7	Sequence 7, Appl
C 143	64.5	5.7	2547	6	US-10-750-185-56188	Sequence 56188, A	C 216	63	5.6	5700	6	US-10-513-786-9	Sequence 9, Appl
C 144	64.5	5.7	2552	6	US-10-750-185-26492	Sequence 26492, A	C 217	63	5.6	5777	6	US-10-821-234-51	Sequence 51, Appl
C 145	64.5	5.7	3133	6	US-10-750-185-51444	Sequence 51444, A	C 218	63	5.6	11115	6	US-10-513-786-6	Sequence 6, Appl
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C 147	64.5	5.7	3687	6	US-10-750-185-38844	Sequence 38844, A	C 220	63	5.6	14911	7	US-11-112-908-63	Sequence 63, Appl
C 148	64.5	5.7	4053	6	US-10-131-826A-351	Sequence 351, App	C 221	63	5.6	157230	7	US-11-112-908-64	Sequence 64, Appl
C 149	64.5	5.7	10373	6	US-10-821-234-64	Sequence 64, Appl	C 222	63	5.6	170508	7	US-11-112-908-62	Sequence 62, Appl
C 150	64.5	5.7	23907	7	US-11-186-731-6	Sequence 6, Appl	C 223	62.5	5.5	484	7	US-11-108-172-252	Sequence 252, App
C 151	64.5	5.7	24120	7	US-11-186-731-4	Sequence 4, Appl	C 224	62.5	5.5	867	6	US-10-750-185-28541	Sequence 28541, A
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C 153	64	5.7	921	7	US-11-017-550-24	Sequence 24, Appl	C 226	62.5	5.5	1352	6	US-10-750-185-51740	Sequence 51740, A
C 154	64	5.7	1297	6	US-10-750-185-32030	Sequence 32030, A	C 227	62.5	5.5	1466	6	US-10-750-185-58911	Sequence 58911, A

228	62.5	5.5	1576	6	US-10-131-826A-301	Sequence 301, App	c 301	61.5	5.4	3501	6	US-10-793-626-3614	Sequence 3614, Ap
229	62.5	5.5	1795	6	US-10-750-185-27375	Sequence 27375, A	c 302	61.5	5.4	4248	6	US-10-793-626-3885	Sequence 3885, Ap
c 230	62.5	5.5	1859	6	US-10-750-185-25504	Sequence 25504, A	c 303	61.5	5.4	4417	6	US-10-750-185-49683	Sequence 49683, A
231	62.5	5.5	2263	6	US-10-750-185-43360	Sequence 43360, A	c 304	61	5.4	856	6	US-10-750-185-28518	Sequence 28518, A
232	62.5	5.5	2993	6	US-10-645-441-10	Sequence 10, Appl	c 305	61	5.4	1042	6	US-10-750-185-29649	Sequence 29649, A
233	62.5	5.5	3055	6	US-10-793-626-4075	Sequence 4075, Ap	c 306	61	5.4	1091	6	US-10-750-185-33817	Sequence 33817, A
234	62.5	5.5	3058	6	US-10-750-185-48442	Sequence 48442, A	c 307	61	5.4	1306	6	US-10-750-185-63579	Sequence 63579, A
235	62.5	5.5	4516	6	US-10-821-234-125	Sequence 125, App	c 308	61	5.4	1437	6	US-10-750-185-29994	Sequence 29994, A
236	62.5	5.5	5134	6	US-11-060-005-1	Sequence 1, Appl	c 309	61	5.4	1518	6	US-10-821-234-435	Sequence 435, App
c 237	62.5	5.5	161994	7	US-11-112-908-57	Sequence 57, Appl	c 310	61	5.4	1616	6	US-10-750-185-45154	Sequence 45154, A
c 238	62.5	5.5	173115	7	US-11-112-908-65	Sequence 65, Appl	c 311	61	5.4	1754	6	US-10-750-185-58125	Sequence 58125, A
c 239	62.5	5.5	319608	7	US-11-145-703-1	Sequence 1, Appl	c 312	61	5.4	1801	6	US-10-750-185-51573	Sequence 51573, A
c 240	62	5.5	678	6	US-10-209-208-2	Sequence 2, Appl	c 313	61	5.4	1845	6	US-10-519-447-1	Sequence 1, Appl
241	62	5.5	726	6	US-10-793-626-3147	Sequence 3147, Ap	c 314	61	5.4	1888	6	US-10-750-185-59957	Sequence 59957, A
c 242	62	5.5	744	6	US-10-131-826A-283	Sequence 283, App	c 315	61	5.4	1962	6	US-10-821-234-434	Sequence 434, App
c 243	62	5.5	855	6	US-10-750-185-50099	Sequence 50099, A	c 316	61	5.4	2124	6	US-10-750-185-31641	Sequence 31641, A
244	62	5.5	877	6	US-10-750-185-60109	Sequence 60109, A	c 317	61	5.4	2152	9	US-11-076-187-1	Sequence 1, Appl
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246	62	5.5	956	7	US-11-055-822-845	Sequence 845, App	c 319	61	5.4	2465	6	US-10-750-185-35775	Sequence 35775, A
247	62	5.5	963	7	US-11-055-822-843	Sequence 843, App	c 320	61	5.4	3214	6	US-10-750-185-44076	Sequence 44076, A
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249	62	5.5	1223	6	US-10-750-185-58273	Sequence 58273, A	c 322	61	5.4	3328	6	US-10-793-626-4195	Sequence 4195, Ap
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251	62	5.5	1279	6	US-10-750-185-43208	Sequence 43208, A	c 324	61	5.4	3459	7	US-11-108-172-1097	Sequence 1097, Ap
c 252	62	5.5	1279	6	US-10-750-185-60775	Sequence 60775, A	c 325	61	5.4	3973	6	US-10-750-185-34094	Sequence 34094, A
c 253	62	5.5	1299	6	US-10-750-185-57299	Sequence 57299, A	c 326	61	5.4	14770	6	US-10-821-234-268	Sequence 268, App
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259	62	5.5	1882	6	US-10-750-185-53598	Sequence 53598, A	c 332	60.5	5.3	1065	6	US-10-750-185-40891	Sequence 40891, A
260	62	5.5	1915	6	US-10-750-185-34691	Sequence 34691, A	c 333	60.5	5.3	1158	6	US-10-392-234A-21	Sequence 21, Appl
261	62	5.5	2031	7	US-11-135-855-5	Sequence 5, Appl	c 334	60.5	5.3	1258	6	US-10-750-185-48396	Sequence 48396, A
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c 267	62	5.5	2638	6	US-10-750-185-43568	Sequence 43568, A	c 340	60.5	5.3	1790	6	US-10-750-185-57305	Sequence 57305, A
268	62	5.5	2762	6	US-10-750-185-34426	Sequence 34426, A	c 341	60.5	5.3	1983	7	US-11-044-051-104	Sequence 104, App
269	62	5.5	2828	6	US-10-957-569-30	Sequence 30, Appl	c 342	60.5	5.3	2033	6	US-10-750-185-49737	Sequence 49737, A
c 270	62	5.5	3194	6	US-10-793-626-4136	Sequence 4136, Ap	c 343	60.5	5.3	2052	6	US-10-821-234-462	Sequence 462, App
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c 272	62	5.5	3310	6	US-10-793-626-4143	Sequence 4143, Ap	c 345	60.5	5.3	2887	7	US-11-044-051-76	Sequence 76, Appl
273	62	5.5	3349	6	US-10-793-626-4175	Sequence 4175, Ap	c 346	60.5	5.3	3098	6	US-10-750-185-46414	Sequence 46414, A
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c 276	62	5.5	4982	6	US-10-276-233A-17	Sequence 17, Appl	c 349	60.5	5.3	3859	7	US-11-137-465-10	Sequence 155, App
c 277	62	5.5	191343	7	US-11-112-908-53	Sequence 53, Appl	c 350	60.5	5.3	13672	7	US-11-055-035-2	Sequence 2, Appl
c 278	61.5	5.4	735	6	US-10-750-185-25116	Sequence 25116, A	c 351	60.5	5.3	340000	7	US-11-102-978-3	Sequence 3, Appl
c 279	61.5	5.4	747	6	US-10-750-185-30779	Sequence 30779, A	c 352	60.5	5.3	442	6	US-10-821-234-373	Sequence 373, App
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284	61.5	5.4	1062	6	US-10-750-185-44168	Sequence 44168, A	c 357	60	5.3	987	6	US-10-467-657-2239	Sequence 2239, Ap
c 285	61.5	5.4	1178	6	US-10-750-185-29213	Sequence 29213, A	c 358	60	5.3	1074	6	US-10-750-185-25003	Sequence 25003, A
c 286	61.5	5.4	1218	6	US-10-821-234-505	Sequence 505, App	c 359	60	5.3	1085	6	US-10-750-185-25003	Sequence 463, App
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c 288	61.5	5.4	1221	6	US-10-821-234-497	Sequence 497, App	c 361	60	5.3	1245	6	US-10-750-185-50481	Sequence 50481, A
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c 294	61.5	5.4	2008	6	US-10-750-185-35465	Sequence 35465, A	c 367	60	5.3	1496	6	US-10-750-185-58238	Sequence 58238, A
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c 297	61.5	5.4	2381	6	US-10-750-185-43961	Sequence 43961, A	c 370	60	5.3	1664	6	US-11-099-691-18	Sequence 18, Appl
c 298	61.5	5.4	3119	6	US-10-750-185-34459	Sequence 34459, A	c 371	60	5.3	2097	6	US-10-750-185-60539	Sequence 60539, A
c 299	61.5	5.4	3213	7	US-11-147-047-23	Sequence 23, Appl	c 372	60	5.3	2097	6	US-10-750-185-29804	Sequence 29804, A
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[illegible]

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; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 25698
; LENGTH: 952
; TYPE: DNA
; ORGANISM: Bovine 19866881510436
US-10-750-185-25698

Alignment Scores:
Pred. No.: 2,26e-14 Length: 952
Score: 196.00 Matches: 38
Percent Similarity: 91.30% Conservative: 4
Best Local Similarity: 82.61% Mismatches: 4
Query Match: 17.33% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-10-750-185-25698 (1-952)

QY 116 GluIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysSerArg 135
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Db 800 CAAATACCTGAAGTCTGTAAGAAGGATATTTACACAGCTATATGTTGAAGAAATCAAGA 741

QY 136 ValLysLeuLysSerGlnGluIleProPheProSerThrLysMetMetArgAsnLeu 155
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Db 680 TTTGTGTTCATGTAAGT 663

RESULT 2
US-10-821-234-746
; Sequence 746, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes version 1.0
; SEQ ID NO 746
; LENGTH: 3828
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-746

Alignment Scores:
Pred. No.: 5.93 Length: 3828
Score: 88.50 Matches: 42
Percent Similarity: 47.17% Conservative: 33
Best Local Similarity: 26.42% Mismatches: 65
Query Match: 7.82% Indels: 19
DB: Gaps: 7

US-10-757-745-2_COPY_54_273 (1-220) x US-10-821-234-746 (1-3828)

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QY 77 SerGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePhe 96
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; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 25698
; LENGTH: 952
; TYPE: DNA
; ORGANISM: Bovine 19866881510436
US-10-750-185-25698

Alignment Scores:
Pred. No.: 2,26e-14 Length: 952
Score: 196.00 Matches: 38
Percent Similarity: 91.30% Conservative: 4
Best Local Similarity: 82.61% Mismatches: 4
Query Match: 17.33% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-10-750-185-25698 (1-952)

QY 116 GluIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysSerArg 135
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Db 800 CAAATACCTGAAGTCTGTAAGAAGGATATTTACACAGCTATATGTTGAAGAAATCAAGA 741

QY 136 ValLysLeuLysSerGlnGluIleProPheProSerThrLysMetMetArgAsnLeu 155
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QY 156 LeuCyValHisValAsn 161
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RESULT 3
US-11-112-908-19
; Sequence 19, Application US/11112908
; Publication No. US20050260859A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Lisa M.
; APPLICANT: Harris, Cole
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 212805
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-19

Alignment Scores:
Pred. No.: 3.51e+03 Length: 212805
Score: 87.50 Matches: 44
Percent Similarity: 44.38% Conservative: 35
Best Local Similarity: 24.72% Mismatches: 80
Query Match: 7.74% Indels: 20
DB: Gaps: 6

US-10-757-745-2_COPY_54_273 (1-220) x US-11-112-908-19 (1-212805)

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QY 58 GlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSer 77
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Db 76775 AATTCACATAACATATTAACCTTAATATGTAATGGACTA-----AATGCTCCA 76825

QY 78 GluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeu 97
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Db 76826 ATTAAGAAGACACAGACTGCGCAAAATTTGATAAAGAGTCAAGACCCATCAGTGTGTGTATT 76885
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Qy 98 GlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIle 117
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Qy 118 IleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLys 137
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Qy 138 LeuLysSerGlnGluIleProPheProSerThrLysMetMetArgAsnLeuLys 157
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Qy 158 ValHisValAsnValSerGlyAsn-----GluLeuLysLysMetThrSerHis 173
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Qy 174 LeuGluSerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLys 193
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Qy 194 LysMetGlnGluAlaProGluSerAlaThrValIlePheAlaGlyAspThrAsn 211
Db 77153 GACCTACAAAGAGACTTAGACTCCACACATAATAATG---GGAGACTTTTAAC 77203

RESULT 4

US-11-112-908-18
; Sequence 18, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 165883
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-18

Alignment Scores:
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Score: 85.50 Matches: 46
Percent Similarity: 44.94% Conservative: 34
Best Local Similarity: 25.84% Mismatches: 79
Query Match: 7.56% Indels: 20
DB: 7 Gaps: 7

US-10-757-745-2_COPY_54_273 (1-220) x US-11-112-908-18 (1-165883)

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Qy 58 GlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSer 77
Db 93316 AATTACACATAACATAATTAACCTTAATGTAATGGA-----CTAAATCTCCCAATT 93369
Qy 78 GluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeu 97
Db 93370 AAAGACACAGA---CTGGCAAGTTGGATAAGAGTCAAGACCCCATCATGCTGCTGATT 93426

Qy 98 GlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIle 117
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Db 93469 ATAAAGAGTGGAGGAAGATCTACCAAGCAAAATGGAAAAACAAMAGCGAGGGTTGCA 93528
Qy 138 LeuLysSerGlnGluIleProPheProSerThrLysMetMetArg-----153
Db 93529 ATCTAGTCTCTGATAAAACAGACTTTAAACCAACAAAGATCAAAAGAGAAAAAGAGGC 93588
Qy 154 AsnLeuLysValHisValAsnValSerGlyAsnGlnLeuLysLeuMetThrSerHis 173
Db 93589 CATTACATAATGGTAAAGGGATCAATCAACCAAGAGAGCTTAATCTCTAAATATATAT 93648
Qy 174 LeuGluSerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLys 193
Db 93649 GCACCAATACA-----GGAGCACCAGATTC-----ATAAGCAAGTCTCTGAGT 93693
Qy 194 LysMetGlnGluAlaProGluSerAlaThrValIlePheAlaGlyAspThrAsn 211
Db 93694 GACCTACAAAGAGACTTAGACTCCACACATAATAATG---GGAGACTTTTAAC 93744

RESULT 5

US-11-112-908-21/c
; Sequence 21, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 207908
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-21

Alignment Scores:
Pred No.: 6.98e+03 Length: 207908
Score: 85.00 Matches: 43
Percent Similarity: 44.89% Conservative: 36
Best Local Similarity: 24.43% Mismatches: 79
Query Match: 7.52% Indels: 19
DB: 7 Gaps: 6

US-10-757-745-2_COPY_54_273 (1-220) x US-11-112-908-21 (1-207908)

Qy 38 GluThrThrAspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsn 57
Db 72865 GAAGAACTGCATCAACTAACAGGCAAAATGA-CCAGCTAACATCATATAATGACAGGATCA 72807
Qy 58 GlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSer 77
Db 72806 AATTACACGTAACATAATTAACCTTAATGTAATGGGCTA-----AATGCCCCA 72756
Qy 78 GluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeu 97
Db 72755 ATTAAGACACACAGACTAGCAAAATGGATAAGGTCAGAGCCCATCATGCTGCTGATT 72696

```
QY 98 GlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIle 117
Db 72695 CAGGAG-----ACCCATCTCACATGTCAGAGACACATAGGCTCAGA 72654

QY 118 IleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLys 137
Db 72653 ATAAAGGATGGAGGAAGATCTACCAAGCAAAATGGAAGCAAAAAAAGCAGGGTTGCA 72594

QY 138 LeuLysSerGlnGluIleIleProPheProSerThrLysMetMetMetArgAsnLeuLeuCys 157
Db 72593 ATCTAGTCTCTGATAAAGACAGACTTTAAACCAACCAAGATCAAAAGACAGCAAGAGGC 72534

QY 158 ValHisValAsnValSerGlyAsn-----GluLeuCysLeuMetThrSerHis 173
Db 72533 CATTACATATGTAAGGATCAATTCACAAAGAGAGCTAACTACTCTTAATATGTAT 72474

QY 174 LeuGluSerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLys 193
Db 72473 GTACCAACCAATGCAGG-----GCACCTAGATTC-----ATAAGCAAGTCCTTAGA 72426

QY 194 LysMetGlnGluAlaProGluSerAlaThrValIlePheAlaGlyAsp 209
Db 72425 GACCTACAAAGAGACTTAGACTCCACACAGTAATAATG---GGAGAC 72381
```

RESULT 6

```
US-11-112-908-22
; Sequence 22, Application US/11112908
; Publication No. US20050260659A1
```

GENERAL INFORMATION:

```
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 172147
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-22
```

Alignment Scores:

Pred. No.:	1.44e+04	Length:	172147
Score:	81.50	Matches:	38
Percent Similarity:	42.51%	Conservative:	33
Best Local Similarity:	22.75%	Mismatches:	77
Query Match:	7.21%	Indels:	19
DB:	7	Gaps:	6

US-10-757-745-2_COPY_54_273 (1-220) x US-11-112-908-22 (1-172147)

```
QY 49 ProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIle 68
Db 3492 CCAGCTAACATCATATATGACAGGATCAATTCACATATAACAATATTAATGTA 3551

QY 69 AspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeuAla 88
Db 3552 AATGGACTA-----AATGCTCCCAATTAAGATACAGACTGGCAAAATGGATAAAG 3602

QY 89 LeuTyrSerProAspValIlePheLeuGlnGluValIleProProTyrTyrSerTyrLeu 108
Db 3603 AGTCAAGACCCATCAGTGTGCTGATTATTCAGGA-----ACCATCTC 3644
```

RESULT 7

```
US-11-112-908-21
; Sequence 21, Application US/11112908
; Publication No. US20050260659A1
```

GENERAL INFORMATION:

```
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 207908
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-21
```

Alignment Scores:

Pred. No.:	1.92e+04	Length:	207908
Score:	81.50	Matches:	57
Percent Similarity:	42.60%	Conservative:	38
Best Local Similarity:	25.56%	Mismatches:	85
Query Match:	7.21%	Indels:	46
DB:	7	Gaps:	9

US-10-757-745-2_COPY_54_273 (1-220) x US-11-112-908-21 (1-207908)

```
QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAla----- 17
Db 184690 CTGAAGGAAGCGCTAAACATGGAAG-GAACAAACAGTAGTACCAGCCGCTGCAAAATCATGC 184748

QY 18 -----LeuGluArgArgProGluThrIleSerGluProLysThrTyrVal 32
Db 184749 CAAATGTAAAGACCATCGAGACTAGAA-GAAACTGCATCA----- 184789

QY 33 AspLeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSerProSerGluAsp 52
Db 184790 -----ACTAAACGCAAAATAACAGCTAAACATCATCA----- 184822
```

Qy 53 ThrGlnGlnGluAenGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAsp 72
Db 184823 ---TGACAGGATCA-AATTACACATACATATTAATTTAAATGTAAATGGACTA--- 184875
Qy 73 LeuAsnAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerPro 92
Db 184876 ---AATGCTCCAATTAAAGACACACAGACTGGCAAGTTGGATAAAGAGTCAAGACCCA 184929
Qy 93 AspValIlePheLeuGlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSer 112
Db 184930 TCAGTGTCTGCTATTTCAGGAA-----ACCCATCTCACGTGCAGAGAC 184971
Qy 113 SerAsnTyrGluIleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLys 132
Db 184972 ACACATAGGCTCAAAATAAAGGATGGAGGAGATCTTACCAAGCAAAATGGAAAAACAAAA 185031
Qy 133 LysSerArgValLysLeuLysSerGlnGluIleIleProPheProSerThrLysMetMet 152
Db 185032 AAGGCAGGGTTCATCTAGTCTCTGATATAAAGACAGCGTTAAACCCACAAAGATCAAA 185091
Qy 153 ArgAsnLeuLeuCysValHisValAsnValSerGlyAsn-----GluLeuCys 168
Db 185092 AGAGACAAAGAGGCCATTACATATGTTAAAGGATCAATTCACCAAGAGAGCTAACT 185151
Qy 169 LeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeu 188
Db 185152 ATACTAAATATATATGACCCCAATACA-----GGAGCACCAGATTC-----ATA 185196
Qy 189 LysMetValLeuLysLysMetGlnGluAlaProGluSerAlaThrValIlePheAlaGly 208
Db 185197 AAGCAAGTCTCTGAGTGACCTACAAAGAGACTAGACTCCCAACATTAATAATG---GGA 185253
Qy 209 AspThrAsn 211
Db 185254 GACTTTTAAC 185262

RESULT 8

US-11-112-908-19/c
; Sequence 19, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 212805
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-19

Alignment Scores:

Pred No.:	1.99e+04	Length:	212805
Score:	81.50	Matches:	57
Percent Similarity:	43.50%	Conservative:	40
Best Local Similarity:	25.56%	Mismatch:	83
Query Match:	7.21%	Indels:	46
DB:	7	Gaps:	10

US-10-757-745-2_COPY_54_273 (1-220) x US-11-112-908-19 (1-212805)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAla----- 17
Db 122845 CTGAAGGAGACATAACATCGGAAG-GAACACCGGTACCAGCCACTGCAAAATCATGC 122787
Qy 18 -----LeuGluArgArgProGluThrIleSerGluProLysThrTyrVal 32
Db 122786 CAAATTGTAAGACCATCGAGGCTAGGAA-GAAACTGTATCA----- 122746
Qy 33 AspLeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSerProSerGluAsp 52
Db 122745 -----ACTAACGAGCAAA---AATAACGAGCTAATCAATAA----- 122713
Qy 53 ThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAsp 72
Db 122712 ---TGACAGGATCA-AATTACACATACATTAATTTAAATGTAAATGGACTA--- 122660
Qy 73 LeuAsnAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerPro 92
Db 122659 -----AATGCTCCAATTAAAGACACAGACTGGCAAAATGGATAAAGAGTCAAGACCCA 122606
Qy 93 AspValIlePheLeuGlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSer 112
Db 122605 TCAGTGTGCTGTATTTCAGGAA-----ACCCATCTCACGTGCAGAGAC 122564
Qy 113 SerAsnTyrGluIleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLys 132
Db 122563 ACACATAGGCTCAAAATAAAGGATGGAGGAGATCTTACCAAGCAAAATGGAAAAACAAAA 122504
Qy 133 LysSerArgValLysLeuLysSerGlnGluIleIleProPheProSerThrLysMetMet 152
Db 122503 AAGCAGGGTTCGAATCTCTGCTGATATAAAGACACTTTAAACCAACAAAGATCAAA 122444
Qy 153 ArgAsnLeuLeuCysValHisValAsnValSerGlyAsn-----GluLeuCys 168
Db 122443 AGAGACAAAGAGGCCATTACATATGTTGAAGGATCAATTCACCAAGAGAGCTAACT 122384
Qy 169 LeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeu 188
Db 122383 GTCTTAAATATATATGACCCCAATACA-----GGAGCACCAGATTC-----ATA 122339
Qy 189 LysMetValLeuLysLysMetGlnGluAlaProGluSerAlaThrValIlePheAlaGly 208
Db 122338 AAGCAAGTCTCTGAGTGACCTACATAGAGACTTAGACTCCCAACATTAATAATG---GGA 122282
Qy 209 AspThrAsn 211
Db 122281 GACTTTTAAC 122273
RESULT 9
US-11-112-908-53
; Sequence 53, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 53
; LENGTH: 191343
; TYPE: DNA

; ORGANISM: Homo sapiens		; ORGANISM: Homo sapiens	
US-11-112-908-53		US-10-821-234-301	
Alignment Scores:		Alignment Scores:	
Pred. No.:	4.03e+04	Pred. No.:	116
Score:	78.50	Score:	78.00
Percent Similarity:	44.10%	Percent Similarity:	48.53%
Best Local Similarity:	24.10%	Best Local Similarity:	38.24%
Query Match:	6.94%	Query Match:	6.90%
DB:	7	DB:	6
US-10-757-745-2_COPY_54_273 (1-220) x US-11-112-908-53 (1-191343)		US-10-757-745-2_COPY_54_273 (1-220) x US-10-821-234-301 (1-3672)	
QY	38 GluThrThrAspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsn 57	QY	7 SerTyrPheGluProValGluSerAlaLeuGluArg-ArgProGluThrIleSe 26
DB	141430 GAAGAACTGCATCACTAATGAGCAAAATAA-CCAGCTTAACATCATATGACAGATCA 141488	DB	1760 TCACGTGTTCTTCCACCCATCTCCCTTGCATCTTGAGCAGTTATCCAACTAGGATCTG 1819
QY	58 GlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSer 77	QY	26 rGluProLysThrTyrValAspLeuThrAsnGluThrAspSerThrThrSerly 46
DB	141489 AATTACACATACATATTAATTTAAATGTAATGGA-----CGAATGCTCCA 141539	DB	1820 CCAAGTGATAGTGGGTGCCACTCCCTGAGAAAGACTGAGCCAGGAATACAAAGCTC 1879
QY	78 GluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeu 97	QY	46 s-----IleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeu 64
DB	141540 ATTAAGAATACAGACTGCATAATGATAAGAGTCAAGACCCATCAGTGTGTATT 141599	DB	1880 CCCCCACATCTCTCCAGCCTGGACCTAAATTCTTGAGAGGGGCTCTCTCTCAGGACTG 1939
QY	98 GlnGluValIleProProTyrTyrSerTyrLeuLysIleArgSerSerAsnTyrGluIle 117	QY	64 eThrTrpAsnIleAspGlyLeu 71
DB	141600 CAGGAATC-----CATCTCATGTGCAGAGACACACATAGGCTCAA 141641	DB	1940 TGTCTGGACTTTGACGAGCTT 1961
QY	118 IleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysIleSerArgValLys 137	RESULT 11	
DB	141642 ATAAAGAGTGGAGGAGATCTTACCAGCAATGGAACAAACAAAAGGCGGGTTGCA 141701	US-10-510-386-71	
QY	138 LeuLysSerGlnGluIleProPheProSerThrLysMetMetArgAsnLeuLeuCys 157	; Sequence 71, Application US/10510386	
DB	141702 ATCTAGTCTCTGATGAACAGACTTTAAACCAACAAAGATCAAAAGAGACAAAGAGGC 141761	; Publication No. US2005024922A1	
QY	158 ValHisValAsnValSerGlyAsn-----GluLeuCysLeuMetThrSerHis 173	; GENERAL INFORMATION:	
DB	141762 CATTACATATGTAAGGGATCAATTCACAGAGAGGCTTAATCTCTTAATATATAT 141821	; APPLICANT: Andersen, Jens Tonne	
QY	174 LeuGluSerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLys 193	; APPLICANT: Clausen, Ib Groth	
DB	141822 GCACCAATACA-----GGAGCACCAGATTC-----ATAAGCAAGTCTCTGAGT 141866	; APPLICANT: Jorgensen, Steen Troels	
QY	194 LysMetGlnGluAlaProGluSerAlaThrValIlePheAlaGlyAsp----- 209	; APPLICANT: Olsen, Peter Bjarke	
DB	141867 GACCTACAGAGACTTAGACTCACACATTAATATG---GGAGACTTTAATACCCCA 141923	; APPLICANT: Rasmussen, Michael Dolberg	
QY	210 -----ThrAsnLeuArgAspArgGluValThrArg 219	; TITLE OF INVENTION: Improved Bacillus Host Cell	
DB	141924 CTGTCAACATTAGACATCAACGAGACAGAGAAAGTTAAACAAGG 141966	; FILE REFERENCE: 10294.204-US	
RESULT 10		; CURRENT APPLICATION NUMBER: US/10/510,386	
US-10-821-234-301		; CURRENT FILING DATE: 2004-10-04	
; Sequence 301, Application US/10821234		; NUMBER OF SEQ ID NOS: 248	
; Publication No. US2005025511A1		; SOFTWARE: PatentIn version 3.3	
; GENERAL INFORMATION:		; SEQ ID NO 71	
; APPLICANT: Labat, Ivan		; LENGTH: 1621	
; APPLICANT: Stache-Crain, Birgit		; TYPE: DNA	
; APPLICANT: Andarmani, Susan		; ORGANISM: Bacillus licheniformis	
; APPLICANT: Tang, Y. Tom		; FEATURE:	
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia		; NAME/KEY: CDS	
; FILE REFERENCE: 821A		; LOCATION: (271)...(1122)	
; CURRENT APPLICATION NUMBER: US/10/821,234		US-10-510-386-71	
; CURRENT FILING DATE: 2004-04-07		Alignment Scores:	
; PRIOR APPLICATION NUMBER: US 60/462,047		Pred. No.:	
; PRIOR FILING DATE: 2003-04-07		Score:	
; NUMBER OF SEQ ID NOS: 1704		Percent Similarity:	
; SOFTWARE: pt_seq_genes Version 1.0		Best Local Similarity:	
; SEQ ID NO 301		Query Match:	
; LENGTH: 3672		DB:	
; TYPE: DNA		US-10-757-745-2_COPY_54_273 (1-220) x US-10-510-386-71 (1-1621)	
		QY	
		9 PheGluProValGluGlu-----SerAlaLeuGluArgArg--- 21	
		DB	
		691 TTTCCGCCCTGTTGAAAGGCCGTATGGAAGCTGATCGCGCTTAACAATCGATTT 750	
		QY	
		22 ProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr--- 40	
		DB	
		751 CCGGAATGGATC-----TTTAAGAAATATCTATCTCTTACTACTACTT 795	
		QY	
		41 -----AspSerThrThrSerLysIleSerProSerGlu----- 51	


```
Db 724 GAGGTTCCCGTACCAAGACCCAAACAGGCTGTGAGCGCTGAGGACGAGCACTG 783
      |||      |||      |||      |||      |||      |||      |||      |||
Qy 189 LysMetValLeuLysLysMetGlnGluAlaProGluSerAlaThrValIlePheAlaGly 208
      |||      |||      |||      |||      |||      |||      |||      |||
Db 784 GACACATCTCGACAGCTGGCGGAGTCTCGCGCGTGTGGTGATATCTCGCGG 843
      |||      |||      |||      |||      |||      |||      |||      |||
Qy 209 AspThrAsnLeuArgAsp-----ArgGluValThrArg 219
      |||      |||      |||      |||      |||      |||      |||      |||
Db 844 GAGCTGAGCCTGCACAACTTCTTCGCTGAGGTGCTGCGC 882
      |||      |||      |||      |||      |||      |||      |||      |||

RESULT 17
US-10-485-517-118
; Sequence 118, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Poster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P1006290
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 118
; LENGTH: 2361
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-485-517-118

Alignment Scores:
Pred. No.: 252 Length: 2361
Score: 73.00 Matches: 38
Percent Similarity: 41.44% Conservative: 37
Best Local Similarity: 20.99% Mismatches: 73
Query Match: 6.45% Indels: 33
DB: 6 Gaps: 8

US-10-757-745-2_COPY_54_273 (1-220) x US-10-485-517-118 (1-2361)
Qy 24 ThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThrAspSerThr 43
      |||      |||      |||      |||      |||      |||      |||      |||
Db 200 ACTTTAGTTTCACCTACCGCTTATGCTGATACACCTCAAAAGATGACTACAGTAAGACA 259
      |||      |||      |||      |||      |||      |||      |||      |||
Qy 44 Thr-----SerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
      |||      |||      |||      |||      |||      |||      |||      |||
Db 260 ACATCTCATGATTCAAAATAATCTAATGACGATGAATCTTCAAGGATACTACAAAGTAAA 319
      |||      |||      |||      |||      |||      |||      |||      |||
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
      |||      |||      |||      |||      |||      |||      |||      |||
Db 320 -----GATATTGATAAGACGACAAATAATAACAAGTAACTACCAAGAC 361
      |||      |||      |||      |||      |||      |||      |||      |||
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
      |||      |||      |||      |||      |||      |||      |||      |||
Db 362 AATAACGACAAAATAATTAATAACTATA---GACGACAGCACTTCAGACTTAACAATATC 418
      |||      |||      |||      |||      |||      |||      |||      |||
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerAsnTyrGluIleIleThr--- 119
      |||      |||      |||      |||      |||      |||      |||      |||
Db 419 ATTGATTATTTATTAAGATTTTACCACAAACCAATATAAC---CAATTGTCAACCAA 475
      |||      |||      |||      |||      |||      |||      |||      |||
Qy 120 ---GlyHisGluGluGlyTyrPheThrAlaIleMetLeu-LysLys-----Se 134
      |||      |||      |||      |||      |||      |||      |||      |||
Db 476 AATAAATACCATGATATTAATCTATTAAACAACCTTTATTCACAAAACCTTTATTCAAT 535
      |||      |||      |||      |||      |||      |||      |||      |||
Qy 134 ArgValLysLysSerGlnGluIleIleProPheProSerThrLysMetMetArgAs 154
      |||      |||      |||      |||      |||      |||      |||      |||
Db 536 TCGGATATTCTGATTACGAACAACTCGTAAATGGCGGAAAAGTCAACAAATGATTCA-- 593
      |||      |||      |||      |||      |||      |||      |||      |||
```

```
Qy 154 nLeuLeuCysValHisValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLe 174
      |||      |||      |||      |||      |||      |||      |||      |||
Db 594 -----ATAAAACAGTGACAAATAGCATCAAAATAGCACTGATACGCAATCATCT 643
      |||      |||      |||      |||      |||      |||      |||      |||
Qy 174 uGluSerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLy 194
      |||      |||      |||      |||      |||      |||      |||      |||
Db 644 A-----AACAAAGATAAAGCAGACAATCAAAAA 670
      |||      |||      |||      |||      |||      |||      |||      |||
Qy 194 S 194
      |||      |||      |||      |||      |||      |||      |||      |||
Db 671 G 671

RESULT 18
US-10-821-234-606
; Sequence 606, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 606
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-606

Alignment Scores:
Pred. No.: 147 Length: 1503
Score: 72.50 Matches: 47
Percent Similarity: 37.22% Conservative: 36
Best Local Similarity: 21.08% Mismatches: 84
Query Match: 6.41% Indels: 57
DB: 6 Gaps: 10

US-10-757-745-2_COPY_54_273 (1-220) x US-10-821-234-606 (1-1503)
Qy 8 TyrPheGluProProValGluGluSerAlaLeuGluArgArgProGluThrIle---Ser 26
      |||      |||      |||      |||      |||      |||      |||      |||
Db 163 TTTCGTTGAACCCATCCTGGAGGTTTCCAGCTTGGCCGACCAACCAACTCAACCAATTCA 222
      |||      |||      |||      |||      |||      |||      |||      |||
Qy 27 GluProLysThrTyrValAspLeuThrAsnGluGluThrThrAspSerThrThrSer--- 45
      |||      |||      |||      |||      |||      |||      |||      |||
Db 223 GCCACCAAAATAACAGCTAATACCACTGATGAACCCACCACCAACCACTACCCAG 282
      |||      |||      |||      |||      |||      |||      |||      |||
Qy 46 -----LysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPhe 61
      |||      |||      |||      |||      |||      |||      |||      |||
Db 283 ACCACCAACCCACCATCAACCCACCACCAACCACTACCCAG----- 324
      |||      |||      |||      |||      |||      |||      |||      |||
Qy 62 SerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArg 81
      |||      |||      |||      |||      |||      |||      |||      |||
Db 325 -----CTCCCAACAGATTCTCTACCCAGCCCACTACT 357
      |||      |||      |||      |||      |||      |||      |||      |||
Qy 82 Gly-----ValCysSerTyrLeuAlaLeuTyrSerProAsp 93
      |||      |||      |||      |||      |||      |||      |||      |||
Db 358 GGGTCCTTCTGCCAGGACCTGTACTCTCTGCTCTGACTGGAGAGTCAATCAACAGAG 417
      |||      |||      |||      |||      |||      |||      |||      |||
Qy 94 ValIlePheLeuGlnGluValIleProProTyr-----TyrSer 106
      |||      |||      |||      |||      |||      |||      |||      |||
Db 418 GCGGTG---TTGGGGATGCTTTGGTAGATTCTCTCGAGCTCTACCAAGCTTCTCA 474
      |||      |||      |||      |||      |||      |||      |||      |||
Qy 107 TyrLeuLysLysArgSerAsnTyrGluIleIleThrGlyHisGluGluGlyTyrPhe 126
      |||      |||      |||      |||      |||      |||      |||      |||
Db 475 GCAATGAGAAGGTGGAGACCAACATGGCGCTTTTCCCATTCAGATCGCAGCCTCCTT 534
      |||      |||      |||      |||      |||      |||      |||      |||
```


QY 116 GluIlelleThrGlyHisGluGluGlyTyrPheThr 127
Db 1556 CAATACCTT-----TATTTTACT 1539

RESULT 21

US-10-793-626-3737
; Sequence 3737, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3737
; LENGTH: 4434
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3737

Alignment Scores:
Pred. No.: 875 Length: 4434
Score: 72.00 Matches: 50
Percent Similarity: 36.52% Conservative: 34
Best Local Similarity: 21.74% Mismatches: 61
Query Match: 6.37% Indels: 86
DB: 6 Gaps: 12

US-10-757-745-2_COPY_54_273 (1-220) x US-10-793-626-3737 (1-4434)

QY 5 LeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArgProGluThr 24
Db 3641 CTTAATAAGATTATAATAAGCTTTAAAGAGC-----ATTGAGAAAGCTCCAGAGAAT 3694
QY 25 IleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThrAspSerThr 44
Db 3695 AAAAAAGCATACAAAAAGGAAATTTA-----GAACAACATCGATGCAATCAG 3748
QY 45 SerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySer----- 59
Db 3749 CAAAAAATTAATGAGCTAAAAAATCTTAAACAGACATGGCAATGCAATACCCATCTCT 3808
QY 59 ----- 59
Db 3809 GCTGGCTCTTTATATTAATTCGTTTGAAGTAGTTTACTACGCTGGTGAACCTTCAAAAT 3868
QY 60 -----MetPheSerLeuIleThrTrpAsnIle 68
Db 3869 CGTTATCGCCATTTTCAGGAGCTATGCGGTTCAATGGAAGATGATTAAGTCAAT 3928
QY 69 Asp---GlyLeuAspLeuAsnAn-----LeuSerGluArgAla 80
Db 3929 GAACATGGTATTATTCGGTATATTTCTATGTTATTAGTGGTCACTTTAGTGAAGATGCT 3988
QY 81 Arg-----GlyValCysSerTyrLeuAlaLeuTyrSerProAspValIle----- 95
Db 3989 GAAGATGCTGGCGTAGTTAAGTTTAAAAAGGGCTATGATCCGATGTTATAGAATACGTT 4048
QY 96 -----PheLeuGlnGluValIleProProTyrTyrSer----- 106
Db 4049 GGTGACTTTATTAACCTTATTAACCAATGATATAACATTTATAGAACACATTAATAAAA 4108
QY 107 -----TyrLeuLysLysArgSerSerAsnTyrGluIleThrGlyHisGlu 122
Db 4109 CTAAGAAATAGATTTTAAAGAGGAATTAATCTAATTAAGAAATT----- 4153

QY 123 GluGlyTyrPheThrAlaIleMetLeuLysLysSerArgVal-----LysLeuLysSerGln 141
Db 4154 -----TACAGAGTTAAACAGTTAAAGAAATTTGAAACTTTTGTACAAA 4195
QY 142 GluIlellePro-----PheProSerThrLysMetMetArgAsnLeuLeuCysVal 158
Db 4196 TCCATCATTAGAAAGTCATTATTTTCCAAGT-----GAAGGAAATATTGCTA- 4242
QY 159 HisValAsnValSerGlyAsnGluLeuCys 168
Db 4243 CACGGAATCAGATGGGTTTCAAGTAGTGT 4272

RESULT 22

US-10-750-185-50641/c
; Sequence 50641, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50641
; LENGTH: 1611
; TYPE: DNA
; ORGANISM: Bovine 19866880585640
US-10-750-185-50641

Alignment Scores:
Pred. No.: 218 Length: 1611
Score: 71.50 Matches: 57
Percent Similarity: 37.13% Conservative: 31
Best Local Similarity: 24.05% Mismatches: 65
Query Match: 6.32% Indels: 84
DB: 6 Gaps: 14

US-10-757-745-2_COPY_54_273 (1-220) x US-10-750-185-50641 (1-1611)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSer----- 16
Db 703 CTTGACAGGCGCTTTAATAGTTATTACTGGAAGAGCTGAAGAGTCTAAAAGAGTGCA 644
QY 17 -----AlaLeuGluArgPro---GluThrIleSerGluProLysThrTyrVal 32
Db 643 TTTCTGTTTCTCGTTCTGTGCCCCCACTCCAAAGGGTCAAGTGGGCAAGAACTAT--- 587
QY 33 AspLeuThrAsnGluGluThrThrAspSerThrSerLysIleSerProSerGluAsp 52
Db 587 ----- 587
QY 53 ThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAsp 72
Db 586 -----AATTACAACTCAAGTGGTTTTTAATACACCGAGGAGGAATTTCTGAAGCCCTAGGC 533
QY 73 LeuAsnAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerPro 92
Db 532 TGGAAC-----AAAGCAGAGGCGCTATGTTCA-----GCTGGGCATAGCTCA 491
QY 93 AspValIlePheLeuGlnGluVal-----Ile 101
Db 490 CAAATCTCTAGCTTTTCCAGTTAAACACAGCTCCTGAGAAATTCCTGAGGGCAAGGTTTC 431

```
Qy 102 ProPro-----TyrTyrSerTyrLeuLysArg 111
|||
Db 430 CTGGAGAGGGCCAGAGATGGAATAGATGCAATTTATTAAGCAGCTTGTAAACCTG 371
|||
Qy 112 SerSerAntyrGluIleThrGly-----HisGluGluGly 124
|||
Db 370 GCCTCCAGGCCACCTTCAACTCTGGGTAAATAGGACTTGGAGACAGTGGAAATTTGGG 311
|||
Qy 125 TyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGlnGluIle 144
|||
Db 310 TGGTTTTCCATAACTCTTGGGGAACAACTATTCTCTGA-----AGTGAATCTT 263
|||
Qy 145 ProPhe-Pro---SerThrLysMetMetArgAsnLeuLysValHisValAsnValSe 163
|||
Db 262 AGTCTCTCCCTGAGAACAGAGTCATCAGAAAT---GTGTGTGTGTATGTATGTGTG 206
|||
Qy 163 rGlyAsnGluLeuCysLeuMet-----ThrSerHisLeuGluSe 176
|||
Db 205 T-----TTGTGTATGTCTTGGGGCAGGGATGATGCCAAATGATCATCTG---- 160
|||
Qy 176 rThrArgGlyHisAlaGluArgMetAsnGlnLeuLysMetValLeu 192
|||
Db 159 -TCTAGAGGCCACCTTCTGCTTCCCTTGGCTGCTGCAATTTCTGCTT 112
|||
```

RESULT 23

```
US-10-750-185-63174/c
; Sequence 63174, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
```

```
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63174
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Bovine 19866880424799
US-10-750-185-63174
```

```
Alignment Scores:
Pred. No.: 675 Length: 3396
Score: 71.50 Matches: 38
Percent Similarity: 45.21% Conservative: 28
Best Local Similarity: 26.03% Mismatches: 68
Query Match: 6.32% Indels: 12
DB: 6 Gaps: 4
```

```
US-10-757-745-2_COPY_54_273 (1-220) x US-10-750-185-63174 (1-3396)
```

```
Qy 46 LysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThr 65
|||||
Db 3075 GAGTGTGACAGCTCCAGGATGCTGAAGACAGGAGGAACTGCGCAATCCAG 3016
|||||
Qy 66 TrpAsnIleAspGlyLeuAspLeu-----AsnAsnLeuSerGluArgAla 80
|||||
Db 3015 TGGATCAGAAGAGCTTGGACATGCTGAGTTACTGACACACAACTGCTCTTGAACTATA 2956
|||||
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
|||||
Db 2955 GCTGATGGTTCTGTCAAGTCAGCTATTATCTCTTCTCTCTTCTTCTTCTTCTGTCACAGCAA 2896
|||||
Qy 101 IleProProTyrTyrSerTyrLeuLys-LysArgSerSerAsnTyrGluIleIleThrGl 120
|||||
```

```
Db 2895 ATATTAGAGTGCAGACCAAGAGTGTAAAGTGCACAGCAAGTCACAGCTCAGTTAGGC 2836
|||
Qy 120 yHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSe 140
|||
Db 2835 TCAAGCAGCAAGATATTTTATTAGACAGAGTACTCCAAAAATACAGGAGCAAGCTGATCCC 2776
|||
Qy 140 rGlnGluIle--IleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHi 159
|||
Db 2775 AAGGAAGTCTCTCTATTTTCTTACTGAGCCTGTTGG-----CTTCTTGCTTTTCAT 2722
|||
Qy 159 sValAsnValSerGlyAsnGluLeuCysLeuMetThr-----SerHisLeuGluSe 176
|||
Db 2721 CGTCCAGTCTCTCTTTTGGTTATGTGTGTGCAAGTAGAGCTTGTACACATCACCAGTC 2662
|||
Qy 176 rThrArgGlyHisAla 181
|||
Db 2661 AACGAAAGAAATGCA 2646
|||
```

RESULT 24

```
US-10-793-626-3009/c
; Sequence 3009, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
```

```
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR FILING DATE: 2004-03-04
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3009
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3009
```

```
Alignment Scores:
Pred. No.: 74.2 Length: 720
Score: 71.00 Matches: 27
Percent Similarity: 41.94% Conservative: 12
Best Local Similarity: 29.03% Mismatches: 42
Query Match: 6.28% Indels: 12
DB: 6 Gaps: 2
```

```
US-10-757-745-2_COPY_54_273 (1-220) x US-10-793-626-3009 (1-720)
```

```
Qy 12 ProValGluGluSerAlaLeuGluArgProGluThrIleSerGluProLysThrTyr 31
|||||
Db 368 CCAGTTTCTCTATCTAAGTACAACTATTACCACCACCTACCGTCTGAACCCATTTTCATAG 309
|||||
Qy 32 ValAspLeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSerProSerGlu 51
|||
Db 308 CTAATGATGATCACCAGCCTCTCCAGCAACTCTCCCATGACACAGCTCCAGCACCCTCCA 249
|||||
Qy 52 AspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeu 71
|||
Db 248 AATAATACAGCAGTAGAACCGTTCAGTCATATTCGGTAATC----- 210
|||||
Qy 72 AspLeuAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSer 91
|||
Db 209 ---TTAGATAATTATTCAGCACCCCACTAAAATATGT-----TTGTAATCA 165
|||||
Qy 92 ProAspValIlePheLeuGlnGluValIleProProTyr 104
|||||
Db 164 CCAGATTGTATATATTGTTTTCAGCAGTAATCATTTGAATAC 126
|||||
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RESULT 25

[illegible]

D**b** 1598 ACTAAAGTTGATTCCTAAAAAGCTA 1622

Search completed: December 4, 2005, 21:00:28
Job time : 823.959 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 12:45:51 ; Search time 943.306 Seconds
(without alignments)
1928.603 Million cell updates/sec

Title: US-10-757-745-2_COPY_54_273

Perfect score: 1131

Sequence: 1 MERALNSYFEPVPSALER.....SATVIFAGTNLDRDREVRTC 220

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

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-MATRIX=blosum62 -TRANS=human40.cdi -LIST=500 -DOCALLIGN=200 -THR_SCORE=pct
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database :

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3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1131	100.0	1920	9	US-10-757-745-1
2	1131	100.0	1940	9	US-10-783-271-28
3	1131	100.0	1948	5	US-10-037-270-889
4	1131	100.0	1948	6	US-10-117-722-889
5	1131	100.0	1948	9	US-10-122-851-889
6	1131	100.0	3152	3	US-09-981-353-88
7	1123	99.3	1296	3	US-09-925-299-170
					Sequence 1, Appli
					Sequence 28, Appl
					Sequence 889, App
					Sequence 889, App
					Sequence 889, App
					Sequence 88, Appl
					Sequence 170, App

8	1123	99.3	1296	3	US-09-925-299-170	Sequence 170, App
9	766.5	67.8	1312	9	US-10-757-745-3	Sequence 3, Appli
10	728	64.4	553	5	US-10-066-543-983	Sequence 983, App
11	726	64.2	625	5	US-10-066-543-1031	Sequence 1031, Ap
12	726	64.2	633	5	US-10-066-543-1084	Sequence 1084, Ap
13	723	63.9	644	5	US-10-066-543-1070	Sequence 1070, Ap
14	713	63.0	674	5	US-10-066-543-1067	Sequence 1067, Ap
C 15	711	62.9	1079	3	US-09-745-288-63	Sequence 63, Appl
C 16	711	62.9	1079	3	US-10-453-919-63	Sequence 22058, A
17	710	62.8	1088	9	US-10-450-763-22058	Sequence 548, App
18	708	62.6	625	5	US-10-066-543-548	Sequence 1363, Ap
19	651	57.6	401	5	US-10-066-543-1363	Sequence 22059, A
20	466	41.2	1227	9	US-10-450-763-22059	Sequence 826, App
C 21	414	36.6	391	5	US-10-066-543-836	Sequence 783536,
C 22	299.5	26.5	634	4	US-09-925-065A-783536	Sequence 121, App
23	298	26.3	176	3	US-09-878-722-121	Sequence 50, Appl
C 24	298	26.3	176	3	US-09-878-178-50	Sequence 1367, Ap
25	298	26.3	176	3	US-09-904-456-121	Sequence 121, App
C 26	298	26.3	176	5	US-10-046-935-50	Sequence 50, Appl
C 27	298	26.3	176	5	US-10-146-502-50	Sequence 1367, Ap
C 28	298	26.3	176	5	US-10-060-036-1367	Sequence 783537,
C 29	296	26.2	606	4	US-09-925-065A-783537	Sequence 8082, Ap
30	254	22.5	400	7	US-10-242-535A-8082	Sequence 8082, Ap
31	254	22.5	400	7	US-10-085-783A-8082	Sequence 132360,
32	183	16.2	1686	7	US-10-424-599-132360	Sequence 16762, A
33	182.5	16.1	444	3	US-09-864-761-16762	Sequence 33229, A
34	182.5	16.1	691	3	US-09-864-761-33229	Sequence 14543, A
35	154	13.6	525	7	US-10-021-323-14543	Sequence 42449, A
36	133.5	11.8	1497	7	US-10-437-963-42449	Sequence 105489,
37	129	11.4	898	8	US-10-425-115-105489	Sequence 21056, A
C 38	114	10.1	725	8	US-10-363-345A-21056	Sequence 21056, A
C 39	114	10.1	725	8	US-10-363-483A-21056	Sequence 21056, A
C 40	114	10.1	725	9	US-10-363-483A-21056	Sequence 165873,
41	114	10.1	725	9	US-10-425-115-165873	Sequence 1725, Ap
42	105.5	9.3	1577	8	US-10-425-115-105488	Sequence 105488,
43	104.5	9.2	9737	9	US-10-425-115-105488	Sequence 662, App
44	103.5	9.2	800	8	US-10-484-577-662	Sequence 60, Appl
C 45	103.5	9.2	96960	8	US-10-275-595A-60	Sequence 39, Appl
46	102.5	9.1	3640	6	US-10-172-118-39	Sequence 39, Appl
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; PRIOR FILING DATE: 1998-04-29
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US-10-757-745-1

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; Sequence 28, Application US/10783271
; Publication No. US20050186577A1
; GENERAL INFORMATION:
; APPLICANT: Veridex, LLC
; APPLICANT: Wang, Yixin
; TITLE OF INVENTION: BREAST CANCER PROGNOSTICS
; FILE REFERENCE: VDX-5003 USNP
; CURRENT APPLICATION NUMBER: US/10/783,271
; CURRENT FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 111
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; SEQ ID NO 28
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US-10-783-271-28

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; Publication No. US20030104529A1
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; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Yang, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghast, John
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt FL_genes Version 1.0
; SEQ ID NO 889
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(1127)
US-10-037-270-889

Alignment Scores:
Pred. No.: 5,28e-139 Length: 1948
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_copy_54_273 (1-220) x US-10-037-270-889 (1-1948)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 198 ATGGAAGGGCTCTGAATCTCTACTTCGAGGCTCCGGTGGAGGAGCGCTTGAACGC 257

Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 258 CGACTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAACACT 317

Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 318 GATTCACCACTTCTAATAATCAGCCCATCTGAAGTACTCTAGCAAGAAATGGCAGCATG 377

Qy 61 PheSerIleThrThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 378 TTCCTCTCATCTACCTGGAATATTGATGGATTAGATCTTAAACAATCTCTCAGAGGGCT 437

Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
```

```
Db 438 CGAGGGGTGTGTTCTCTACTTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTT 497
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 498 ATTCCCCCATATTATAGCTACCTTAAAGAAGAGATCAAGTAATTATGAGATTATTACAGGT 557
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 558 CATCAAGAAGGATATTTTCAGACTATTAATGTTGAAGAAATCAAGAGTGAATTAAGAAGC 617
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysValHisVal 160
Db 618 CAAGAGATTATTCCTTTTCCAAAGTACCAGAAATGATGAGAAACCTTTTATGTGTCATGTG 677
Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 678 AATGTGTTCAGAAATGAGCTTTTGCCTTTATGACATCCCATTTGGAGAGCACCCAGAGGCAT 737
Qy 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 738 GCTGGGGAACGAATGATCAGTTTAAATGGTTTAAAGAAATGCAAGAGGCTCCAGAG 797
Qy 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 798 TCAGCTACAGTTATATTTCGAGGAGATACAAATCTAAGGATCGAGAGGTTACCAAGATGT 857

RESULT 4
US-10-117-722-889
; Sequence 889, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt FL_genes Version 1.0
; SEQ ID NO 889
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(1127)
US-10-117-722-889

Alignment Scores:
Pred. No.: 5,28e-139 Length: 1948
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_copy_54_273 (1-220) x US-10-117-722-889 (1-1948)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 198 ATGGAAGGGCTCTGAATCTCTACTTCGAGGCTCCGGTGGAGGAGCGCTTGAACGC 257

Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
```



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Db 258 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAAACCAATGAAGAAACAAC 317
Qy 41 AspSerThrThrSerLysLysSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 318 GATTCCACCATCTTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATG 377
Qy 61 PheSerLeuLeuThrTrpAsnLeuAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 378 TTCTCTCATCTGGAATATTGATGATTAGATCTTAAACATCTGTCCAGAGGGCT 437
Qy 81 ArgGlyValCysSerThrLeuAlaLeuThrSerProAspValIlePheLeuGlnGluVal 100
Db 438 CGAGGGGTGTCTCTACTAGCTTTGACGCCCAGATGATGATATTCTACAGGAAGTT 497
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 498 ATTCCCCCATATTATAGCTTACCTAAAGAGAGATCAAGTAATTAATGAGATTATTACAGGT 557
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 558 CATGAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAAGAAAGC 617
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysValHisVal 160
Db 618 CAAGAGATTATTCCTTTCCAGTACCAAAATGATGAGAACTTTTATGTGTGATGTG 677
Qy 161 AnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 678 AATGTGTGAGAAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCACCAGAGGCAT 737
Qy 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 738 GCTGCGGAACGAATGAATCAGTTAAATGGTTTTAAAGAAATGCAAGAGGCTCCAGAG 797
Qy 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 798 TCAGCTACAGTTATATTTCAGGAGAGATACAAATCTTAAGGATCGAGAGGTTACCAGATGT 857
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RESULT 5

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US-10-122-851-889
; Sequence 889, Application US/10122851
; Publication No. US20050239060A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2BDV3
; CURRENT APPLICATION NUMBER: US/10/122,851
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 889
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(1127)
US-10-122-851-889
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Alignment Scores: 5.28e-139 Length: 1948
Pred. No.:

```
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Db: 9 Gaps: 0
```

US-10-757-745-2_COPY_54_273 (1-220) x US-10-122-851-889 (1-1948)

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Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 198 ATGGAAGGGCTCTGAACTCTACTTCGAGCCTCGGTGGAGGAGCGCCTTGGACGC 257
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db 258 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAAACCAATGAAGAAACAAC 317
Qy 41 AspSerThrThrSerLysLysSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 318 GATTCCACCATCTTAAATCAGCCCATCTCAAGATCTCAGCAAGAAATGGCAGCATG 377
Qy 61 PheSerLeuLeuThrTrpAsnLeuAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 378 TTCTCTCATCTGGAATATTGATGATTAGATCTTAAACATCTGTCCAGAGGGCT 437
Qy 81 ArgGlyValCysSerThrLeuAlaLeuThrSerProAspValIlePheLeuGlnGluVal 100
Db 438 CGAGGGGTGTCTCTACTAGCTTTGACGCCCAGATGATGATATTCTACAGGAAGTT 497
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 498 ATTCCCCCATATTATAGCTTACCTAAAGAGAGATCAAGTAATTAATGAGATTATTACAGGT 557
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 558 CATGAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAAGAAAGC 617
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysValHisVal 160
Db 618 CAAGAGATTATTCCTTTCCAGTACCAAAATGATGAGAACTTTTATGTGTGATGTG 677
Qy 161 AnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 678 AATGTGTGAGAAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCACCAGAGGCAT 737
Qy 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 738 GCTGCGGAACGAATGAATCAGTTAAATGGTTTTAAAGAAATGCAAGAGGCTCCAGAG 797
Qy 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 798 TCAGCTACAGTTATATTTCAGGAGAGATACAAATCTTAAGGATCGAGAGGTTACCAGATGT 857
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RESULT 6

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US-09-981-353-88
; Sequence 88, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 88
; LENGTH: 3152
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 232992.1
; NAME/KEY: unsure
```

```
; LOCATION: 1171
; OTHER INFORMATION: a, t, c, g, or other
US-09-981-353-88

Alignment Scores:      1.15e-138      Length:      3152
Pred. No.:      1131.00      Matches:      220
Score:      1131.00      Mismatches:      0
Percent Similarity:      100.00%      Conserved:      0
Best Local Similarity:      100.00%      Indels:      0
Query Match:      100.00%      Gaps:      0
DB:      3

US-10-757-745-2_COPY_54_273 (1-220) x US-09-981-353-88 (1-3152)

Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 1411 ATGGAAGGGCTCTGAACCTCTACTTCAGAGCTCCGGTGGAGAGCGCTTGGAAACGC 1470

Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAenGluGluThr 40
Db 1471 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACT 1530

Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAenGlySerMet 60
Db 1531 GATTCCACCATCTTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATG 1590

Qy 61 PheSerLeuIleThrTrpAenIleAspGlyLeuAspLeuAenLeuSerGluArgAla 80
Db 1591 TTCTCTCTCATTTACCTGGAATATTGATGGATTAGATCTAAACAATCTGTGCAGAGGGCT 1650

Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 1651 CGAGGGGTGTTCCTACTTAGCTTTGTACAGCCCATGTGATATTCTACAGGAAGTT 1710

Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 1711 ATTCCCCCATATTATAGTACTACCTAAAGAGAGATCAAGTAATATTAGATTATTACAGGT 1770

Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 1771 CATGAAGAAGGATATTTACAGCTATTAATGTTGAAGAAATCAAGAGTGAAATTAAGAAAGC 1830

Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAenLeuLeuCysValHisVal 160
Db 1831 CAAGAGATTATTCCTTTTCCAAAGTACCAGAAATGATGAGAAACCTTTTATGTGTGCATGTG 1890

Qy 161 AsnValSerGlyAenGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 1891 AATGTGTGAGGAATGAGCTTTGCTTTATGCATCCCATTTGGAGAGCACCCAGAGGGCAT 1950

Qy 181 AlaAlaGluArgMetAenGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 1951 GCTGCGGAACGAATGAATCAGTTAAAAATGTTTTAAAGAAATGCAAGAGGGCTCCAGAG 2010

Qy 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 2011 TCAGCTACAGTTATATTTCAGGAGAGATACAAATCTAAGGGATCGAGAGGTTTACAGATGT 2070

RESULT 7
US-09-925-299-170
; Sequence 170, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P4102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 170
; LENGTH: 1296
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1261)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1276)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-170

Alignment Scores:      3.18e-138      Length:      1296
Pred. No.:      1123.00      Matches:      219
Score:      1123.00      Mismatches:      0
Percent Similarity:      99.55%      Conserved:      0
Best Local Similarity:      99.55%      Indels:      0
Query Match:      99.29%      Gaps:      0
DB:      3

US-10-757-745-2_COPY_54_273 (1-220) x US-09-925-299-170 (1-1296)

Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 183 ATGGAAGGGCTCTGAACCTCTACTTCAGACCTCCGGTGGAGAGCGCTTGGAAACGC 242

Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAenGluGluThr 40
Db 243 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACT 302

Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAenGlySerMet 60
Db 303 GATTCCACCATCTTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATG 362

Qy 61 PheSerLeuIleThrTrpAenIleAspGlyLeuAspLeuAenLeuSerGluArgAla 80
Db 363 TTCTCTCTCATTTACCTGGAATATTGATGGATTAGATCTAAACAATCTGTGCAGAGGGCT 422

Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 423 CGAGGGGTGTGTTCCTACTTAGCTTTGTACAGCCCATGTGATATTCTACAGGAAGTT 482

Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 483 ATTCCCCCATATTATAGTACTACCTAAAGAGAGATCAAGTAATATTAGATTATTACAGGT 542

Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 543 CATGAAGAAGGATATTTACAGCTATTAATGTTGAAGAAATCAAGAGTGAAATTAAGAAAGC 602

Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAenLeuLeuCysValHisVal 160
Db 603 CAAGAGATTATTCCTTTTCCAAAGTACCAGAAATGATGAGAAACCTTTTATGTGTGCATGTG 662

Qy 161 AsnValSerGlyAenGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 663 AAYGTGTGAGGAATGAGCTTTGCTTTATGCATCCCATTTGGAGAGCACCCAGAGGGCAT 722

Qy 181 AlaAlaGluArgMetAenGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 723 GCTGCGGAACGAATGAATCAGTTAAAAATGTTTTAAAGAAATGCAAGAGGGCTCCAGAG 782

Qy 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 783 TCAGCTACAGTTATATTTCAGGAGAGATACAAATCTAAGGGATCGAGAGGTTTACAGATGT 842

RESULT 8
US-09-925-299-170
; Sequence 170, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 170
LENGTH: 1296
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1261)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1276)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-170

Alignment Scores:
Pred. No.: 3,18e-138 Length: 1296
Score: 1123.00 Matches: 219
Percent Similarity: 99.55% Conservative: 0
Best Local Similarity: 99.55% Mismatches: 1
Query Match: 99.29% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-09-925-299-170 (1-1296)

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Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluSerAlaLeuGluArg 20
Db 183 ATGGAAGGCTCTGAACCTCTACTTCGAGCTCCGGTGGAGAGAGCGCTTGGAAACG 242
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
Db 243 CGACCTGAAACCACTCTCGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACA 302
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 303 GATTCCACCACCTCTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATG 362
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 363 TTCTCTCTCATTAACCTGGAATATTGATGGATTAGATCTAAACAATCTGTCAAGAGGGCT 422
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 423 CGAGGGGTGTGTTCTCTACTTAGCTTTGTACAGCCAGATGTGATATTCTTACAGGAAGTT 482
Qy 101 IleProProTyrTyrSerTyrLeuValAspSerSerAsnTyrGluIleThrGly 120
Db 483 ATTCCCCCATATTATAGCTACCTTAAAGAGAGATCAAGTAATTATGAGATTATACAGGT 542
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 543 CATGAAGAGGAKATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAGAGC 602
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db 603 CAAGAGATTATTCCTTTTCCAGTACCTCCAAATGATGAGAAACCTTTTATGTGTCATGTG 662
Qy 161 AsnValSerGlyAsnGlnLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 663 AATGTGTGAGAAATGAGCTTTGCTTTATGACATCCCATTTGGAGAGACACAGAGGCAT 722
Qy 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 723 GCTCCGGNACGATGAATCAGTTTAAATAATGTTTAAAGAAATGCAAGAGGCTCCAGAG 782
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Qy 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 783 TCAGCTACAGTTATATTGTCAGGAGATACAAATCTTAGGGATCGAGAGGTTACCAGATGT 842
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RESULT 9

US-10-757-745-3
Sequence 3, Application US/10757745
Publication No. US20050101769A1
GENERAL INFORMATION:
APPLICANT: Vlaams Interuniversitair Instituut Voor Biotechnologie VZW
TITLE OF INVENTION: CD-40 INTERACTING AND TRAP-INTERACTING PROTEINS
FILE REFERENCE: 2676-4555US
CURRENT APPLICATION NUMBER: US/10/757,745
CURRENT FILING DATE: 2004-01-15
PRIOR APPLICATION NUMBER: US/09/697,863A
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: PCT/EP99/03025
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: EPO 98201392.2
PRIOR FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent in version 3.1
SEQ ID NO 3
LENGTH: 1312
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (122)..(1234)
OTHER INFORMATION:
US-10-757-745-3

Alignment Scores:

Pred. No.: 8,77e-91 Length: 1312
Score: 766.50 Matches: 150
Percent Similarity: 81.28% Conservative: 28
Best Local Similarity: 68.49% Mismatches: 40
Query Match: 67.77% Indels: 1
DB: Gaps: 1

US-10-757-745-2_COPY_54_273 (1-220) x US-10-757-745-3 (1-1312)

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Qy 2 GluArgAlaLeuAsnSerTyrPheGluProValGluSerAlaLeuGluArgArg 21
Db 317 CAGAAGCCCTCAGCGCTACTTCGAGCTGCCAGAGAACGACCAAGGGTGGCGGCCG 376
Qy 22 ProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThrAsp 41
Db 377 CCTCCACGCTCTTCAAGTCCGAGGCTATGTTGATCTTAACCAACGAGGATGCAAAATGAT 436
Qy 42 SerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPhe 61
Db 437 ACAACCATTTTGAAGACCCAGTCCATCT---GGAACCTCTCTAGAAGATAGCAGCACTATT 493
Qy 62 SerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArg 81
Db 494 TCTTTCATTAATCTGGNATATTATGATGATGATGATGATGATGATGATGATGATGATGAT 553
Qy 82 GlyValCysSerTyrIleAlaLeuTyrSerProAspValIlePheLeuGlnGluValIle 101
Db 554 GGGGTGTGTTCTCGCTAGCTTTGTATAGTCCAGATGTGTATTTCTTACAGGAAGTTATC 613
Qy 102 ProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGlyHis 121
Db 614 CCCCCATCTGTGCTTACCTAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 673
Qy 122 GluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGln 141
Db 674 GAAGAAGGATATTTCACAGCTATCTATTGAGAAAGGAGAGAGTGAATTTTAAAGTTCAG 733
Qy 142 GluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsn 161
```


Db 222 AGCCAAGAGATTATTCCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTGCAT 281
Qy 160 ValAenValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGly 179
Db 282 GTGAATGTGTGAGGAATGAGCTTTTGCCTTATGACATCCCATTTGGAGAGCCACGAGGG 341
Qy 180 HisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaPro 199
Db 342 CATGCTGGGAGCAAGATGATCAGTTAAATGGTTTAAAGAAATGCAAGAGGCTCCA 401
Qy 200 GluSerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArg 219
Db 402 GAGTCAGCTACAGTTATATTTGAGGAGATACAAATCTAAGGATCGAGAGGTTACCAGA 461
Qy 220 Cys 220
Db 462 TGT 464

RESULT 12

US-10-066-543-1084
; Sequence 1084, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1084
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-1084

Alignment Scores:
Pred. No.: 6.63e-86 Length: 633
Score: 726.00 Matches: 141
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 64.19% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-10-066-543-1084 (1-633)

Qy 80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99
Db 34 GCTCGAGGGGTGTCTTCTACTTAGCTTTGTACAGCCAGATGTGATTTCTACAGGAA 93
Qy 100 ValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleThr 119
Db 94 GTTATTTCCCATATATAGCTACCTAAAGAGAGATCAAGTAATTTATGAGATTATACA 153
Qy 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLys 139
Db 154 GGTCAATGAGAGAGATTTTTCACAGCTATTAATGTTGAAGAAATCAAGAGTGAATTAATA 213

Qy 140 SerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHis 159
Db 214 AGCCAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCAT 273
Qy 160 ValAenValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGly 179
Db 274 GTGAATGTGTGAGGAATGAGCTTTTGCCTTATGACATCCCATTTGGAGAGCCACGAGGG 333
Qy 180 HisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaPro 199
Db 334 CATGCTGGGAGCAAGATGATCAGTTAAATGGTTTAAAGAAATGCAAGAGGCTCCA 393
Qy 200 GluSerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArg 219
Db 394 GAGTCAGCTACAGTTATATTTGAGGAGATACAAATCTAAGGATCGAGAGGTTACCAGA 453
Qy 220 Cys 220
Db 454 TGT 456

RESULT 13

US-10-066-543-1070
; Sequence 1070, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1070
; LENGTH: 644
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-066-543-1070

Alignment Scores:
Pred. No.: 1.71e-85 Length: 644
Score: 723.00 Matches: 140
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.29% Mismatches: 0
Query Match: 63.93% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-10-066-543-1070 (1-644)

Qy 80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99
Db 32 GCTCGAGGGGTGTCTTCTACTTAGCTTTGTACAGCCAGATGTGATTTCTACAGGAA 91
Qy 100 ValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleThr 119
Db 92 GTTATTTCCCATATATAGCTACCTAAAGAGAGATCAAGTAATTTATGAGATTATACA 151
Qy 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLys 139
Db 152 GGTCAATGAGAGAGATTTTTCACAGCTATTAATGTTGAAGAAATCAAGAGTGAATTAATA 211
Qy 140 SerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHis 159

Db 212 AGCCAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCAT 271
Qy 160 ValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGly 179
Db 272 GTGAATGTGTGAGAAATAGCTTTTGCCTTATGACATCCCATTTTGGAGAGCACCAGAGGG 331
Qy 180 HisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaPro 199
Db 332 CATCTCGGGAACCAATGAATCAGTTAAATGTTTTAAAGAAATGGAGAGGCTCCA 391
Qy 200 GluSerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArg 219
Db 392 GAGTCAGCTACAGTTATATTTCAGGAGATACAAATCTAAGGGATCGAGAGTTACCAGA 451
Qy 220 Cys 220
Db 452 TGT 454
RESULT 14
US-10-066-543-1067
; Sequence 1067, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Pyrie, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secret, Heather
; APPLICANT: Carter, Derrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1067
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 11, 377, 640, 654
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-1067
Alignment Scores:
Pred. No.: 3.94e-84 Length: 674
Score: 713.00 Matches: 141
Percent Similarity: 99.30% Conservative: 0
Best Local Similarity: 99.30% Mismatches: 0
Query Match: 63.04% Indels: 1
DB: 5 Gaps: 0
US-10-757-745-2_COPY_54_273 (1-220) x US-10-066-543-1067 (1-674)
Qy 80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99
Db 18 GCTCAGGGGTGTGTTCTTACTAGCTTTGTACAGCCAGATGTGATATTCTACAGAA 77
Qy 100 ValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleThr 119
Db 78 GTTATTCCTCCATATTATAGCTACCTAAAGAGAGATCAAGTAATTATGAGATTATTACA 137
Qy 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLys 139
Db 138 GGTCAATGAAGAGATATTTCACAGCTATATGTTGAAGAAATCAAGAGTGAATTAATA 197

Qy 140 SerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHis 159
Db 198 AGCCAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCAT 257
Qy 160 ValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGly 179
Db 258 GTGAATGTGTGAGAAATAGCTTTTGCCTTATGACATCCCATTTTGGAGAGCACCAGAGGG 317
Qy 180 HisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaPro 199
Db 318 CATCTCGGGAACCAATGAATCAGTTAAATGTTTTAAAGAAATGGAGAGGCTCCN 377
Qy 200 -GluSerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrAr 219
Db 378 TGAGTCAGCTACAGTTATATTTCAGGAGATACAAATCTAAGGGATCGAGAGTTACCAG 437
Qy 219 qCys 220
Db 438 ATGT 441
RESULT 15
US-09-745-288-63/c
; Sequence 63, Application US/09745288
; Patent No. US20010018058A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.446D1
; CURRENT APPLICATION NUMBER: US/09/745,288
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 1079
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-745-288-63
Alignment Scores:
Pred. No.: 1.55e-83 Length: 1079
Score: 711.00 Matches: 138
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 62.86% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_54_273 (1-220) x US-09-745-288-63 (1-1079)
Qy 83 ValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIlePro 102
Db 1077 GTGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTCCC 1018
Qy 103 ProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleThrGlyHisGlu 122
Db 1017 CCATATTATAGCTACCTAAAGAGAGATCAAGTAATTATGAGATTATTACAGGTCATGAA 958
Qy 123 GluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLysSerGlnGlu 142
Db 957 GAAGGATATTTCACAGCTATAAATGTTGAAGAAATCAAGAGTGAATTAAGAACAGAG 898
Qy 143 IleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsnVal 162
Db 897 ATTATTCCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTGAATGTG 838
Qy 163 SerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAla 182
Db 837 TCAGGAATAGCTTTTGCCTTATGACATCCCATTTTGGAGAGCACCAGAGGCGCTGCG 778
Qy 183 GluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGluSerAla 202

Db 777 GAACGAATGATCAGTTAAATAATGGTTTTAAAGAAAAATGCAAGAGGCTCCAGAGTCAGCT 718
QY 203 ThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 717 ACAGTTATATTTGTCAGGAGATACAAATCTTAAGGGATCGAGAGGTATACCAAGATGT 664

RESULT 16

US-10-453-919-63/c
; Sequence 63, Application US/10453919
; Publication No. US2004003320A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.446C7
; CURRENT APPLICATION NUMBER: US/10/453,919
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 1079
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-453-919-63

Alignment Scores:
Pred. No.: 1,55e-83 Length: 1079
Score: 711.00 Matches: 138
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 62.86% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-10-453-919-63 (1-1079)

QY 83 ValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIlePro 102
Db 1077 GTGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTCCTC 1018
QY 103 ProTyrTyrSerTyrLeuLysArgSerSerAsnTyrGluIleThrGlyHisGlu 122
Db 1017 CCATATTATAGCTTACCTAAAGAGAGATCAAGTAATATTAGATATTATACAGTCAAGAA 958
QY 123 GluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGlnGlu 142
Db 957 GAAGGATATTTACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAAGCCCAAGAG 898
QY 143 IleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsnVal 162
Db 897 ATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTGAATGTG 838
QY 163 SerGlyAsnGluLeuCysLeuMetThrSerHisLeuGlnSerThrArgGlyHisAlaAla 182
Db 837 TCAGGAAATGAGCTTTTGCCCTTATGACATCCCATTTGGAGAGCCAGAGGGCATGTGGC 778
QY 183 GluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGluSerAla 202
Db 777 GAACGAATGAATCAGTTTAAATAATGGTTTTTAAAGAAATGCAAGAGGCTCCAGAGTCAGCT 718
QY 203 ThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 717 ACAGTTATATTTGTCAGGAGATACAAATCTTAAGGGATCGAGAGGTATACCAAGATGT 664

RESULT 17

US-10-450-763-22058
; Sequence 22058, Application US/10450763
; Publication No. US2005019675A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790IEP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22058
; LENGTH: 1088
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1)..(687)
; OTHER INFORMATION: 98% homologous to Homo sapiens dj30M3.3 (novel protein
; similar to C. elegans Y63D3A.4), accession number AL031775, Smith-
; OTHER INFORMATION: Waterman Score=1199.
US-10-450-763-22058

Alignment Scores:
Pred. No.: 2.14e-83 Length: 1088
Score: 710.00 Matches: 138
Percent Similarity: 98.58% Conservative: 1
Best Local Similarity: 97.87% Mismatches: 2
Query Match: 62.78% Indels: 0
DB: 9 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-10-450-763-22058 (1-1088)

QY 80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99
Db 1 GCTCGAGGGGTGTGTCTTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAA 60
QY 100 ValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThr 119
Db 61 GTTATTTCCCCATATTATTAGCTTACCTTAAGAGAGATCAAGTAATATTATGAGATTATTA 120
QY 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLys 139
Db 121 GGTCTGATGAGAGAGGATATTTTACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAACA 180
QY 140 SerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHis 159
Db 181 AGCCAAGAGATTTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCAT 240
QY 160 ValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGly 179
Db 241 GTGAATGTGTGAGGAAATGAGCTTTTGCCCTTATGACATCCCATTTTGAGAGACCAAGGG 300
QY 180 HisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaPro 199
Db 301 CATGCTGCGGAACGATGAATCAGTTTAAATAATGGGTTTAAAGAAATGCAAGAGGCTCCA 360
QY 200 GluSerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArg 219
Db 361 GAGTCAGCTACAGTTATATTTTGCAGGAGATACAAATCTTAAGGGATCGAGAGGTATACAGA 420
QY 220 Cys 220
Db 421 TGT 423

RESULT 18

US-10-066-543-548
; Sequence 548, Application US/10066543
; Publication No. US2003008781A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.

; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secret, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 548
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: misc feature
; NAME/KEY: LOCATION: 19, 71
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-548

Alignment Scores:
Pred. No.: 1.61e-83 Length: 625
Score: 708.00 Matches: 140
Percent Similarity: 98.59% Conservative: 0
Best Local Similarity: 98.59% Mismatches: 1
Query Match: 62.60% Indels: 1
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-10-066-543-548 (1-625)

Qy 80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99
Db 26 GCTCAGGGGTGTTCTTACTTAGCTTTGACAGCCAGATGTGNTATTCTACAGGAA 85
Qy 100 ValIleProTyrTyrSerTyrLeuLysLysArgSerAsnTyrGluIleThr 119
Db 86 GTTATTCCTCCCATATTATAGTACTTAAGAGAGATCAAGTATTATGAGATTATACA 145
Qy 120 -GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLy 139
Db 146 GGGTCATGAAGAGGATATTTACAGCTATATAATGTTGAAGAAATCAAGAGTGAATAA 205
Qy 139 sSerGlnGluIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHi 159
Db 206 AAGCCAGAGATTATTCCTTTTCCAAAGTACCAGAAATGATGAGAAACCTTTTATGTGCA 265
Qy 159 sValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGl 179
Db 266 TGTGAATGTGCAGGAAATGAGCTTTGCCTTATGACATCCCATTTGGAGAGCACCAGAG 325
Qy 179 yHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaPr 199
Db 326 GCATGCTCGCGAAGCAATGAATCAGTTAAAAATGGTTTAAAGAAATGCAAGAGGCTCC 385
Qy 199 oGluSerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrAr 219
Db 386 AGAGTCAGTCACAGTTATATTTCAGGAGATACAAATCTAAGGGATCGAGAGGTACCAG 445
Qy 219 qCys 220
Db 446 ATGT 449

RESULT 19
US-10-066-543-1363
; Sequence 1363, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:

; APPLICANT: Jiang, Yuciu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secret, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1363
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-066-543-1363

Alignment Scores:
Pred. No.: 3.03e-76 Length: 401
Score: 651.00 Matches: 127
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.56% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-10-066-543-1363 (1-401)

Qy 80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99
Db 19 GCTCAGGGGTGTTCTTACTTAGCTTTGACAGCCAGATGTGNTATTCTACAGGAA 78
Qy 100 ValIleProTyrTyrSerTyrLeuLysLysArgSerAsnTyrGluIleThr 119
Db 79 GTTATTCCTCCCATATTATAGTACTTAAGAGAGATCAAGTATTATGAGATTATACA 138
Qy 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLy 139
Db 139 GGTCAATGAAGAGGATATTTACAGCTATATAATGTTGAAGAAATCAAGAGTGAATAA 198
Qy 140 SerGlnGluIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHis 159
Db 199 AGCCAGAGATTATTCCTTTTCCAAAGTACCAGAAATGATGAGAAACCTTTTATGTGCA 258
Qy 160 ValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGly 179
Db 259 GTGAATGTGCAGGAAATGAGCTTTGCCTTATGACATCCCATTTGGAGAGCACCAGAGG 318
Qy 180 HisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaPro 199
Db 319 CATGCTCGGAGCAATGAATCAGTTAAAAATGGTTTAAAGAAATGCAAGAGGCTCCA 378
Qy 200 GluSerAlaThrValIlePhe 206
Db 379 GAGTCAGTCACAGTTATATT 399

RESULT 20
US-10-450-763-22059
; Sequence 22059, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631


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; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22059
; LENGTH: 1227
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (84)..(203)
; OTHER INFORMATION: 85% homologous to Homo sapiens dj30M3.3 (novel protein
; OTHER INFORMATION: similar to C. elegans f63D3A.4), accession number AL031775, Smith-
; OTHER INFORMATION: Waterman Score=164.
US-10-450-763-22059

Alignment Scores:
Pred. No.: 7,55e-51 Length: 1227
Score: 466.00 Matches: 125
Percent Similarity: 57.52% Conservative: 5
Best Local Similarity: 55.31% Mismatches: 11
Query Match: 41.20% Indels: 85
DB: 3 Gaps: 3

US-10-757-745-2_COPY_54_273 (1-220) x US-10-450-763-22059 (1-1227)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluAr 20
Db 235 ATGGAAGGCTCTGAACTCTACTTCTGAGCCTCCGGCGGAGAGAGCGCTTGAACG 294
QY 20 gAtgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrTh 40
Db 295 CCGACCTGAACCATCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAAGAAACAAC 354
QY 40 rAspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsn-GlySerM 60
Db 355 TGATTCACCACTTCTAAATACGCCCATCTGAAGATACCTCAGCAAGAAATGGGCAGCA 414
QY 60 etPheSerLeu-IleThrTrp-AsnIle-AspGlyLeuAsp---LeuAsnAsnLeu-Ser 77
Db 415 TGTTCTCTCTCAATACCTGGGAATATTGATGGGATAGGATCTTAACAATCTGTTC 474
QY 78 Glu-ArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLe 97
Db 475 GAGGAGGCTCGAGGGGTGTTCCTACTTAGCTTTGTAGTATTATCACTTCTATTAA 534
QY 97 uGlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIl 117
Db 535 TAGTAATGTG-----TCTTATGTA----- 553
QY 117 eIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgVally 137
Db 553 ----- 553
QY 137 sLeuLysSerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCy 157
Db 553 ----- 553
QY 157 sValHisValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerTh 177
Db 553 ----- 553
QY 177 rArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGl 197
Db 554 -----TATACGGAACCAATGCAATCAGTTCTTAAATAATGGTTTAAAGAAATGCAAGA 603
QY 197 uAlaProGluSerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluVa 217
Db 604 GGCTCCAGATCAGCTACAGTTATTTATTTGCGGAGATACAAATCTAAGGATCGAGAGGT 663
```

```
QY 217 lThr 218
Db 664 GAGT 667

RESULT 21
US-10-066-543-826/c
; Sequence 826, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Xuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 826
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 373_
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-826

Alignment Scores:
Pred. No.: 9,93e-45 Length: 391
Score: 414.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 36.60% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-10-066-543-826 (1-391)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluAr 20
Db 286 ATGGAAGGCTCTGAACTCTACTTCTGAGCCTCCGGTGGAGAGAGCGCTTGAACGC 227
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
Db 226 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 167
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 166 GATTCCACCACCTCTTAAATACGCCCATCTGAAGATACCTCAGCAAGAAATGCGCAGCATG 107
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 106 TTCTCTCTCATTAACCTGGATATTGATGGATTAGATCTTAACAATCTGTCTCAGAGAGGCT 47
QY 81 Arg 81
Db 46 CGA 44

RESULT 22
US-09-925-065A-783536
; Sequence 783536, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

;
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 783536
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-783536

Alignment Scores:
Pred. No.: 3,71e-29 Length: 634
Score: 299.50 Matches: 63
Percent Similarity: 83.33% Conservatives: 2
Best Local Similarity: 80.77% Mismatches: 10
Query Match: 26.48% Indels: 3
DB: 4 Gaps: 1

US-10-757-745-2_COPY_54_273 (1-220) x US-09-925-065A-783536 (1-634)

Qy 32 ValAspLeuThrAsnGluThrThrAspSerThrThrSerLysIleSerProSerGlu 51
Db 265 GTTGACCTTAACCAATGAAGAAACAACTGATTCACCACTTCTAAATCAGCCCATCTGAA 324
Qy 52 AspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeu 71
Db 325 GATCTCTACGCAAGAAATGGCAGCATGTTCTCTCATACCTGGAATATGATGGATTA 384
Qy 72 AspLeuAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSer 91
Db 385 GATCTAAACATCTGTACAGAGGGCTCGAGGGGTGTTCTCTACTAGCTTTTGAAGTA 444
Qy 92 ProAspValIlePheLeuGlnGluValIleProProTyrTyrSerTyrLeuLys 109
Db 445 TTATCAGCTCTCTATTAATAGTAATGTG-----TCTTATGTATATACAAAG 489

RESULT 23
US-09-878-722-121
; Sequence 121, Application US/09878722
; Publication No. US20020040127A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Hepler, William T.
; APPLICANT: Clapper, Jonathan
; APPLICANT: Wang, Aijun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.524
; CURRENT APPLICATION NUMBER: US/09/878,722
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-878-722-121
Alignment Scores:

Pred. No.: 7.45e-30 Length: 176
Score: 298.00 Matches: 58
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.35% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-09-878-722-121 (1-176)

Qy 91 SerProAspValIlePheLeuGlnGluValIleProProTyrTyrSerTyrLeuLys 110
Db 3 AGCCAGATGTGATATTCTACAGGAAGTTATTCCCCCATATTATAGTACCTAAAGAAG 62
Qy 111 ArgSerSerAsnTyrGluIleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMet 130
Db 63 AGATCAAGTAATTATGAGATTATTACAGGTCATGAGAGAGATATTTTCACAGCTATAATG 122
Qy 131 LeuLysLysSerArgValLysLeuLysSerGlnGluIleIleProPheProSer 148
Db 123 TTGAAGAAATCAAGAGTGAAATTAATAAAGCCAGAGATTATTCCTTTTCCAAGT 176

RESULT 24
US-09-878-178-50/c
; Sequence 50, Application US/09878178
; Patent No. US20020177552A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527
; CURRENT APPLICATION NUMBER: US/09/878,178
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 2237
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-878-178-50

Alignment Scores:
Pred. No.: 7.45e-30 Length: 176
Score: 298.00 Matches: 58
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.35% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-09-878-178-50 (1-176)

Qy 91 SerProAspValIlePheLeuGlnGluValIleProProTyrTyrSerTyrLeuLys 110
Db 174 AGCCAGATGTGATATTCTACAGGAAGTTATTCCCCCATATTATAGTACCTAAAGAAG 115
Qy 111 ArgSerSerAsnTyrGluIleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMet 130
Db 114 AGATCAAGTAATTATGAGATTATTACAGGTCATGAGAGAGATATTTTCACAGCTATAATG 55
Qy 131 LeuLysLysSerArgValLysLeuLysSerGlnGluIleIleProPheProSer 148
Db 54 TTGAAGAAATCAAGAGTGAAATTAATAAAGCCAGAGATTATTCCTTTTCCAAGT 1

RESULT 25
US-09-904-456-121
; Sequence 121, Application US/09904456
; Publication No. US20030017167A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.524C1
; FILE REFERENCE: 210121.524C1

```
; CURRENT APPLICATION NUMBER: US/09/904,456
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-904-456-121

Alignment Scores:
Pred. No.: 7,45e-30 Length: 176
Score: 298.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.35% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-09-904-456-121 (1-176)

Qy 91 SerProAspValIlePheLeuGlnGluValIleProProTyrTyrSerTyrLeuLysLys 110
Db 3 AGCCAGATGTGATATTTCTACAGGAAGTTATTTCCCCCATATATAGCTACCTAAAGAG 62
Qy 111 ArgSerSerAsnTyrGluIleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMet 130
Db 63 AGATCAAGTAATATATGAGATTATTACAGGTCTATGAAGAGGATATTTTCACAGCTAATG 122
Qy 131 LeuLysLysSerArgValIlePheLeuGlnGluValIleProProTyrTyrSerTyrLeuLysLys 148
Db 123 TTGAAGAATCAAGAGTGAATTTAAAGCCCAAGAGATATTCTCTTTTCCAAGT 176

RESULT 26
US-10-046-935-50/c
; Sequence 50, Application US/10046935
; Publication No. US20020156011A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527C1
; CURRENT APPLICATION NUMBER: US/10/046,935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2239
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-046-935-50

Alignment Scores:
Pred. No.: 7,45e-30 Length: 176
Score: 298.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.35% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-10-046-935-50 (1-176)

Qy 91 SerProAspValIlePheLeuGlnGluValIleProProTyrTyrSerTyrLeuLysLys 110
Db 174 AGCCAGATGTGATATTTCTACAGGAAGTTATTTCCCCCATATATAGCTACCTAAAGAG 115
Qy 111 ArgSerSerAsnTyrGluIleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMet 130
Db 114 AGATCAAGTAATATATGAGATTATTACAGGTCTATGAAGAGGATATTTTCACAGCTAATG 55

US-10-046-935-50/c
; Sequence 50, Application US/10046935
; Publication No. US20020156011A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527C1
; CURRENT APPLICATION NUMBER: US/10/046,935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2239
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-046-935-50

Alignment Scores:
Pred. No.: 7,45e-30 Length: 176
Score: 298.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.35% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-10-046-935-50 (1-176)

Qy 91 SerProAspValIlePheLeuGlnGluValIleProProTyrTyrSerTyrLeuLysLys 110
Db 174 AGCCAGATGTGATATTTCTACAGGAAGTTATTTCCCCCATATATAGCTACCTAAAGAG 115
Qy 111 ArgSerSerAsnTyrGluIleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMet 130
Db 114 AGATCAAGTAATATATGAGATTATTACAGGTCTATGAAGAGGATATTTTCACAGCTAATG 55

US-10-046-935-50/c
; Sequence 50, Application US/10046935
; Publication No. US20020156011A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527C2
; CURRENT APPLICATION NUMBER: US/10/146,502
; CURRENT FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-502-50

Alignment Scores:
Pred. No.: 7,45e-30 Length: 176
Score: 298.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.35% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-10-146-502-50 (1-176)

Qy 91 SerProAspValIlePheLeuGlnGluValIleProProTyrTyrSerTyrLeuLysLys 110
Db 174 AGCCAGATGTGATATTTCTACAGGAAGTTATTTCCCCCATATATAGCTACCTAAAGAG 115
Qy 111 ArgSerSerAsnTyrGluIleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMet 130
Db 114 AGATCAAGTAATATATGAGATTATTACAGGTCTATGAAGAGGATATTTTCACAGCTAATG 55

US-10-146-502-50/c
; Sequence 50, Application US/10146502
; Publication No. US20030069180A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527C2
; CURRENT APPLICATION NUMBER: US/10/146,502
; CURRENT FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-502-50

Alignment Scores:
Pred. No.: 7,45e-30 Length: 176
Score: 298.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.35% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-10-146-502-50 (1-176)

Qy 91 SerProAspValIlePheLeuGlnGluValIleProProTyrTyrSerTyrLeuLysLys 110
Db 174 AGCCAGATGTGATATTTCTACAGGAAGTTATTTCCCCCATATATAGCTACCTAAAGAG 115
Qy 111 ArgSerSerAsnTyrGluIleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMet 130
Db 114 AGATCAAGTAATATATGAGATTATTACAGGTCTATGAAGAGGATATTTTCACAGCTAATG 55

US-10-146-502-50/c
; Sequence 50, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1367
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-1367/c
; Sequence 1367, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1367
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-1367
```

Alignment Scores:

Pred. No.: 7,45e-30 Length: 176
Score: 298.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.35% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-10-060-036-1367 (1-176)

Qy 91 SerProaspValIlePheLeuGlnGluValIleProProTyrTyrSerTyrLeuLysLys 110
Db 174 AGCCAGATGATATTCTTACAGGAAGTTATTCCTCCCATATTATAGTACCTAAAGAAG 115
Qy 111 ArgSerSerAsnTyrGluIleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMet 130
Db 114 AGATCAAGTATTATGATGATTATTACAGGTTCATGAAGAAGGATATTTACACAGCTATAATG 55
Qy 131 LeuLysLysSerArgValLysLeuLysSerGlnGluIleIleProPheProSer 148
Db 54 TTGAAGAATCAAGAGTGAATTAATAAAGCCCAAGAGATTATTCCTTTTCCAGT 1

RESULT 29

US-09-925-065A-783537
; Sequence 783537, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 783537
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-925-065A-783537

Alignment Scores:
Pred. No.: 1.01e-28 Length: 606
Score: 296.00 Matches: 58
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.17% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-09-925-065A-783537 (1-606)

Qy 32 ValAspLeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSerProSerGlu 51
Db 414 GTTGACCTAACCAATGAAGAAACCACTGATTCACCACTTCTAAANTCAGCCCATCTGAA 473
Qy 52 AspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeu 71
Db 474 GATACTCAGCAAGAAATGGCAGCATGTTCTCTCTCATCTGGAATATTGATGGATTA 533
Qy 72 AspLeuAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeu 89
Db 534 GATCTAAACAATCTGTCTCAGAGAGGCGTCGAGGGGTGTGTTCTCTTACTAGCTTTG 587

RESULT 30

US-10-242-535A-8082
; Sequence 8082, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242.535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8082
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Human

US-10-242-535A-8082

Alignment Scores:
Pred. No.: 2e-23 Length: 400
Score: 254.00 Matches: 50
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.04% Mismatches: 0
Query Match: 22.46% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-10-242-535A-8082 (1-400)

Qy 170 MetThrSerHisLeuGluSerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeuLys 189
Db 65 GTGACATCCCATTGGAGAGACACAGAGGGCTCCAGAGTCACGTATATTTGCAGGAGAT 124
Qy 190 MetValLeuLysLysMetGlnGluAlaProGluSerAlaThrValIlePheAlaGlyAsp 209
Db 125 ATGGTTTTAAAGAAAATGCAAGAGGCTCCAGAGTCACGTATATTTGCAGGAGAT 184
Qy 210 ThrAsnLeuArgAspArgGluValThrArgCys 220
Db 185 ACAAAATCTAAGGGATCGAGAGGTTACCAGATGT 217

Search completed: December 4, 2005, 20:43:40
Job time : 1006.31 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 00:49:56 ; Search time 204.735 Seconds
(without alignments)
1910.099 Million cell updates/sec

Title: US-10-757-745-2_COPY_54_273

Perfect score: 1131

Sequence: 1 MERALNSYEPFVBSALER.....SATVIFAGDTNLRDREVRTC 220

Scoring table:

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40 cdi
-LIST=500 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30
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Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	711	62.9	1079	3	US-09-118-627-63
6	711	62.9	1079	3	US-09-602-877A-63
7	145	12.8	379	3	US-09-621-976-8403
8	105	9.3	232547	3	US-09-949-016-16603
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c 85	89.5	7.9	312470	3	US-09-949-016-14043	Sequence 14043, A	c 158	83.5	7.4	107926	3	US-09-949-016-15405	Sequence 15405, A
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c 89	88.5	7.8	678533	3	US-09-949-016-14577	Sequence 14577, A	c 162	83.5	7.4	117937	3	US-09-949-016-12762	Sequence 12762, A
c 90	88.5	7.8	678533	3	US-09-949-016-14578	Sequence 14578, A	c 163	83.5	7.4	117937	3	US-09-949-016-15775	Sequence 15775, A
c 91	88	7.8	13188	3	US-08-961-527-70	Sequence 70, Appl	c 164	83.5	7.4	120609	3	US-09-949-016-13915	Sequence 13915, A
c 92	88	7.8	58829	3	US-09-949-016-13146	Sequence 13146, A	c 165	83.5	7.4	120609	3	US-09-949-016-12415	Sequence 12415, A
c 93	87.5	7.7	727	3	US-09-328-475C-279	Sequence 279, App	c 166	83.5	7.4	363032	3	US-09-949-016-12515	Sequence 12515, A
c 94	87.5	7.7	748	3	US-09-328-475C-278	Sequence 278, App	c 167	83	7.3	1053	3	US-09-248-796A-4227	Sequence 4227, Ap
c 95	87.5	7.7	147321	3	US-09-949-016-15450	Sequence 15450, A	c 168	82.5	7.3	2257	3	US-10-104-047-1677	Sequence 1677, Ap
c 96	87.5	7.7	260286	3	US-09-949-016-17037	Sequence 17037, A	c 169	82.5	7.3	26354	3	US-09-949-016-12746	Sequence 12746, A
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c 99	87	7.7	29384	3	US-09-902-540-1229	Sequence 1229, Ap	c 172	82.5	7.3	76264	3	US-09-949-016-15773	Sequence 15773, A
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c 117	85.5	7.6	87352	3	US-09-949-016-15693	Sequence 15693, A	c 190	81.5	7.2	2604	3	US-10-101-464A-834	Sequence 834, App
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c 122	85	7.5	3018	3	US-10-415-147-11	Sequence 11, Appl	c 195	81	7.2	2439	3	US-09-513-783A-3	Sequence 3, Appli
c 123	85	7.5	3346	3	US-10-104-047-1298	Sequence 1298, Ap	c 196	81	7.2	2439	3	US-09-513-783A-5	Sequence 5, Appli
c 124	85	7.5	51770	3	US-09-949-016-13668	Sequence 13668, A	c 197	81	7.2	2439	3	US-09-430-656-3	Sequence 3, Appli
c 125	85	7.5	9916	3	US-09-816-095-3	Sequence 3, Appli	c 198	81	7.2	2439	3	US-09-430-656-5	Sequence 5, Appli
c 126	85	7.5	374159	3	US-09-949-016-15868	Sequence 15868, A	c 199	81	7.2	2439	3	US-10-100-957A-5	Sequence 5, Appli
c 127	84.5	7.5	2637	3	US-10-101-464A-881	Sequence 881, App	c 200	81	7.2	2439	3	US-10-100-957A-5	Sequence 5, Appli
c 128	84.5	7.5	40328	3	US-08-742-185-102	Sequence 102, App	c 201	81	7.2	2601	3	US-09-134-001C-2093	Sequence 2093, Ap
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c 134	84.5	7.5	161124	3	US-09-949-016-11760	Sequence 11760, A	c 207	81	7.2	3378	3	US-10-100-957A-151	Sequence 151, App
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c 138	84	7.4	212139	3	US-09-949-016-16065	Sequence 16065, A	c 211	81	7.2	103934	3	US-09-949-016-14433	Sequence 14433, A
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c 142	83.5	7.4	700	3	US-09-735-271-298	Sequence 298, App	c 215	80.5	7.1	2307	3	US-09-433-826B-468	Sequence 468, App
c 143	83.5	7.4	42410	3	US-09-949-002-616	Sequence 616, App	c 216	80.5	7.1	2307	3	US-09-604-287A-468	Sequence 468, App
c 144	83.5	7.4	42411	3	US-09-949-002-727	Sequence 727, App	c 217	80.5	7.1	2307	3	US-09-834-759-468	Sequence 468, App
c 145	83.5	7.4	107329	3	US-09-949-016-12663	Sequence 12663, A	c 218	80.5	7.1	2307	3	US-09-590-751A-468	Sequence 468, App
c 146	83.5	7.4	107329	3	US-09-949-016-12664	Sequence 12664, A	c 219	80.5	7.1	2307	3	US-09-551-621-468	Sequence 468, App
c 147	83.5	7.4	107330	3	US-09-949-016-15408	Sequence 15408, A	c 220	80.5	7.1	2307	3	US-09-551-621A-468	Sequence 468, App
c 148	83.5	7.4	107330	3	US-09-949-016-15409	Sequence 15409, A	c 221	80.5	7.1	2307	3	US-10-076-622-468	Sequence 468, App
c 149	83.5	7.4	107330	3	US-09-949-016-15410	Sequence 15410, A	c 222	80.5	7.1	3045	2	US-10-076-622-548	Sequence 548, App
c 150	83.5	7.4	107330	3	US-09-949-016-15411	Sequence 15411, A	c 223	80.5	7.1	4540	2	US-08-770-761A-6	Sequence 6, Appli
c 151	83.5	7.4	107750	3	US-09-949-016-12662	Sequence 12662, A	c 224	80.5	7.1	94830	3	US-09-949-016-12414	Sequence 12414, A
c 152	83.5	7.4	107751	3	US-09-949-016-15412	Sequence 15412, A	c 225	80.5	7.1	94847	3	US-09-949-016-16336	Sequence 16336, A
c 153	83.5	7.4	107751	3	US-09-949-016-15413	Sequence 15413, A	c 226	80.5	7.1	636591	3	US-09-949-016-11808	Sequence 11808, A
c 154	83.5	7.4	107751	3	US-09-949-016-15414	Sequence 15414, A	c 227	80.5	7.1	636591	3	US-09-949-016-13388	Sequence 13388, A
c 155	83.5	7.4	107751	3	US-09-949-016-15415	Sequence 15415, A	c 228	80	7.1	1743	3	US-09-032-365A-18	Sequence 18, Appl

229	80	7.1	2032	3	US-09-241-581B-5	Sequence 5, Appli	c 302	76.5	6.8	2313	3	US-09-370-838-157	Sequence 157, App
230	80	7.1	2032	3	US-08-265-428-5	Sequence 5, Appli	c 303	76.5	6.8	2313	3	US-09-854-133-157	Sequence 157, App
231	80	7.1	2032	6	PCT-US95-07721-5	Sequence 5, Appli	c 304	76.5	6.8	2397	3	US-09-221-017B-272	Sequence 272, App
232	79.5	7.0	1365	2	US-08-114-072-1	Sequence 1, Appli	c 305	76.5	6.8	2847	3	US-09-902-540-5588	Sequence 7588, Ap
233	79.5	7.0	1365	6	PCT-US94-09361-1	Sequence 1, Appli	c 306	76.5	6.8	5238	3	US-03-080-855-1	Sequence 1, Appli
234	79.5	7.0	1493	3	US-09-376-781-24	Sequence 24, Appli	c 307	76.5	6.8	5238	3	US-03-566-076-1	Sequence 1, Appli
235	79.5	7.0	71387	3	US-09-949-016-16754	Sequence 16754, A	c 308	76.5	6.8	7704	3	US-09-902-540-743	Sequence 743, App
236	79.5	7.0	86980	3	US-09-949-016-15344	Sequence 15344, A	c 309	76.5	6.8	39299	3	US-09-949-016-16625	Sequence 16625, App
237	79.5	7.0	106380	3	US-09-949-016-17553	Sequence 17553, A	c 310	76.5	6.8	162841	3	US-09-949-016-13733	Sequence 13733, A
238	79.5	7.0	179904	3	US-09-949-002-577	Sequence 577, App	c 311	76.5	6.8	312474	3	US-09-949-016-17434	Sequence 17434, A
239	79.5	7.0	179905	3	US-09-949-002-705	Sequence 705, App	c 312	76	6.7	471	3	US-08-982-285-21	Sequence 21, Appl
240	79.5	7.0	246444	3	US-09-949-016-13113	Sequence 13113, A	c 313	76	6.7	471	3	US-10-100-057-16	Sequence 16, Appl
241	79.5	7.0	258775	3	US-09-949-016-16435	Sequence 16435, A	c 314	76	6.7	601	3	US-09-949-016-156022	Sequence 156022, App
242	79	7.0	168575	3	US-09-426-290-1	Sequence 1, Appli	c 315	76	6.7	828	3	US-09-583-110-345	Sequence 345, App
243	79	7.0	373182	3	US-09-949-016-117371	Sequence 117371, A	c 316	76	6.7	828	3	US-09-252-991A-14967	Sequence 14967, A
244	79	7.0	373694	3	US-09-949-016-12062	Sequence 12062, A	c 317	76	6.7	1065	3	US-09-328-352-3136	Sequence 3136, Ap
245	78.5	6.9	1053	3	US-09-248-796A-4335	Sequence 4335, Ap	c 318	76	6.7	1149	3	US-09-252-931A-14783	Sequence 14783, A
246	78.5	6.9	1350	3	US-09-248-796A-4759	Sequence 4759, Ap	c 319	76	6.7	1461	3	US-09-252-931A-14833	Sequence 14833, A
247	78.5	6.9	2160	3	US-09-583-110-1312	Sequence 1312, Ap	c 320	76	6.7	193169	3	US-09-949-016-15091	Sequence 15091, A
248	78.5	6.9	2166	3	US-09-107-433-1102	Sequence 1102, Ap	c 321	76	6.7	205163	3	US-09-949-016-17009	Sequence 17009, A
249	78.5	6.9	7881	2	US-08-751-189-1	Sequence 1, Appli	c 322	75.5	6.7	864	3	US-09-902-540-5281	Sequence 5281, Ap
250	78.5	6.9	7881	2	US-09-060-836-1	Sequence 1, Appli	c 323	75.5	6.7	1036	3	US-09-270-767-13028	Sequence 13028, A
251	78.5	6.9	7881	2	US-09-184-445-1	Sequence 1, Appli	c 324	75.5	6.7	1449	3	US-09-134-000C-2192	Sequence 2192, Ap
252	78.5	6.9	51547	3	US-09-949-016-16405	Sequence 16405, A	c 325	75.5	6.7	1836	3	US-09-601-198-69	Sequence 69, Appl
253	78.5	6.9	54707	3	US-09-949-016-11861	Sequence 11861, A	c 326	75.5	6.7	1983	3	US-09-248-796A-5863	Sequence 5863, Ap
254	78.5	6.9	79824	3	US-09-949-016-13919	Sequence 13919, A	c 327	75.5	6.7	2152	3	US-09-830-902-106	Sequence 106, App
255	78.5	6.9	86936	3	US-09-949-016-17314	Sequence 17314, A	c 328	75.5	6.7	4437	2	US-08-559-303B-72	Sequence 72, Appl
256	78.5	6.9	145241	3	US-09-949-016-17394	Sequence 17394, A	c 329	75.5	6.7	4437	3	US-09-175-828-72	Sequence 72, Appl
257	78.5	6.9	145241	3	US-09-949-016-17395	Sequence 17395, A	c 330	75.5	6.7	4437	3	US-09-798-096-3	Sequence 3, Appli
258	78	6.9	797	3	US-09-328-475C-167	Sequence 167, App	c 331	75.5	6.7	4437	3	US-09-753-143-72	Sequence 72, Appl
259	78	6.9	1560	3	US-09-248-796A-4631	Sequence 4631, Ap	c 332	75.5	6.7	13815	3	US-10-149-736-2	Sequence 2, Appli
260	78	6.9	2304	3	US-09-543-681A-2296	Sequence 2296, Ap	c 333	75.5	6.7	19307	3	US-08-836-022A-10	Sequence 10, Appl
261	78	6.9	3127	3	US-09-620-312D-613	Sequence 613, App	c 334	75.5	6.7	19307	3	US-09-427-048A-10	Sequence 10, Appl
262	78	6.9	3356	3	US-09-379-523-4	Sequence 29, Appli	c 335	75.5	6.7	30783	3	US-09-902-540-1258	Sequence 1258, Ap
263	78	6.9	6696	3	US-10-272-459-29	Sequence 30, Appl	c 336	75.5	6.7	39113	3	US-09-949-016-16661	Sequence 16661, A
264	78	6.9	6757	3	US-10-272-459-30	Sequence 30, Appl	c 337	75.5	6.7	81819	3	US-09-949-016-16662	Sequence 16662, A
265	78	6.9	7478	3	US-10-104-966-15	Sequence 15, Appli	c 338	75.5	6.7	81819	3	US-09-949-016-16662	Sequence 16662, A
266	78	6.9	7478	3	US-09-929-955-15	Sequence 15, Appli	c 339	75.5	6.7	95648	3	US-09-949-016-13139	Sequence 13139, A
267	78	6.9	36643	3	US-09-949-016-11860	Sequence 11860, A	c 340	75.5	6.7	9370	3	US-09-949-016-12816	Sequence 12816, A
268	78	6.9	36821	3	US-09-949-016-16403	Sequence 16403, A	c 341	75.5	6.7	9370	3	US-09-949-016-12816	Sequence 12816, A
269	78	6.9	36821	3	US-09-949-016-16404	Sequence 16404, A	c 342	75.5	6.7	9370	3	US-09-949-016-12816	Sequence 12816, A
270	78	6.9	135667	3	US-09-949-016-15051	Sequence 15051, A	c 343	75.5	6.7	105050	3	US-09-949-016-17540	Sequence 17540, A
271	78	6.9	152486	3	US-09-949-016-12869	Sequence 12869, A	c 344	75.5	6.7	203632	3	US-09-949-002-574	Sequence 574, App
272	77.5	6.9	1569	2	US-08-680-728A-57	Sequence 57, Appli	c 345	75.5	6.7	203632	3	US-09-949-002-802	Sequence 802, App
273	77.5	6.9	1569	2	US-09-092-409-57	Sequence 57, Appli	c 346	75.5	6.7	678533	3	US-09-949-016-14577	Sequence 14577, A
274	77.5	6.9	1575	3	US-09-774-528-260	Sequence 260, App	c 347	75.5	6.7	678533	3	US-09-949-016-14578	Sequence 14578, A
275	77.5	6.9	1575	3	US-10-120-988-260	Sequence 260, App	c 348	75	6.6	678533	3	US-09-248-796A-1829	Sequence 1829, Ap
276	77.5	6.9	3391	6	PCT-US96-03940-10	Sequence 10, Appli	c 349	75	6.6	678533	3	US-09-248-796A-1829	Sequence 1829, Ap
277	77.5	6.9	3705	6	PCT-US96-03940-7	Sequence 7, Appli	c 350	75	6.6	1730	3	US-09-672-785-3	Sequence 3, Appli
278	77.5	6.9	5648	6	PCT-US96-03940-1	Sequence 1, Appli	c 351	75	6.6	1730	3	US-09-107-532A-472	Sequence 472, App
279	77.5	6.9	5984	3	US-09-949-016-2745	Sequence 2745, Ap	c 352	75	6.6	1812	3	US-09-248-796A-637	Sequence 637, App
280	77.5	6.9	6635	3	US-09-949-016-773	Sequence 773, App	c 353	75	6.6	2484	3	US-09-134-000C-1207	Sequence 1207, Ap
281	77.5	6.9	10592	2	US-08-726A-51	Sequence 51, Appli	c 354	75	6.6	2817	6	PCT-US93-05944-1	Sequence 1, Appli
282	77.5	6.9	10592	2	US-08-680-726A-52	Sequence 52, Appli	c 355	75	6.6	3139	3	US-09-949-016-303	Sequence 303, App
283	77.5	6.9	10592	3	US-09-092-409-51	Sequence 51, Appli	c 356	75	6.6	3139	3	US-09-949-016-4130	Sequence 4130, App
284	77.5	6.9	10592	3	US-09-092-409-52	Sequence 52, Appli	c 357	75	6.6	3786	3	US-09-919-039-351	Sequence 351, App
285	77.5	6.9	30843	3	US-09-949-016-14487	Sequence 14487, A	c 358	75	6.6	4074	2	US-08-471-033-19	Sequence 19, Appl
286	77.5	6.9	56147	3	US-09-949-016-16352	Sequence 16352, A	c 359	75	6.6	4074	2	US-08-471-044-19	Sequence 19, Appl
287	77.5	6.9	76472	3	US-09-949-016-15896	Sequence 15896, A	c 360	75	6.6	4074	2	US-08-463-483A-19	Sequence 19, Appl
288	77.5	6.9	86980	3	US-09-949-016-15344	Sequence 15344, A	c 361	75	6.6	4074	2	US-08-471-046A-19	Sequence 19, Appl
289	77.5	6.9	92276	3	US-09-949-016-12166	Sequence 12166, A	c 362	75	6.6	4074	2	US-08-470-566B-19	Sequence 19, Appl
290	77.5	6.9	193303	3	US-09-497-855A-37	Sequence 37, Appli	c 363	75	6.6	4074	2	US-08-469-334-19	Sequence 19, Appl
291	77.5	6.9	193303	3	US-09-497-855A-44	Sequence 44, Appli	c 364	75	6.6	4074	2	US-09-300-529-19	Sequence 19, Appl
292	77	6.8	471	3	US-08-982-285-19	Sequence 20, Appli	c 365	75	6.6	4358	3	US-09-308-453-1	Sequence 1, Appli
293	77	6.8	471	3	US-08-982-285-20	Sequence 20, Appli	c 366	75	6.6	7963	3	US-08-956-171B-168	Sequence 168, App
294	77	6.8	601	3	US-10-100-057-14	Sequence 14, Appli	c 367	75	6.6	7963	3	US-08-781-986A-168	Sequence 168, App
295	77	6.8	1053	3	US-09-540-236-1180	Sequence 1180, Ap	c 368	75	6.6	150597	2	US-09-949-016-15379	Sequence 15379, A
296	77	6.8	1242	3	US-09-489-039A-537	Sequence 537, App	c 369	74.5	6.6	586	2	US-08-463-115-51	Sequence 51, Appl
297	77	6.8	3292	3	US-09-620-312D-165	Sequence 165, App	c 370	74.5	6.6	586	2	US-08-465-388-51	Sequence 51, Appl
298	77	6.8	29231	3	US-09-949-016-16263	Sequence 16263, A	c 371	74.5	6.6	894	3	US-09-543-681A-4070	Sequence 4070, Ap
299	77	6.8	1896	3	US-09-949-016-5744	Sequence 5744, Ap	c 372	74.5	6.6	1194	3	US-09-270-767-13562	Sequence 13562, A
300	76.5	6.8	2220	3	US-09-543-681A-2265	Sequence 2265, Ap	c 373	74.5	6.6	1279	2	US-08-872-719-1	Sequence 1, Appli
301	76.5	6.8	2220	3	US-09-543-681A-2265	Sequence 2265, Ap	c 374	74.5	6.6	1279	3	US-08-957-302A-11	Sequence 11, Appl

375	74.5	6.6	1279	3	US-09-336-890-1	Sequence 1, Appl
376	74.5	6.6	1279	3	US-09-542-403-11	Sequence 11, Appl
377	74.5	6.6	1279	3	US-09-668-499-1	Sequence 1, Appl
378	74.5	6.6	1337	3	US-09-620-405B-467	Sequence 467, App
379	74.5	6.6	1337	3	US-09-433-826B-467	Sequence 467, App
380	74.5	6.6	1337	3	US-09-604-287A-467	Sequence 467, App
381	74.5	6.6	1337	3	US-09-834-759-467	Sequence 467, App
382	74.5	6.6	1337	3	US-09-530-751A-467	Sequence 467, App
383	74.5	6.6	1337	3	US-09-551-621-467	Sequence 467, App
384	74.5	6.6	1337	3	US-09-551-621A-467	Sequence 467, App
385	74.5	6.6	1337	3	US-10-076-622-467	Sequence 467, App
386	74.5	6.6	1698	3	US-09-248-796A-1657	Sequence 1657, Ap
387	74.5	6.6	2030	3	US-09-451-739B-15	Sequence 15, Appl
388	74.5	6.6	2030	3	US-09-602-362B-15	Sequence 15, Appl
389	74.5	6.6	4047	3	US-10-076-622-566	Sequence 566, App
390	74.5	6.6	4458	3	US-10-076-622-564	Sequence 564, App
391	74.5	6.6	2693	3	US-09-949-016-16750	Sequence 16750, A
392	74.5	6.6	27009	3	US-09-949-016-11848	Sequence 11848, A
393	74.5	6.6	56147	3	US-09-949-016-16352	Sequence 16352, A
394	74.5	6.6	103712	3	US-09-949-016-13058	Sequence 13058, A
395	74.5	6.6	105733	3	US-09-949-016-13080	Sequence 13080, A
396	74.5	6.6	126176	3	US-09-949-016-16137	Sequence 16137, A
397	74.5	6.6	126176	3	US-09-949-016-16138	Sequence 16138, A
398	74.5	6.6	136917	3	US-09-949-016-16369	Sequence 16369, A
399	74.5	6.6	161652	3	US-09-497-855A-40	Sequence 40, Appl
400	74.5	6.6	168174	3	US-10-071-411A-63	Sequence 63, Appl
401	74.5	6.6	168273	3	US-10-071-411A-2	Sequence 2, Appl
402	74.5	6.6	228896	3	US-09-949-016-17217	Sequence 17127, A
403	74.5	6.6	238815	3	US-09-949-016-16724	Sequence 16274, A
404	74.5	6.6	285478	3	US-09-949-016-13362	Sequence 13362, A
405	74.5	6.6	390890	3	US-09-949-016-14720	Sequence 14720, A
406	74	6.5	471	3	US-08-982-285-16	Sequence 16, Appl
407	74	6.5	1605	3	US-09-107-532A-2895	Sequence 2895, Ap
408	74	6.5	2422	3	US-09-949-016-3805	Sequence 3805, Ap
409	74	6.5	2624	3	US-09-919-039-113	Sequence 113, App
410	74	6.5	2757	3	US-09-248-796A-4868	Sequence 4868, Ap
411	74	6.5	3697	2	US-08-571-758-1	Sequence 1, Appl
412	74	6.5	3697	2	US-08-909-984A-1	Sequence 1, Appl
413	74	6.5	3697	2	US-08-909-983-1	Sequence 1, Appl
414	74	6.5	3821	3	US-09-949-016-817	Sequence 817, App
415	74	6.5	3850	3	US-09-644-947A-1	Sequence 1, Appl
416	74	6.5	4228	3	US-09-949-016-1239	Sequence 1239, Ap
417	74	6.5	10432	3	US-09-919-172-97	Sequence 97, Appl
418	74	6.5	10432	3	US-09-976-594-21	Sequence 21, Appl
419	74	6.5	10432	3	US-09-919-039-20	Sequence 20, Appl
420	74	6.5	11230	3	US-09-949-016-12981	Sequence 12981, A
421	74	6.5	92227	3	US-09-949-016-11929	Sequence 11929, A
422	74	6.5	92232	3	US-09-949-016-15421	Sequence 15421, A
423	74	6.5	98701	3	US-09-949-016-15989	Sequence 15989, A
424	74	6.5	98730	3	US-09-949-016-15999	Sequence 15999, A
425	74	6.5	129380	3	US-09-949-016-12544	Sequence 12544, A
426	74	6.5	222691	3	US-09-949-016-11762	Sequence 11762, A
427	74	6.5	222697	3	US-09-949-016-15842	Sequence 15842, A
428	73.5	6.5	648	3	US-09-248-796A-8852	Sequence 8852, Ap
429	73.5	6.5	893	3	US-09-869-677B-1	Sequence 1, Appl
430	73.5	6.5	1101	3	US-09-248-796A-1389	Sequence 1389, Ap
431	73.5	6.5	1102	3	US-09-016-434-1131	Sequence 1131, Ap
432	73.5	6.5	1102	3	US-09-023-655-943	Sequence 943, App
433	73.5	6.5	1102	3	US-09-949-016-224	Sequence 224, App
434	73.5	6.5	1104	3	US-09-949-016-4635	Sequence 4635, Ap
435	73.5	6.5	1120	3	US-08-884-324-2	Sequence 2, Appl
436	73.5	6.5	1120	3	US-08-832-180-6	Sequence 6, Appl
437	73.5	6.5	1120	3	US-09-479-862-2	Sequence 2, Appl
438	73.5	6.5	1492	3	US-09-976-594-937	Sequence 937, App
439	73.5	6.5	1575	3	US-08-957-302A-1	Sequence 1, Appl
440	73.5	6.5	1575	3	US-09-542-403-1	Sequence 1, Appl
441	73.5	6.5	1656	3	US-09-270-767-13277	Sequence 13277, A
442	73.5	6.5	1752	3	US-09-949-016-4922	Sequence 4922, Ap
443	73.5	6.5	1796	3	US-09-767-767-30632	Sequence 30632, A
444	73.5	6.5	1800	3	US-09-519-878-1	Sequence 1, Appl
445	73.5	6.5	1810	2	US-07-755-573C-7	Sequence 7, Appl
446	73.5	6.5	2179	3	US-09-620-312D-78	Sequence 78, Appl
447	73.5	6.5	2232	3	US-09-620-405B-491	Sequence 491, App

448	73.5	6.5	2232	3	US-09-834-759-491	Sequence 491, App
449	73.5	6.5	2232	3	US-10-076-622-491	Sequence 491, App
450	73.5	6.5	2307	3	US-09-793-024-43	Sequence 43, Appl
451	73.5	6.5	2351	3	US-09-270-767-14459	Sequence 14459, A
452	73.5	6.5	2436	3	US-09-248-796A-5862	Sequence 5862, Ap
453	73.5	6.5	2490	3	US-09-487-556B-323	Sequence 323, App
454	73.5	6.5	2532	3	US-09-361-631-4	Sequence 4, Appl
455	73.5	6.5	2598	3	US-10-104-047-448	Sequence 448, App
456	73.5	6.5	3288	3	US-09-620-405B-490	Sequence 490, App
457	73.5	6.5	3288	3	US-09-834-759-490	Sequence 490, App
458	73.5	6.5	3288	3	US-10-076-622-490	Sequence 490, App
459	73.5	6.5	3320	3	US-10-104-047-111	Sequence 111, App
460	73.5	6.5	3681	3	US-09-620-405B-463	Sequence 463, App
461	73.5	6.5	3681	3	US-09-433-826B-463	Sequence 463, App
462	73.5	6.5	3681	3	US-09-604-287A-463	Sequence 463, App
463	73.5	6.5	3681	3	US-09-834-759-463	Sequence 463, App
464	73.5	6.5	3681	3	US-09-590-751A-463	Sequence 463, App
465	73.5	6.5	3681	3	US-09-551-621-463	Sequence 463, App
466	73.5	6.5	3681	3	US-09-551-621A-463	Sequence 463, App
467	73.5	6.5	3681	3	US-10-076-622-463	Sequence 463, App
468	73.5	6.5	3865	3	US-09-620-405B-474	Sequence 474, App
469	73.5	6.5	3865	3	US-09-604-287A-474	Sequence 474, App
470	73.5	6.5	3865	3	US-09-834-759-474	Sequence 474, App
471	73.5	6.5	3865	3	US-09-590-751A-474	Sequence 474, App
472	73.5	6.5	3865	3	US-09-551-621-474	Sequence 474, App
473	73.5	6.5	3865	3	US-09-551-621A-474	Sequence 474, App
474	73.5	6.5	3865	3	US-10-076-622-474	Sequence 474, App
475	73.5	6.5	4080	3	US-09-134-000C-2969	Sequence 2969, Ap
476	73.5	6.5	4731	2	US-08-488-706-2	Sequence 2, Appl
477	73.5	6.5	4731	3	US-08-772-270A-9	Sequence 9, Appl
478	73.5	6.5	4731	3	US-09-062-126-6	Sequence 6, Appl
479	73.5	6.5	4792	3	US-08-781-891-205	Sequence 205, App
480	73.5	6.5	4792	3	US-08-618-166-205	Sequence 205, App
481	73.5	6.5	4836	3	US-09-799-451-519	Sequence 519, App
482	73.5	6.5	5433	3	US-09-562-702A-15	Sequence 15, Appl
483	73.5	6.5	5433	3	US-09-561-818A-15	Sequence 15, Appl
484	73.5	6.5	5433	3	US-10-037-182A-13	Sequence 7, Appl
485	73.5	6.5	5613	3	US-09-563-702A-13	Sequence 13, Appl
486	73.5	6.5	5613	3	US-09-561-818A-13	Sequence 13, Appl
487	73.5	6.5	5613	3	US-09-561-709B-10	Sequence 10, Appl
488	73.5	6.5	5613	3	US-10-037-182-5	Sequence 5, Appl
C 489	73.5	6.5	44208	3	US-09-949-016-12240	Sequence 12240, A
C 490	73.5	6.5	44208	3	US-09-949-016-15941	Sequence 15941, A
C 491	73.5	6.5	79595	3	US-09-949-016-15318	Sequence 15318, A
C 492	73.5	6.5	107421	3	US-09-949-016-15532	Sequence 15532, A
C 493	73.5	6.5	126200	3	US-09-949-016-11824	Sequence 11824, A
C 494	73.5	6.5	126200	3	US-09-949-016-13193	Sequence 13193, A
C 495	73.5	6.5	148794	3	US-09-949-016-13751	Sequence 12751, A
C 496	73.5	6.5	278866	3	US-09-949-016-13922	Sequence 13922, A
C 497	73.5	6.5	278866	3	US-09-949-016-13923	Sequence 13923, A
C 498	73.5	6.5	278866	3	US-09-949-016-13924	Sequence 13924, A
C 499	73.5	6.5	278866	3	US-09-949-016-13925	Sequence 13925, A
C 500	73.5	6.5	278866	3	US-09-949-016-13926	Sequence 13926, A

ALIGNMENTS

RESULT 1

```

US/09-697-863A-1
; Sequence 1, Application US/09697863A
; Patent No. 6812203
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Inst
; TITLE OF INVENTION: CD-40 INTERACTING AN
; FILE REFERENCE: 2676-45550S
; CURRENT APPLICATION NUMBER: US/09/697.86
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: PCT/EP99/03025
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EPO 98201392.2
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ IDS NOS: 6
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 1
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1627)..(1627)
; OTHER INFORMATION: N stands for any nucleotide.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1108)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1849)..(1849)
; OTHER INFORMATION: N stands for any nucleotide.
US-09-697-863A-1

Alignment Scores:
Pred. No.: 2,36e-137 Length: 1920
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-09-697-863A-1 (1-1920)
QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 179 ATGGAAGGCTCTGAACCTCTTCCGAGCCTCCGGTGGAGAGAGCGCTTGGAAACG 238
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
Db 239 CGACCTGAAACCACTCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACT 298
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 299 GATTCACCACTCTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGACGATG 358
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 359 TTCTCTCTCATTTACCTGGAATATTGATGATTAGATTCTAAACAATCTGTGACAGAGGGCT 418
QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 419 CGAGGGGTGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATATTCTTACAGGAAGTT 478
QY 101 IleProProTyrTyrSerTyrLeuLysValSerSerAsnTyrGluIleIleThrGly 120
Db 479 ATTCCCCCATATTATAGCTACCTTAAAGAGAGATCAAGTAATATGAGATTATTACAGGT 538
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 539 CATGAAGAGGATATTTCACAGCTATAATGTTGAGAAATCAGAGTGAATTAAGAAAGC 598
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db 599 CAAGAGATTATTCCTTTTCCCAAGTACCATAATGATGAGAAACCTTTTATGTGTGCATGTG 658
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 659 AATGTGTGAGAAATGAGCTTTGCTTATGACATCCCATTTGGAGAGCACACAGAGGGCAT 718
QY 181 AlaAlaGluArgMetAsnGlnLeuLysMetValIleLysLysMetGlnGluAlaProGlu 200
Db 719 GCTGCGGAACGAATGATGATTAATGTTTTAAAGAAATGCAAGAGGCTCCAGAG 778
QY 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 779 TCAGCTACAGTTATATTTCAGGAGATACAAATCTAAGGGATCGAGAGGTTTACAGATGT 838

RESULT 2
```

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US-09-620-312D-889
; Sequence 889, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 889
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(1127)
US-09-620-312D-889

Alignment Scores:
Pred. No.: 2,42e-137 Length: 1948
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-09-620-312D-889 (1-1948)
QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 198 ATGGAAGGCTCTGAACCTCTTCCGAGCCTCCGGTGGAGAGAGCGCTTGGAAACG 257
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
Db 258 CGACCTGAAACCACTCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAGAAACAACT 317
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 318 GATTCACCACTCTTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGACGATG 377
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 378 TTCTCTCTCATTTACCTGGAATATTGATGATTAGATTCTAAACAATCTGTGACAGAGGGCT 437
QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 438 CGAGGGGTGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATATTCTTACAGGAAGTT 497
QY 101 IleProProTyrTyrSerTyrLeuLysValSerSerAsnTyrGluIleIleThrGly 120
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Db 498 ATTCCCATATTATAGCTACTAAAGAGAGATCAAGTAATTATGAGATTATTACAGGT 557
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 558 CATGAAGAAGAGATATTTCACAGCTATATATGTTGAAGAAATCAAGAGTGAATTTAAAGC 617
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db 618 CAAGAGATTATTCCTTTCCAGTACCCAAATGATGAGAACTTTTATGTGTGATGTG 677
Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 678 AATGTGTGAGAAATGAGCTTTGCTTATGACATCCCATTTGGAGAGCACCAGAGGGCAT 737
Qy 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 738 GCTCGGGAACCAATGAATCACTTAAATATGTTTAAAGAAATGCAAGAGGCTCCAGAG 797
Qy 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 798 TCAGCTACAGTTATTTTCAGGAGATACAAATCTTAGGGATCGAGAGGTTACCAAGATGT 857

RESULT 3
US-09-697-863A-3
; Sequence 3, Application US/09697863A
; Patent No. 6812203
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut Voor Biotechnologie VZW
; TITLE OF INVENTION: CD-40 INTERACTING AND TRAP-INTERACTING PROTEINS
; FILE REFERENCE: 2676-4555US
; CURRENT APPLICATION NUMBER: US/09/697,863A
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: PCT/EP99/03025
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EPO 98201392.2
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1312
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (122)..(1234)
; OTHER INFORMATION:
US-09-697-863A-3

Alignment Scores:
Pred. No.: 5, 8e-90 Length: 1312
Score: 766.50 Matches: 150
Percent Similarity: 81.28% Conservative: 28
Best Local Similarity: 68.49% Mismatches: 40
Query Match: 67.77% Indels: 1
DB: 3 Gaps: 1

US-10-757-745-2_COPY_54_273 (1-220) x US-09-697-863A-3 (1-1312)
Qy 2 GluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArgArg 21
Db 317 CAGAAGCCCTGAGCGCTACTTCGAGCTGCAGAGAACGACCAAGGGTGGCCGGCCAG 376
Qy 22 ProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThrAsp 41
Db 377 CCTCCACGCTCTCAAGTCCGAGCGCTATGTCATCTAACCACGAGGATGCAATGAT 436
Qy 42 SerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPhe 61
Db 437 ACAACACATTTAGAACCCAGTCCATCT---GGAACTCTCTTAGAAGATGACGACGATTT 493
Qy 62 SerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArg 81
Db 494 TCTTTTACCTGGAATATTGATGGATTAGATGATGATCAATCTGCCCGAGAGGGCTCGA 553
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Qy 82 GlyValCysSerTyrIleuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIle 101
Db 554 GGGGTGTGTTCTCGCCCTAGCTTTGTATAGTCCAGATGTGGTATTTCTACAGGAAGTTATC 613
Qy 102 ProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGlyHis 121
Db 614 CCCCCTACTGTCTTACCTACCTAAAGAGAGAGCAGCCAGTTTACACAATTTATTACAGGTAAT 673
Qy 122 GluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGln 141
Db 674 GAAGAGAGATATTTCACAGCTATCTATTGAAGAAAGAGAGAGTGAATTTAAAGTCAG 733
Qy 142 GluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsn 161
Db 734 GAGATTATTCCTTTTCCAAATACCAAAATGATGAGAACTCTGCTATCGGTAATGTGAGT 793
Qy 162 ValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAla 181
Db 794 TTGGTGGAAATGAATTTTGGCTTATGACATCCCATTTGGAGAGCACCAGAGAACATCTCT 853
Qy 182 AlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGluSer 201
Db 854 GCGGAACCAATAAGACAAATTTAAAAAAGCTGTTCTTGGAAAAATGCAAGAGGCTCCAGATTCA 913
Qy 202 AlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 914 ACCACGGTTATATTTCAGGAGATACAAATTTAAGAGATCAAGAAAGTTATCAAAATGT 970

RESULT 4
US-09-118-554-63/c
; Sequence 63, Application US/09118554A
; Patent No. 6365348
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOUNDS FOR DIAGNOSIS OF BREAST CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.450C1
; CURRENT APPLICATION NUMBER: US/09/118,554A
; CURRENT FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 08/988,255
; EARLIER FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 1079
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-118-554-63

Alignment Scores:
Pred. No.: 7, 67e-83 Length: 1079
Score: 711.00 Matches: 138
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 62.86% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-09-118-554-63 (1-1079)
Qy 83 ValCysSerTyrIleuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIlePro 102
Db 1077 GTGTGTTCTTACTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTATCCC 1018
Qy 103 ProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGlyHisGlu 122
Db 1017 CCATATTTATAGTACCTTAAAGAGAGATCAAGTAATTTATGAGATTATTACAGGTCATGAA 958
Qy 123 GluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGlnGlu 142
Db 957 GAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAAAGCAAGAG 898
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Qy	143	IleIleProPheProSerThrIysMetMetArgAsnLeuLeuCysValHisValAsnVal	162
Db	897	ATTATTCTCTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCATGTGAATGTG	938
Qy	163	SerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAla	182
Db	837	TCAGGAATAGAGCTTTGGCTTTATGACATCCCATTTGGAGAGCACGAGGGCATGCTCGG	778
Qy	183	GluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGluSerAla	202
Db	777	GAACGATGATCAGTTTAAATAATGTTTTAAAGAAATGCAGAGGGCTCCAGAGTCAGCT	718
Qy	203	ThrValIlePheAlaGlyAspThrAsnLeuArgPheArgGluValThrArgCys	220
Db	717	ACAGTTTATTTTTCAGGAGATCAAACTCTTAAGCATTCGAGAGGTTACCAATGT	664

! SOFTWARE: Patent.pm
! SEQ ID NO 8403
! LENGTH: 379
! TYPE: DNA
! ORGANISM: Homo sapiens
US-09-621-976-8403

Alignment Scores:
Pred. No.: 1.44e-09 Length: 379
Score: 145.00 Matches: 28
Percent Similarity: 100.00% Conservatives: 1
Best Local Similarity: 96.55% Mismatches: 0
Query Match: 12.82% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x US-09-621-976-8403 (1-379)

Qy 2 GluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 21
Db 19 CAGAGGGCTCTGAACCTCTACTTTCAGCCTCCGGTGGAGGAGCGCCTTGGAAAGCCGA 78
Qy 22 ProGluThrIleSerGluProLysThr 30
Db 79 CCTGAACCACTCTCTGAGCCCAAGACC 105

RESULT 8

US-09-949-016-16603/c
! Sequence 16603, Application US/09949016
! Patent No. 6812339

! GENERAL INFORMATION:
! APPLICANT: VENTER, J. Craig et al.
! TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
! WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
! FILE REFERENCE: CL001307
! CURRENT APPLICATION NUMBER: US/09/949,016
! CURRENT FILING DATE: 2000-04-14
! PRIOR APPLICATION NUMBER: 60/241,755
! PRIOR FILING DATE: 2000-10-20
! PRIOR APPLICATION NUMBER: 60/237,768
! PRIOR FILING DATE: 2000-10-03
! PRIOR APPLICATION NUMBER: 60/231,498
! PRIOR FILING DATE: 2000-09-08
! NUMBER OF SEQ ID NOS: 207012
! SOFTWARE: FastSeq for Windows Version 4.0
! SEQ ID NO 16603
! LENGTH: 232547
! TYPE: DNA
! ORGANISM: Human
US-09-949-016-16603

Alignment Scores:
Pred. No.: 6.37 Length: 232547
Score: 105.00 Matches: 51
Percent Similarity: 48.33% Conservatives: 36
Best Local Similarity: 28.33% Mismatches: 71
Query Match: 9.28% Indels: 22
DB: 3 Gaps: 8

US-10-757-745-2_COPY_54_273 (1-220) x US-09-949-016-16603 (1-232547)

Qy 38 GluThrThrAspSerThr-ThrSerLysIleSerProSerGluAspThrGlnGln-GluA 57
Db 72006 GAAGAACTCCATCAACTAAGCAGCAAAATAACAGCCACATCATATGACAGATCAA 71947
Qy 57 snGlySerMetPheSerLeuIleThrTrpAniIleAspGlyLeuAspLeuAsnLeuS 77
Db 71946 AT--TCACACATAACAATATTAACCTTAATGTAAATGGA-----CTAAATCTCCAA 71896
Qy 77 erGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheL 97
Db 71895 TTAAGAAAGACAGA---CTGGCAATTTGGATAAAGAGTCAAGACCCATCAGTGTGCTGA 71839
Qy 97 euGlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluI 117

Db 71838 TTCAGGAA-----ACCATCTCAGTCGACAGACACATAGGCTCA 71797
Qy 117 leIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValL 137
Db 71796 AAATAAAAGGATGGAGGAGATCTACCAAGCAAAATGAAACAAAAAAGCAGGGGTG 71737
Qy 137 ysLeuLysSerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeu 157
Db 71736 CAATCCTAGTCTCTGATAAAACAGACTTTAAACCAACAAGATCAAAAAGAGACAAAGAT 71677
Qy 157 ysValHisValAsnValSerGlyAsn-----GluLeuCysLeuMetThrSerH 173
Db 71676 GCCATTACATAATGTTAAAGGATCAATTCAACAGAGAGCTAATTATCTTAATATAT 71617
Qy 173 isLeuGluSerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuL 193
Db 71616 ATGCACCCCAATACA-----GGAGCACCAGATTG-----ATAAGCAAGTCTCTGA 71572
Qy 193 ysLysMetGlnGluAlaProGluSerAlaThrValIlePheAlaGlyAspThrAsn 211
Db 71571 GTGACCTACAAAGAGACTTAGACTCCACACAATAATAATG---GGAGACTTTTAAC 71519

RESULT 9
US-09-976-594-888
! Sequence 888, Application US/09976594
! Patent No. 6673549
! GENERAL INFORMATION:
! APPLICANT: Furness, Michael
! APPLICANT: Buchbinder, Jenny
! TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
! FILE REFERENCE: PA-0041 US
! CURRENT APPLICATION NUMBER: US/09/976,594
! CURRENT FILING DATE: 2001-10-12
! PRIOR APPLICATION NUMBER: 60/240,409
! PRIOR FILING DATE: 2000-10-12
! NUMBER OF SEQ ID NOS: 1143
! SOFTWARE: PERL Program
! SEQ ID NO 888
! LENGTH: 3640
! TYPE: DNA
! ORGANISM: Homo sapiens
! FEATURE:
! NAME/KEY: misc feature
! OTHER INFORMATION: Incyte ID No. 6673549 5202390CBI
US-09-976-594-888

Alignment Scores:
Pred. No.: 0.0187 Length: 3640
Score: 102.50 Matches: 66
Percent Similarity: 42.17% Conservatives: 39
Best Local Similarity: 26.51% Mismatches: 80
Query Match: 9.06% Indels: 64
DB: 3 Gaps: 16

US-10-757-745-2_COPY_54_273 (1-220) x US-09-976-594-888 (1-3640)

Qy 6 AsnSerTyrPheGluPro-----ProValGlu 14
Db 827 AATCCTTTTATGAACCTCAACTCCTCCTCAAAATAATTGGTAAATCTCTGTCAA 886
Qy 15 GluSerAlaLeuGluArgArg-----ProGluThrIleSerGlu 27
Db 887 GAATAGAAAAGTGAAGGCGAGTGAAGAAAGAGCCCGGCTCCACAGCTCTCTCA--- 943
Qy 28 ProLysThrTyrValAspLeuThrAsnGluGluThrThrAsp-----Ser 42
Db 944 CCAAAAACAGAGTA-----TTAATGAAACACACAGTTCTTCAGAGAAAAGATCTCTCT 997
Qy 43 ThrThrSerLysIleSerProSerGluAspThr-----GlnGlnGluAsnGlySer 59
Db 998 ACTTCTCTTAAGCAAGCCCTATACCAAGTCTCTGTTTGGGGCGGAAAGCAAAATGCTAGT 1057

```

QY 60 MetPheSerLeuIleThrTyr-----AsnIleAspGlyLeuAspLeu 73
Db 1058 CAG-----TCTTCTCTGTATGGTGTAAAGAGTACAAAGAACTACCGAGGAGTAAATC 1114
QY 74 AsnAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeu-----Tyr 90
Db 1115 ACCAATTTTACTPACATCGTGGAGAAATGGTTTATCTTTTGTGCAATATTACACCACCTTT 1174
QY 91 SerProAspValIlePheLeuGlnGluValIleProProTyrTyrSerTyrLeuLys 110
Db 1175 AGACCAGATTTAATTAATGACTACAAAGTCTCTGAATCCT----- 1210
QY 111 ArgSerSerAsnTyrGluIleIleThrGlyHisGluGluGlyTyr-----PheThrAla 128
Db 1211 -----CAGATATTAAAGAGAACACAAAGGCGATACATGATGGATTGCCAGC 1258
QY 129 Ile-----MetLeuLysLysSerArgValLysLeuLysSerGlnGluIle 144
Db 1259 ATAGGAATTTCCCGATTATTGGAACCTTCTGATATGGTATTATTAGCA-----ATT 1309
QY 145 ProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsnValSerGly 164
Db 1310 CCTGATAAACTGACT---GTTATGACTTATCTCTATCAATAAAGGCGACATTTCAAGTGC 1366
QY 165 AsnGluLeuCysLeuMetThrSerHisLeuGluSerThr-ArgGlyHis---AlaAlaG 183
Db 1367 CAAGAACTAAATGTCTGATAGAGGAAACAGCAGTAAAGGCGACATATAAAGTTGA 1426
QY 183 uArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGluSerAlaTh 203
Db 1427 AACTATGAACACAGATACAAACAGTCTGTGTGATCAAGAAATTTCTATGCAGAGC---TT 1483
QY 203 rValIlePheAlaGlyAspThrAsn 211
Db 1484 AGTGATCTGAAGCGGAGCCTGAAC 1508

```

RESULT 10

```

US-09-620-312D-363
; Sequence 363, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghaast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: No. 6569662el Nucleic Acids and
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt FL_genes Version 1.0
; SEQ ID NO 363
; LENGTH: 4061
; TYPE: DNA
; ORGANISM: Homo sapiens

```

```

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (72)..(3062)
US-09-620-312D-363
Alignment Scores:
Pred. No.: 0.0222 Length: 4061
Score: 102.50 Matches: 66
Percent Similarity: 42.17% Conservative: 39
Best Local Similarity: 26.51% Mismatches: 80
Query Match: 9.06% Indels: 64
Db: 3 Gaps: 16

```

US-10-757-745-2_COPY_54_273 (1-220) x US-09-620-312D-363 (1-4061)

```

QY 6 AsnSerTyrPheGluPro-----ProValGlu 14
Db 474 AATCTCTTTTATGAACCTTAATCAACTCTCTCCTCAATAATTTGGTAAATCTCTTCAA 533
QY 15 GluSerAlaLeuGluArgArg-----ProGluThrIleSerGlu 27
Db 534 GAACCTAGAACTGAAGCGGAGTGAAGAGAGCGCCGCTCCACCACTCTCTCA--- 590
QY 28 ProLysThrTyrValAspLeuThrAsnGluGluThrAsp-----Ser 42
Db 591 CCMAAAACAGGAGTA-----TTAAATGMAAACACAGTTTCTGCAGGAAAGATCTCTCT 644
QY 43 ThrThrSerLysIleSerProSerGluAspThr-----GlnGluAsnGlySer 59
Db 645 ACTTCTCTAGCCAGCCCTATACCAAGTCTCTGTTGGGCGGAAGCAATGCTAGT 704
QY 60 MetPheSerLeuIleThrTyr-----AsnIleAspGlyLeuAspLeu 73
Db 705 CAG---TCTTGTCTGTATGGTGTAAAGAGTTACAAAGAACTACCGAGGAGTAAATAT 761
QY 74 AsnAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeu-----Tyr 90
Db 762 ACCAATTTTACTACATCGTGGAGAAATGGTTTATCTTTTGTGCAATATTACACCACTTT 821
QY 91 SerProAspValIlePheLeuGlnGluValIleProProTyrTyrSerTyrLeuLys 110
Db 822 AGACCAGATTTAATTTGACTACAAAGTCTCTGAATCTCT----- 857
QY 111 ArgSerSerAsnTyrGluIleIleThrGlyHisGluGluGlyTyr-----PheThrAla 128
Db 858 -----CAGATATTAAAGAGAACACAAAGGCGATACGATGATTTGCGCAGC 905
QY 129 Ile-----MetLeuLysLysSerArgValLysLeuLysSerGlnGluIle 144
Db 906 ATAGGAATTTCCCGATTATTGGAACCTTCTGATATGGTATTATTAGCA-----ATT 956
QY 145 ProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsnValSerGly 164
Db 957 CCTGATAAACTGACT---GTTATGACTTATCTCTATCAATAAAGGCGACATTTCACTGTC 1013
QY 165 AsnGluLeuCysLeuMetThrSerHisLeuGluSerThr-ArgGlyHis---AlaAlaG 183
Db 1014 CAAGAACTAAATGTCTTCCAGATAGAGGAAACAGCAGTAAAGGCGACATATAAAGTTGA 1073
QY 183 uArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGluSerAlaTh 203
Db 1074 AACTATGAACACAGATACAAACAGTCTGTGTGATCAAGAAATTTCTATGCAGAGC---TT 1130
QY 203 rValIlePheAlaGlyAspThrAsn 211
Db 1131 AGTGATCTGAAGCGGAGCCTGAAC 1155

```

RESULT 11

```

US-09-949-016-17522/c
; Sequence 17522, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

```

```
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17522
; LENGTH: 61462
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(61462)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17522
```

```
Alignment Scores:
Pred. No.: 5.48 Length: 61462
Score: 98.50 Matches: 54
Percent Similarity: 42.36% Conservative: 43
Best Local Similarity: 23.58% Mismatches: 91
Query Match: 8.71% Indels: 41
DB: 3 Gaps: 10
```

US-10-757-745-2_COPY_54_273 (1-220) x US-09-949-016-17522 (1-61462)

```
Qy 15 GluSerAlaLeuGluArgProGluThrIleSerGlu----- 27
Db 15084 CAGGCTGCTTCAAGAGCTCCAGAGAGCATAACATGGAAGAAAACCGGTA 15025

Qy 28 -----ProLysThrTyrValAspLeuThrAsnGluGluThr-----Asp 41
Db 15024 CCAGCACTGCAAAACATACCAATTGTAAAGACCATCGACACTGTGAAGAAACTGCAA 14965

Qy 42 SerThrThrSerLysIleSerProSerGluAspThrGlnGluAsnGlySerMetPhe 61
Db 14964 CACTAATGAGCAAAATCAATAGCATCATATATGACA-----GGATCAATTCACATA 14911

Qy 62 SerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArg 81
Db 14910 ACAATATTAACTTGAATATAAATGGGCTA-----AATGTTCCAAATTAACACACAC 14860

Qy 82 GlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIle 101
Db 14859 AGACCGCAAAATTGGATAAGAGTCAAGACCATCAGTGTGTTTTCAGGAG----- 14806

Qy 102 ProProTyrTyrSerTyrLeuLysIleArgSerSerAsnTyrGluIleThrGlyHis 121
Db 14805 -----ACCATCTCATGTGCAAGAGACACACATAGCTCAAAATTAAGGATGG 14758

Qy 122 GluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGln 141
Db 14757 AGGATATTACCAAGCAAAATGGAAGAAAAGAGAGGAGGTTGCAATCTAGTTCTT 14698

Qy 142 GluIleIleProPheProSerThrLysMetMetArgAsn-----LeuLeuCys 157
Db 14697 GATAAAGCAAAATTTAAACCAACAAAGATCAAAAGACAAAGAGGTTATTACATATG 14638

Qy 158 ValHisValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThr 177
Db 14637 GTCAGGAATCAATGCAACAAAGAGAGCTAATCTCCATAATATATATATGCCCCCAATCA 14578

Qy 178 ArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGlu 197
Db 14577 -----GGAGCAACCGATTC-----ATAAGCAAGTCTTAGAGACCTACAAAGA 14533
```

```
Qy 198 AlaProGluSerAlaThrValIlePheAlaGlyAspThrAsnLeu----- 212
Db 14532 GACTTAGACTCCACACAATAATA---GTGGAGACTTTAAACACCCCACTGTCAACATTA 14476

Qy 213 -----ArgAspArgGluValThrArg 219
Db 14475 GATCAACGAGACAGAGAAAATTAACAAGG 14449

RESULT 12
US-09-949-016-12008
; Sequence 12008, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12008
; LENGTH: 331814
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(331814)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12008
```

Alignment Scores:

```
Pred. No.: 79.1 Length: 331814
Score: 98.50 Matches: 49
Percent Similarity: 46.63% Conservative: 34
Best Local Similarity: 27.53% Mismatches: 76
Query Match: 8.71% Indels: 20
DB: 3 Gaps: 7
```

US-10-757-745-2_COPY_54_273 (1-220) x US-09-949-016-12008 (1-331814)

```
Qy 38 GluThrThrAspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsn 57
Db 134994 GAAGAACTGCATCACTAATGAGCAAAA--TCACCAGCTAACTAATGACAGGATCA 135052

Qy 58 GlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSer 77
Db 135053 AATTCACACATAACATATTAACTTTAAATATAATATGGA-----CTAAATTCGCAATT 135106

Qy 78 GluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeu 97
Db 135107 AAAAGACACAGA---CTGGCAAGTTGGATAAGAGTCAAGACCCCATCAGTGTGCTGTATT 135163

Qy 98 GlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIle 117
Db 135164 CAGGAA-----ACCATCTCAGTCGAGACACACATAGGCTCAA 135205

Qy 118 IleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLys 137
Db 135206 ATAAAGGATGGAGGAAGATCTACCAAGCAATGGAACCAAAAGGAGGAGGTTGCA 135265

Qy 138 LeuLysSerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCys 157
Db 135266 ATCTAGTCTCTGACAAAACAGACTTTAAACCAACAAAGATCAAAAGAGACAAAGAGAGGC 135325

Qy 158 ValHisValAsnValSerGlyAsn-----GluLeuCysLeuMetThrSerHis 173
Db 158 ValHisValAsnValSerGlyAsn-----GluLeuCysLeuMetThrSerHis 173
```

Db 135326 CATTACATAATGCTAAAGGATCAATCAACAGAGGAGCTAACTATCCTAAATATTTAT 135385
Qy 174 LeuGlusSerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLys 193
Db 135386 GCACCAATACA-----GGAGCACCAGATTC-----ATAAGCAAGTCTCTCAGT 135430
Qy 194 LysMetGlnGluAlaProGluSerAlaThrValIlePheAlaGlyAspThrAsn 211
Db 135431 CACCTACAAAGAGACTTAGACTCCACACATTAATAATG---GGAGACTTTTAAC 135481

RESULT 13
US-09-949-016-17056
; Sequence 17056, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17056
; LENGTH: 331814
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(331814)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17056

Alignment Scores:
Pred. No.: 79.1 Length: 331814
Score: 98.50 Matches: 49
Percent Similarity: 46.63% Conservative: 34
Best Local Similarity: 27.53% Mismatches: 76
Query Match: 8.71% Indels: 20
DB: 3 Gaps: 7

US-10-757-745-2_COPY_54_273 (1-220) x US-09-949-016-17056 (1-331814)
Qy 38 GluThrThrAspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsn 57
Db 134994 GAAGAACTGCATCACTCAATATGAGCAAAA-TCACCAGCTTAACATCATATGACAGGATCA 135052
Qy 58 GlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSer 77
Db 135053 AATTCCACATACATATTAATTAATTAATAATGGA-----CTAATTCGCAATT 135106
Qy 78 GluArgAlaArgGlyValCysSerTyrrLeuAlaLeuTyrrSerProAspValIlePheLeu 97
Db 135107 AAAAGACACAGA---CTGGCAAGTTGGATAAAGAGTCAAGACCCATCAGTGTCTGTATT 135163
Qy 98 GlnGluValIleProProTyrrTyrrSerTyrrLeuLysIleArgSerAsnTyrrGluIle 117
Db 135164 CAGGAA-----ACCCATCTCAGTCGACGACACACATAGGCTCAAA 135205
Qy 118 IleThrGlyHisGluGluGlyTyrrPheThrAlaIleMetLeuLysIleSerArgValLys 137
Db 135206 ATAAAGGATGGAGGAAGATCTACCAAGCCATGGAACCAAAAGGAGGAGGCTTGA 135265
Qy 138 LeuLysSerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLys 157
Db 135266 ATCTTAGTCTCTGACAAAACAGACTTTAAACCAACCAAGATCAAAAGAGACAAAGAGGC 135325

Qy 158 ValHisValAsnValSerGlyAsn-----GluLeuCysLeuMetThrSerHis 173
Db 135326 CATTACATAATGCTAAAGGATCAATCAACAGAGGAGCTAACTATCCTAAATATTTAT 135385
Qy 174 LeuGlusSerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLys 193
Db 135386 GCACCAATACA-----GGAGCACCAGATTC-----ATAAGCAAGTCTCTCAGT 135430
Qy 194 LysMetGlnGluAlaProGluSerAlaThrValIlePheAlaGlyAspThrAsn 211
Db 135431 CACCTACAAAGAGACTTAGACTCCACACATTAATAATG---GGAGACTTTTAAC 135481

RESULT 14
US-09-949-016-17553/c
; Sequence 17553, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17553
; LENGTH: 106380
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17553

Alignment Scores:
Pred. No.: 17.6 Length: 106380
Score: 97.50 Matches: 49
Percent Similarity: 46.63% Conservative: 34
Best Local Similarity: 27.53% Mismatches: 76
Query Match: 8.62% Indels: 20
DB: 3 Gaps: 7

US-10-757-745-2_COPY_54_273 (1-220) x US-09-949-016-17553 (1-106380)
Qy 38 GluThrThrAspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsn 57
Db 22502 GAAGAACTGCATCACTCAATATGAGCAAAA-TCACCAGCTTAACATCATATGACAGGATCA 22444
Qy 58 GlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSer 77
Db 22443 AATTCCACATACATATTAATTAATTAATAATGGA-----CTAATTCGCAATT 22390
Qy 78 GluArgAlaArgGlyValCysSerTyrrLeuAlaLeuTyrrSerProAspValIlePheLeu 97
Db 22389 AAAAGACACAGA---CTGGCAAGTTGGATAAAGAGTCAAGACCCATCAGTGTCTGTATT 22333
Qy 98 GlnGluValIleProProTyrrTyrrSerTyrrLeuLysIleArgSerAsnTyrrGluIle 117
Db 22332 CAGGAA-----ACCCATCTCATGTGCAGACACACATAGGCTCAAA 22291
Qy 118 IleThrGlyHisGluGluGlyTyrrPheThrAlaIleMetLeuLysIleSerArgValLys 137
Db 22290 ATAAAGGATGGAGGAAGATCTACCAAGCCATAGAAAAACAAAAGGAGGAGGCTTGA 22231
Qy 138 LeuLysSerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLys 157
Db 22230 ATCTTAGTCTCTGATTAACAGACTTTAAACCAACCAAGATCAAAAGAGACAAAGAGGC 22171
Qy 158 ValHisValAsnValSerGlyAsn-----GluLeuCysLeuMetThrSerHis 173

```
Db 22170 CATTACATAATGTTAAAGGGATCAATTCAACAGAGGAGCTAATCTCTAAATATTTAT 22111
Qy 174 LeuGluSerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLys 193
Db 22110 GCACCCCAATACA-----GGAGCACCCAGATTC-----ATAAAGCAAGTCTCTCAGT 22066
Qy 194 LysMetGlnGluAlaProGluSerAlaThrValIlePheAlaGlyAspThrAsn 211
Db 22065 GACTTACAAAGAGCTTAGACTCCACACATAATAATG---GGAGACTTTTAAC 22015

RESULT 15
US-09-949-016-12805/c
; Sequence 12805, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12805
; LENGTH: 421491
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(421491)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12805

Alignment Scores:
Pred. No.: 156 Length: 421491
Score: 97.50 Matches: 39
Percent Similarity: 47.40% Conservative: 34
Best Local Similarity: 25.32% Mismatches: 62
Query Match: 8.62% Indels: 19
DB: 3 Gaps: 6

US-10-757-745-2_COPY_54_273 (1-220) x US-09-949-016-12805 (1-421491)
Qy 62 SerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArg 81
Db 289557 ACAATATTAACTTAAATGTAAATGGGCTA-----AATGCTCCAAATTAAAGACAC 289507
Qy 82 GlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIle 101
Db 289506 AGACTGGCAAAATGGATAAAGAATCAACCAATCAGTGTCTATATTCAGAG----- 289453
Qy 102 ProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleThrGlyHis 121
Db 289452 -----ACCCATCTCACATGCAGACACACATAGGCTCAAAATAAAGGATGG 289405
Qy 122 GluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuSerGln 141
Db 289404 AGGAAATCTACCAAGCAAAATGGAAACAAAGATCAAAAGAGACAAAGAGCCATTACTTAATG 289345
Qy 142 GluIleIleProPheProSerThrLysMetMetArg-----AsnLeuLeuCys 157
Db 289344 GATAAAACAGACTTTAAACCAACAAGAATCAAAAGAGACAAAGAGCCATTACTTAATG 289285
Qy 158 ValHisValAsnValSerGlyAsnGluLeuLeuMetThrSerHisLeuGluSerThr 177
Db 289284 GTAAAGGGATCAATTCAACCAAGAGAGCTAATCTCTCTAAATATATATATGCACAAATACA 289225
Qy 178 ArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGlu 197
```

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Qy 178 ArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGlu 197
Db 289224 AGA-----GCACCCAGATTC-----ATAAAGCAAGTCTCTTAGAGACCTACAAAAA 289180
Qy 198 AlaProGluSerAlaThrValIlePheAlaGlyAspThrAsn 211
Db 289179 GACTTAGATTCACACACATAATAATG---GGAGACTTTTAAC 289141

RESULT 16
US-09-949-016-14060/c
; Sequence 14060, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14060
; LENGTH: 421494
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(421494)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14060

Alignment Scores:
Pred. No.: 156 Length: 421494
Score: 97.50 Matches: 39
Percent Similarity: 47.40% Conservative: 34
Best Local Similarity: 25.32% Mismatches: 62
Query Match: 8.62% Indels: 19
DB: 3 Gaps: 6

US-10-757-745-2_COPY_54_273 (1-220) x US-09-949-016-14060 (1-421494)
Qy 62 SerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArg 81
Db 289557 ACAATATTAACTTAAATGTAAATGGGCTA-----AATGCTCCAAATTAAAGACAC 289507
Qy 82 GlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIle 101
Db 289506 AGACTGGCAAAATGGATAAAGAATCAAGACCCATCAGTGTCTATATTCAGAG----- 289453
Qy 102 ProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleThrGlyHis 121
Db 289452 -----ACCCATCTCACATGCAGACACACATAGGCTCAAAATAAAGGATGG 289405
Qy 122 GluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuSerGln 141
Db 289404 AGGAAATCTACCAAGCAAAATGGAAACAAAGATCAAAAGAGACAAAGAGCCATTACTTAATG 289345
Qy 142 GluIleIleProPheProSerThrLysMetMetArg-----AsnLeuLeuCys 157
Db 289344 GATAAAACAGACTTTAAACCAACAAGAATCAAAAGAGACAAAGAGCCATTACTTAATG 289285
Qy 158 ValHisValAsnValSerGlyAsnGluLeuLeuMetThrSerHisLeuGluSerThr 177
Db 289284 GTAAAGGGATCAATTCAACCAAGAGAGCTAATCTCTCTAAATATATATATGCACAAATACA 289225
Qy 178 ArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGlu 197
```


FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11945
LENGTH: 86439
TYPE: DNA
ORGANISM: Human
US-09-949-016-11945

Alignment Scores:
Pred. No.: 17.2 Length: 86439
Score: 96.50 Matches: 49
Percent Similarity: 46.63% Conservative: 34
Best Local Similarity: 27.53% Mismatches: 76
Query Match: 8.53% Indels: 20
DB: 3 Gaps: 7

US-10-757-745-2_COPY_54_273 (1-220) x US-09-949-016-11945 (1-86439)

QY 38 GluThrThrAspSerThrSerLysIleSerProSerGluAspThrGlnGluAsn 57
Db 28322 GAAGAACTGCATCACTAATGAGCAAAA-TGCCAGCTAACATCATATGACAGATCA 28264
QY 58 GlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSer 77
Db 28263 AATTCACATACATATTAATTAATTAATGA-----CTAAATTCGCAATT 28210
QY 78 GluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeu 97
Db 28209 AAAAGACACAGA---CTGGCAAGTTGGATAAAGAGTCAAGACCCATCAGTGTCTGTATT 28153
QY 98 GlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIle 117
Db 28152 CAGGAA-----ACTCATCTCACGTGCAGAGACACACATAGGCTCAAA 28111
QY 118 IleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLys 137
Db 28110 ATAAAGGATGGAGGAAGATCTACCAAGCCATGGAACCAACAAAAGGAGGCGGTGCA 28051
QY 138 LeuLysSerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCys 157
Db 28050 ATCTAGTCTCTGATAAAACAGACTTTAAACCAACAAAGATCAAAAGACACAAAGAGGC 27991
QY 158 ValHisValAsnValSerGlyAsn-----GluLeuCysLeuMetThrSerHis 173
Db 27990 CATTACATATGTAAGGGATCAATTCAACAGAGGAGCTAACTATCTCTAAATATTAT 27931
QY 174 LeuGluSerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLys 193
Db 27930 GCACCCAAATACA-----GGAGCACCAGATTC-----ATAAGCAAGTCTTGAGT 27886
QY 194 LysMetGlnGluAlaProGluSerAlaThrValIlePheAlaGlyAspThrAsn 211
Db 27885 GACCTACAAAGAGACTTAGACTCCCAACACATTAAATATG---GGAGACTTTTAAC 27835

RESULT 23
US-09-949-016-16990/c
Sequence 16990, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016

PATENT NO. 6900016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
AND USES THEREOF
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 673
LENGTH: 58111
TYPE: DNA
ORGANISM: Human
US-09-949-002-673

Alignment Scores:
Pred. No.: 9.15 Length: 58111
Score: 96.50 Matches: 49
Percent Similarity: 46.63% Conservative: 34
Best Local Similarity: 27.53% Mismatches: 76
Query Match: 8.53% Indels: 20
DB: 3 Gaps: 7

US-10-757-745-2_COPY_54_273 (1-220) x US-09-949-002-673 (1-58111)

QY 38 GluThrThrAspSerThrSerLysIleSerProSerGluAspThrGlnGluAsn 57
Db 39463 GAAGAACTGCATCACTAATGAGCAAAA-TGCCAGCTAACATCATATGACAGATCA 39405
QY 58 GlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSer 77
Db 39404 AATTCACATACATATTAATTAATTAATGA-----CTAAATTCGCAATT 39351
QY 78 GluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeu 97
Db 39350 AAAAGACACAGA---CTGGCAAGTTGGATAAAGAGTCAAGACCCATCAGTGTCTGTATT 39294
QY 98 GlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIle 117
Db 39293 CAGGAA-----ACCCATCTCACGTGCAGAGACACACATAGGCTCAAA 39252
QY 118 IleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLys 137
Db 39251 ATAAAGGATGGAGGAAGATCTACCAAGCCATGGAACCAACAAAAGGAGGCGGTGCA 39192
QY 138 LeuLysSerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCys 157
Db 39191 ATCTAGTCTCTGATAAAACAGACTTTAAACCAACAAAGATCAAAAGACACAAAGAGGC 39132
QY 158 ValHisValAsnValSerGlyAsn-----GluLeuCysLeuMetThrSerHis 173
Db 39131 CATTACATATGTAAGGGATCAATTCAACAGAGGAGCTAACTATCTCTAAATATTAT 39072
QY 174 LeuGluSerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLys 193
Db 39071 GCACCCAAATACA-----GGAGCACCAGATTC-----ATAAGCAAGTCTTGAGT 39027
QY 194 LysMetGlnGluAlaProGluSerAlaThrValIlePheAlaGlyAspThrAsn 211
Db 39026 GACCTACAAAGAGACTTAGACTCCCAACACATTAAATATG---GGAGACTTTTAAC 38976

RESULT 22
US-09-949-016-11945/c
Sequence 11945, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17367
; LENGTH: 102520
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17367

Alignment Scores:
Pred. No.: 22.5 Length: 102520
Score: 96.50 Matches: 49
Percent Similarity: 46.63% Conservative: 34
Best Local Similarity: 27.53% Mismatches: 76
Query Match: 8.53% Indels: 20
DB: 3 Gaps: 7

US-10-757-745-2_COPY_54_273 (1-220) x US-09-949-016-17367 (1-102520)
Qy 38 GluThrThrAspSerThrSerLysIleSerProSerGluAspThrGlnGlnGluAsn 57
Db 57481 GAAGAACTGCATCACTAATGACGAAAAA-TCACCAGCTAACATCAATGACAGGATCG 57423
Qy 58 GlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSer 77
Db 57422 AATTCAACATCAATTAATTAATTAATTAATGA-----CTAAATTCGCAATT 57369
Qy 78 GluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeu 97
Db 57368 AAAAGACACAGA---CTGGCAAGTTGGATAAAGAGTCAAGACCCATCAGTGTGTGATT 57312
Qy 98 GlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIle 117
Db 57311 CAGGAA-----ACCATCTCAGTCGACGAGACACACATAGGCTCAA 57270
Qy 118 IleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLys 137
Db 57369 ATAAAGAGTGGAGGAAGATCTACCAAGCCAAATGGAAAAACAAAAAGGCGGGGTTGCA 57210
Qy 138 LeuLysSerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLys 157
Db 57209 ATCTAGTCTCTGATAAAACAGACTTTTAAACCAAAAGATCAAAAGAGACAAAGAGGC 57150
Qy 158 ValHisValAsnValSerGlyAsn-----GluLeuCysLeuMetThrSerHis 173
Db 57149 CATTACATAATGGTAAAGGATCAATTCAACAGAGGAGGCTACTATCTCTAAATATTAT 57090
Qy 174 LeuGluSerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLys 193
Db 57089 GCACCCCAATACA-----GGAGCACCCAGATTC-----ATAAAGCAAGTCTCAGT 57045
Qy 194 LysMetGlnGluAlaProGluSerAlaThrValIlePheAlaGlyAspThrAsn 211
Db 57044 GACCTACAAAGAGACTTTAGACTCCACACATTAATAATG---GGAGACTTTTAAAC 56994

RESULT 25
US-09-949-016-12448/C
; Sequence 12448, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16990
; LENGTH: 86440
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16990

Alignment Scores:
Pred. No.: 17.2 Length: 86440
Score: 96.50 Matches: 49
Percent Similarity: 46.63% Conservative: 34
Best Local Similarity: 27.53% Mismatches: 76
Query Match: 8.53% Indels: 20
DB: 3 Gaps: 7

US-10-757-745-2_COPY_54_273 (1-220) x US-09-949-016-16990 (1-86440)
Qy 38 GluThrThrAspSerThrSerLysIleSerProSerGluAspThrGlnGlnGluAsn 57
Db 28322 GAAGAACTGCATCACTAATGACGAAAAA-TCACCAGCTAACATCAATGACAGGATCA 28264
Qy 58 GlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSer 77
Db 28263 AATTCAACATCAATTAATTAATTAATTAATGA-----CTAAATTCGCAATT 28210
Qy 78 GluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeu 97
Db 28209 AAAAGACACAGA---CTGGCAAGTTGGATAAAGAGTCAAGACCCATCAGTGTGTGATT 28153
Qy 98 GlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIle 117
Db 28152 CAGGAA-----ACTCATCTCAGTCGACGAGACACACATAGGCTCAA 28111
Qy 118 IleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLys 137
Db 28110 ATAAAGAGTGGAGGAAGATCTACCAAGCCAAATGGAAAAACAAAAAGGCGGGGTTGCA 28051
Qy 138 LeuLysSerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLys 157
Db 28050 ATCTAGTCTCTGATAAAACAGACTTTTAAACCAAAAGATCAAAAGAGACAAAGAGGC 27991
Qy 158 ValHisValAsnValSerGlyAsn-----GluLeuCysLeuMetThrSerHis 173
Db 27990 CATTACATAATGGTAAAGGATCAATTCAACAGAGGAGGCTACTATCTCTAAATATTAT 27931
Qy 174 LeuGluSerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLys 193
Db 27930 GCACCCCAATACA-----GGAGCACCCAGATTC-----ATAAAGCAAGTCTCAGT 27886
Qy 194 LysMetGlnGluAlaProGluSerAlaThrValIlePheAlaGlyAspThrAsn 211
Db 27885 GACCTACAAAGAGACTTTAGACTCCACACATTAATAATG---GGAGACTTTTAAAC 27835

RESULT 24
US-09-949-016-17367/c
; Sequence 17367, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/237,768
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; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14547
 ; LENGTH: 818128
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1)...(818128)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-14547

Alignment Scores:
 Pred. No.: 603 Length: 818128
 Score: 96.50 Matches: 49
 Percent Similarity: 46.63% Conservative: 34
 Best Local Similarity: 27.53% Mismatches: 76
 Query Match: 8.53% Indels: 20
 DB: 3 Gaps: 7

US-10-757-745-2_COPY_54_273 (1-220) x US-09-949-016-14547 (1-818128)

QY	38	GlutThrAspSerThrThrSerLysIleSerProSerGluAspThrGlnGluAsn	57
DB	402114	GAAGAAATGCATCACTAATGACAAA-TACCCAGCTAACATCATATGACAGATCA	402056
QY	58	GlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSer	77
DB	402055	AATTACACATACATATTAATTAATAATATGA-----CTAATTCGCAATT	402002
QY	78	GluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeu	97
DB	402001	AAAAGACACAGA---CTGGCAAGTTGGATAAAGAGTCAAGACCCATCAGTGTCTGTATT	401945
QY	98	GlnGluValIleProProTyrTyrSerTyrLeuLysArgSerSerAsnTyrGluIle	117
DB	401944	CAGGAA-----ACCCATCTCACGTGCAGACACACATAGGCTCAAA	401903
QY	118	IleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLys	137
DB	401902	ATAAAGGATGGAGGAGATCTACCAAGCAATGGAACAAACAAAAGGAGGGTTGCA	401843
QY	138	LeuLysSerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCys	157
DB	401842	ATCTAGTCTCTGATAAAGACAGACTTTAAACCAACAAAGATCAAAAGACAAAGAGGC	401783
QY	158	ValHisValAsnValSerGlyAsn-----GluLeuCysLeuMetThrSerHis	173
DB	401782	CATTACATATGTTAAAGGATCAATTCACAAAGAGGAGTAACTATCTCTAAATATTTAT	401723
QY	174	LeuGluSerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLys	193
DB	401722	GCACCAATATACA-----GGAGCACCCAGATTC-----ATAAGCAAGTCTTGAGT	401678
QY	194	LysMetGlnGluAlaProGluSerAlaThrValIlePheAlaGlyAspThrAsn	211
DB	401677	GACCTACAAAGAGACTTAGACTCCACACATTAATAATG---GGAGACTTTTAAC	401627

RESULT 30

US-09-949-016-14548/c
 ; Sequence 14548, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14548
 ; LENGTH: 818128
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1)...(818128)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-14548

Alignment Scores:
 Pred. No.: 603 Length: 818128
 Score: 96.50 Matches: 49
 Percent Similarity: 46.63% Conservative: 34
 Best Local Similarity: 27.53% Mismatches: 76
 Query Match: 8.53% Indels: 20
 DB: 3 Gaps: 7

US-10-757-745-2_COPY_54_273 (1-220) x US-09-949-016-14548 (1-818128)

QY	38	GlutThrAspSerThrThrSerLysIleSerProSerGluAspThrGlnGluAsn	57
DB	402114	GAAGAAATGCATCACTAATGACAAA-TACCCAGCTAACATCATATGACAGATCA	402056
QY	58	GlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSer	77
DB	402055	AATTACACATACATATTAATTAATAATATGA-----CTAATTCGCAATT	402002
QY	78	GluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeu	97
DB	402001	AAAAGACACAGA---CTGGCAAGTTGGATAAAGAGTCAAGACCCATCAGTGTCTGTATT	401945
QY	98	GlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIle	117
DB	401944	CAGGAA-----ACCCATCTCACGTGCAGACACACATAGGCTCAAA	401903
QY	118	IleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLys	137
DB	401902	ATAAAGGATGGAGGAGATCTACCAAGCAATGGAACAAACAAAAGGAGGGTTGCA	401843
QY	138	LeuLysSerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCys	157
DB	401842	ATCTAGTCTCTGATAAAGACAGACTTTAAACCAACAAAGATCAAAAGACAAAGAGGC	401783
QY	158	ValHisValAsnValSerGlyAsn-----GluLeuCysLeuMetThrSerHis	173
DB	401782	CATTACATATGTTAAAGGATCAATTCACAAAGAGGAGTAACTATCTCTAAATATTTAT	401723
QY	174	LeuGluSerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLys	193
DB	401722	GCACCAATATACA-----GGAGCACCCAGATTC-----ATAAGCAAGTCTTGAGT	401678
QY	194	LysMetGlnGluAlaProGluSerAlaThrValIlePheAlaGlyAspThrAsn	211
DB	401677	GACCTACAAAGAGACTTAGACTCCACACATTAATAATG---GGAGACTTTTAAC	401627

Search completed: December 4, 2005, 16:08:34
 Job time : 1937.73 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 00:41:46 ; Search time 4676.12 Seconds
(without alignments)
2201.217 Million cell updates/sec

Title: US-10-757-745-2_COPY_54_273

Perfect score: 1131

Sequence: 1 MERALNSYEPFPVESSALER.....SATVIFAGDTNLRDREVTTC 220

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Command line parameters:

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-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40 -cdd -LIST=500
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10757745 @CGN 1.1 8148 @runat 01122005_091749_10090 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1131	100.0	810	8	CX166335 HSEC2_39
2	1131	100.0	883	5	BU179107 AGENCOURT
3	1131	100.0	972	3	BM468826 AGENCOURT
4	1131	100.0	981	5	BX338160 BX338160
5	1131	100.0	1089	11	DQ049205 Homo sapi
6	1131	100.0	1168	4	CF601303 full-leng
7	1131	100.0	1620	4	CR592636 full-leng

8	1131	100.0	1894	4	CR597293 full-leng
9	1131	100.0	1909	4	CR595644 full-leng
10	1128	99.7	1067	5	BX337905 BX337905
11	1128	99.7	1081	5	BX444691 BX444691
12	1123	99.3	942	5	BX358707 BX358707
13	1123	99.3	1018	5	BX337141 BX337141
14	1123	99.3	1743	4	CR602029 full-leng
15	1120	99.0	846	7	CR765451 DKFZP469E
16	1120	99.0	1046	3	BM926092 AGENCOURT
17	1118	98.9	870	2	BG740396 602634171
18	1118	98.9	948	1	AL555333 AL555333
19	1115	98.6	883	5	BU169945 AGENCOURT
20	1114	98.5	1192	3	BM553049 AGENCOURT
21	1112	98.3	870	5	BU159911 AGENCOURT
22	1112	98.3	932	2	BG740339 602635289
23	1108	98.0	1089	11	DQ049206 Pan trogl
24	1102	97.4	904	5	BX422491 BX422491
25	1087	96.1	729	7	CN298924 170004244
26	1083	95.8	1090	7	CN641671 ILLUMIGEN
27	1077	95.2	757	3	BI760756 603044763
28	1076	95.1	710	5	BU661472 cl72d11.2
29	1072	94.8	1103	3	BM555041 AGENCOURT
30	1058	93.5	767	2	BI258848 602969663
31	1058	93.5	922	7	CN801806 ILLUMIGEN
32	1042.5	92.2	1035	3	BM554324 AGENCOURT
33	1037	91.7	783	5	BX365835 BX365835
34	1035	91.5	701	7	CR767236 DKFZP469E
35	1030	91.1	780	5	BX374579 BX374579
36	1018	90.0	906	6	CD251503 AGENCOURT
37	1009.5	89.3	838	3	BI908925 603067028
38	1005.5	88.9	927	2	BG119064 602347589
39	990	87.5	581	1	AV717253 AV717253
40	990	87.5	952	5	BX433489 BX433489
41	984	87.0	581	3	BP349936 BP349936
42	983	86.9	711	7	CN298923 170006000
43	975.5	86.3	858	3	BI553412 603193358
44	973	86.0	965	7	CN803230 ILLUMIGEN
45	970	85.8	729	7	CN298922 170006000
46	965.5	85.4	793	2	BG533717 602562373
47	950	84.0	583	3	BP262741 BP262741
48	946	83.6	816	1	AL516230 AL516230
49	933	82.5	704	3	BI334820 602998939
50	932	82.4	657	7	CN298920 170006001
51	930	82.2	570	3	BM172060 imagec 3
52	912.5	80.7	731	8	CX760857 AGENCOURT
53	904	79.9	752	1	AU139147 AU139147
54	904	79.9	937	2	BG541819 602569712
55	899	79.5	634	6	CB157906 K-EST0217
56	897	79.3	798	8	DN122208 1122397 M
57	896	79.2	739	7	CR791801 DKFZP468J
58	889	78.6	1087	7	CN642527 ILLUMIGEN
59	887	78.4	582	3	BP261141 BP261141
60	886	78.3	635	3	BM539358 hb08d09.9
61	883	78.1	581	3	BP270744 BP270744
62	883	78.1	581	3	BP379659 BP379659
63	877	77.5	581	3	BP207751 BP207751
64	875	77.4	583	7	CN789157 4123581 B
65	875	77.4	774	3	BI754101 603027659
66	873	77.2	573	3	BP261500 BP261500
67	869.5	76.9	853	3	BE784416 601473891
68	860	76.0	584	3	BP263059 BP263059
69	851	75.2	678	2	BG119113 602699045
70	847	74.9	570	3	BP221518 BP221518
71	845	74.7	573	3	BP221260 BP221260
72	845	74.7	576	3	BP262642 BP262642
73	840.5	74.3	908	2	BG391213 603417244
74	835	73.8	554	3	BP220985 BP220985
75	835	73.8	554	3	BP220508 BP220508
76	834	73.7	581	6	CB286391 CND36 C09
77	830	73.4	583	3	BP262103 BP262103
78	828	73.2	674	7	CN791432 4126159 B
79	820	72.5	582	3	BM507091 602401.9
80	804	71.1	786	2	BG719977 602691335

81	802	70.9	648	5	CF764797	CF764797	CBS003181	154	662	58.5	394	1	AV661333	AV661333
82	788	69.7	570	3	BP258309	BP258309	BP258309	155	659	58.3	577	1	AW964871	ES37376839
83	777	68.7	621	6	CB069952	CB069952	1s3le1o.Y	156	657.5	58.1	517	9	CC248786	XG1_CABE8
84	775	68.5	995	2	BB892886	BB892886	601435730	157	657.5	58.1	802	8	DN100293	JG1_CABE8
85	773	68.3	572	3	BP262485	BP262485	BP262485	158	657.5	58.1	946	5	BU468774	603371865
86	773	68.3	580	3	BP261787	BP261787	BP261787	159	657	58.1	617	7	CN694288	E0348E09-
87	772.5	68.3	799	8	CK756424	AGENCOURT	AGENCOURT	160	655	57.9	419	2	BP853399	MR3-EN008
88	771	68.2	581	3	BP262638	BP262638	BP262638	C 161	651	57.6	891	1	AL879624	AL879624
89	768	67.9	750	2	BI181461	UNL-P-PN-	UNL-P-PN-	C 162	651	57.6	909	5	EX780455	EX780455
90	766	67.7	491	1	AJ681912	AJ681912	AJ681912	163	650	57.5	973	1	AU279894	AU279894
91	766	67.7	581	3	BP262101	BP262101	BP262101	164	650	57.5	927	6	CA972607	AGENCOURT
92	766	67.7	634	7	CV023369	288_Full1	288_Full1	C 165	647.5	57.3	894	5	EX776016	EX776016
93	763	67.5	582	3	BP263516	BP263516	BP263516	166	645	57.0	583	3	BP319548	BP319548
94	758	67.0	456	2	BF996980	QV3-GN020	QV3-GN020	167	644	56.9	581	3	BP199948	BP199948
95	757	66.9	602	1	AL703449	DKF2p686G	DKF2p686G	168	639.5	56.5	879	8	CK824886	JG1_CAAK4
96	755	66.8	582	3	BP261789	BP261789	BP261789	169	635	56.1	688	2	BE189858	BE189858
97	755	66.8	915	3	BI915865	603184527	603184527	170	635	56.1	866	8	CK843565	JG1_CAAK1
98	754.5	66.7	652	7	CR753214	DKF2p4691	DKF2p4691	171	634	56.1	842	8	CK958091	JG1_CAAO9
99	750	66.3	568	3	BP257211	BP257211	BP257211	C 172	634	56.1	860	8	CK958090	JG1_CAAO9
100	749	66.2	440	2	BG982036	MR3-CN014	MR3-CN014	173	633	56.0	570	5	BU397611	603534313
101	743	65.7	440	2	BG982029	MR3-CN014	MR3-CN014	174	632.5	55.9	847	8	DR867246	JG1_CABG9
102	741	65.5	442	3	BQ315535	PM0-IT001	PM0-IT001	175	632	55.1	530	3	BM846221	K-EST0125
103	737	65.2	583	3	BP275810	BP275810	BP275810	176	630.5	55.7	685	7	CK981492	4114013_B
104	737	65.2	959	2	BI161201	602865659	602865659	177	629	55.6	638	1	AL901140	AL901140
105	731	64.6	534	7	CM298921	170005315	170005315	178	626.5	55.4	1077	5	BU131072	603116142
106	729	64.5	583	5	BU783229	in01a08.Y	in01a08.Y	179	626	55.3	583	3	BP195721	BP195721
107	728.5	64.4	644	2	BG083167	H3085C02-	H3085C02-	180	625	55.3	831	6	CA981008	CA981008
108	725	64.1	463	2	BF852284	MR3-EN008	MR3-EN008	C 181	623	55.1	467	3	BQ329405	MR3-EN008
109	724	64.0	582	3	BP270415	BP270415	BP270415	182	623	55.1	473	6	CB120234	CB120234
110	721	63.7	546	2	BG541031	602570190	602570190	183	616	54.5	654	1	AL895081	AL895081
111	719	63.6	441	2	BF893925	PM1-MT014	PM1-MT014	184	613.5	54.2	634	8	DN091361	JG1_CABE4
112	719	63.6	442	2	BF852788	MR3-EN008	MR3-EN008	185	608	53.8	750	8	CK135641	CK135641
113	715	63.2	577	7	CM298919	170006001	170006001	186	607	53.7	407	6	CB118797	CB118797
114	715	63.2	680	7	CK952220	4091710_B	4091710_B	187	607	53.7	889	1	AW199574	AW199574
115	709.5	62.7	444	2	BF893187	PM1-MT014	PM1-MT014	188	605.5	53.5	789	1	AW199574	da05f07.Y
116	709	62.7	749	7	CR767800	DKF2p469C	DKF2p469C	189	601	53.1	760	5	BU204728	604126221
117	705	62.3	626	2	BF977971	602148451	602148451	C 190	599	53.0	835	8	DR867245	JG1_CABG9
118	703	62.2	441	2	BF892415	PM1-MT014	PM1-MT014	C 191	598	52.9	493	1	AA163045	AA163045
119	701	62.0	582	3	BP219740	BP219740	BP219740	192	596.5	52.7	767	8	CK226137	MM011355
120	697	61.6	454	2	BG982031	MR3-CN014	MR3-CN014	C 193	591.5	52.3	453	2	BF773259	PM0-IT001
121	697	61.6	460	2	BF931150	PM1-MT014	PM1-MT014	194	587.5	51.9	645	5	BY737520	BY737520
122	697	61.6	565	3	BP226620	BP226620	BP226620	195	579.5	51.2	782	5	BU406549	BU406549
123	696	61.5	584	3	BP274942	BP274942	BP274942	196	578	51.1	485	1	AA486032	AA486032
124	694.5	61.4	458	3	CV366782	QV3-GN020	QV3-GN020	C 197	575	50.8	491	2	BI016235	BI016235
125	688.5	60.9	734	7	CV119018	AGENCOURT	AGENCOURT	198	574	50.8	662	2	BI067773	pgfin.pk0
126	688	60.8	581	3	BP225088	BP225088	BP225088	199	572.5	50.6	544	1	AA208842	mw73d02.r
127	684	60.5	770	2	BG498689	602544301	602544301	200	572.5	50.6	817	5	BU111103	603127011
128	683	60.4	413	3	BQ332322	MR4-ET014	MR4-ET014	C 201	572	50.6	435	3	BQ332331	MR4-ET014
129	681	60.2	459	2	BG982034	MR3-CN014	MR3-CN014	202	572	50.6	909	5	BU928818	AGENCOURT
130	681	60.2	582	3	BP233592	BP233592	BP233592	203	571.5	50.5	600	2	BI064472	pgfin.pk0
131	680	60.1	879	7	CK797649	AGENCOURT	AGENCOURT	204	565	50.0	876	7	CK798287	CK798287
132	680	60.1	909	6	CA982823	AGENCOURT	AGENCOURT	205	564	49.9	429	5	BQ582059	BQ582059
133	680	60.1	927	6	CA972288	AGENCOURT	AGENCOURT	206	564	49.9	480	1	AI750554	cn04a01.Y
134	680	60.1	984	5	EX846715	EX846715	EX846715	207	560	49.5	556	3	BP243301	BP243301
135	678	59.9	463	2	BF893919	PM1-MT014	PM1-MT014	208	560	49.5	671	3	BU622975	BU622975
136	678	59.9	584	3	BP348623	BP348623	BP348623	209	559.5	49.5	839	5	EX911124	EX911124
137	678	59.9	919	6	CA973696	AGENCOURT	AGENCOURT	210	554.5	49.0	525	2	BE290901	BE290901
138	675.5	59.7	456	3	BQ332321	MR4-ET014	MR4-ET014	211	552	48.8	558	5	EX258258	EX258258
139	675	59.7	900	6	CA980929	AGENCOURT	AGENCOURT	C 212	549	48.5	368	2	BE694706	BE694706
140	674	59.6	580	3	BP274368	BP274368	BP274368	213	549	48.5	484	5	BU338911	BU338911
141	674	59.6	770	2	BG391295	602417344	602417344	214	549	48.5	571	6	CB125492	CB125492
142	674	59.6	827	8	DN097147	JG1_CABE7	JG1_CABE7	215	549	48.5	640	6	CB505136	CB505136
143	673	59.5	582	3	BP234218	BP234218	BP234218	C 216	548.5	48.5	675	1	AL722584	AL722584
144	672	59.4	896	6	CA971409	AGENCOURT	AGENCOURT	217	547	48.4	625	5	BU471395	603363114
145	671.5	59.4	579	2	BF997052	QV3-GN020	QV3-GN020	218	543	48.0	1110	3	BM476771	AGENCOURT
146	671	59.3	471	2	BF893924	PM1-MT014	PM1-MT014	219	539	47.7	737	1	AV655175	AV655175
147	669	59.2	588	3	BP236074	BP236074	BP236074	C 220	535	47.3	737	3	BU639656	BU639656
148	668	59.1	644	3	BI333830	602999339	602999339	C 221	533	47.1	942	2	BG298330	602397112
149	667.5	59.0	1289	4	AK009089	Mus_muscul	Mus_muscul	C 222	531.5	47.0	422	2	BG982044	MR3-CN014
150	666	58.9	559	2	BE162174	IL2-HT044	IL2-HT044	C 223	531.5	47.0	431	7	BF768820	BF768820
151	665.5	58.8	447	2	BF8991509	PM1-MT014	PM1-MT014	C 224	530	46.9	471	7	CF543841	DKF2p4590
152	665	58.8	588	3	BP348796	BP348796	BP348796	225	529	46.8	580	3	BM503555	BM503555
153	664	58.7	650	2	BG431303	602499879	602499879	C 226	528	46.7	850	6	CF378639	AGENCOURT

227	527.5	46.6	751	2	BF243927	601877278	300	372.5	32.9	621	2	BF182465	BF192455	601804232
228	525	46.3	811	8	DN122554	1122781 M	301	370	32.7	615	3	BM425735	BM425735	pgf2c.pk0
229	524	46.3	891	3	BI648868	603275826	302	370	32.7	846	3	CNI75478	AGENCOURT	CNI75478
230	522.5	46.2	639	6	CB545297	AMGNNUC.N	303	369.5	32.7	424	4	AK180792	Mus muscu	AK180792
231	522	46.2	581	3	BI444674	G27d10.Y	304	368.5	32.6	682	10	C2905189	NAIStrap	C2905189
232	519	45.9	815	5	BU936308	AGENCOURT	305	367	32.4	892	5	BU309561	603539613	BU309561
233	519	45.9	857	7	BN017421	AGENCOURT	306	362.5	32.1	911	2	BF101875	601753033	BF101875
234	518.5	45.8	410	2	BG091909	mac18c11.	307	360	31.8	321	1	AA243535	z815f09.Y	AA243535
235	515	45.5	827	8	CV805216	AGENCOURT	308	360	31.8	614	2	BE188941	db561e10.X	BE188941
236	514.5	45.5	712	1	AL725543	AL725543	309	358	31.7	728	5	BU118538	603143186	BU118538
237	513	45.4	623	5	BU228796	603399341	310	350	30.9	826	5	BU943127	fu16b12.Y	BU943127
238	511	45.2	749	5	BF753763	BX753763	311	346	30.6	556	3	BM036121	fy36R04.Y	BM036121
239	505.5	44.7	461	2	BG982012	MR3-CN014	312	346	30.6	644	3	BM860342	u87b07.Y	BM860342
240	494.5	43.7	842	8	DN597142	AGENCOURT	313	345	30.5	552	2	BG148976	uu87b07.Y	BG148976
241	489	43.2	614	2	BG659251	NTSC.iV14	314	345	30.5	565	3	BP226464	BP226464	BP226464
242	489	43.2	841	2	BF784792	602111139	315	343	30.3	688	6	CF789017	B66258 MA	CF789017
243	488	43.1	841	2	BD562430	602581056	316	340	30.1	936	5	BY708937	8567208937	BY708937
244	486.5	43.0	1174	6	CD509260	CD495-D02	317	339.5	30.0	627	6	CB577890	AMGNNUC.N	CB577890
245	486	43.0	568	1	AL727624	AL727624	318	338	29.9	325	8	T31666	EST36732 Hu	T31666
246	482.5	42.7	718	4	CNS0B551	Tetraodon	319	338	29.9	699	1	AL722490	AL722490	AL722490
247	481	42.5	296	2	BP992136	QV3-GN020	320	336	29.7	834	7	CO795546	AGENCOURT	CO795546
248	479	42.4	963	3	BI656151	603283518	321	335	29.6	521	3	BJ079453	BJ079453	BJ079453
249	476	42.1	388	1	AV659558	AV659558	322	333	29.4	623	2	BG816763	dad67906.	BG816763
250	474	41.9	634	1	AL858410	AL858410	323	329	29.1	614	8	CN788690	4123052 B	CN788690
251	472	41.7	782	8	CX937111	JGI.CAA05	324	325	28.7	654	7	CK682762	Yae05908.	CK682762
252	469	41.5	640	1	AL854676	AL854676	325	325	28.7	860	2	CO918949	AGENCOURT	CO918949
253	464	41.0	1445	8	DN716144	CNB111-B0	326	322	28.5	833	2	BG573470	602595261	BG573470
254	462.5	40.9	1236	8	DN716145	CNB111-B0	327	320	28.3	574	3	BI345352	374149 MA	BI345352
255	456	40.3	578	1	AV602300	AV602300	328	319.5	28.2	827	5	BQ443284	UI-M-EV0-	BQ443284
256	454	40.1	463	8	DN851694	4147331 B	329	316	27.9	549	1	AM669835	113421 MA	AM669835
257	453	40.1	724	6	CB443087	693950 MA	330	313.5	27.7	600	2	BG800090	2112-54 M	BG800090
258	452	40.0	468	1	AA636415	Yq86D01.s	331	312	27.6	416	8	R14990	Yq45c11.r1	R14990
259	452	40.0	471	1	AA681654	vr43d12.s	332	311	27.5	652	8	W02878	za06a07.r1	W02878
260	447	39.5	898	2	BG623866	602649018	333	311	27.5	732	5	BX115672	BL115672	BX115672
261	443.5	39.2	838	7	CV482470	AGENCOURT	334	310	27.4	581	3	BP270589	BP270589	BP270589
262	442	39.1	327	1	AA690934	vr83e05.s	335	309	27.3	886	5	BU328780	603494664	BU328780
263	441.5	39.0	835	5	CX937110	JGI.CAA05	336	304	26.9	573	3	BP379251	BP379251	BP379251
264	437.5	38.7	736	5	EX306203	EX306203	337	298	26.3	365	7	CR767008	DXF2p469G	CR767008
265	437	38.6	310	8	T26956	ld155proJ	338	294	26.0	531	1	AA824213	VY20h08.r	AA824213
266	436	38.5	718	6	CB512714	sealfpB54	339	288	25.5	637	2	BF471995	UI-M-BH3-	BF471995
267	434	38.4	714	2	BG070243	H3085C02-	340	287	25.4	839	5	BU222688	603575804	BU222688
268	431	38.1	645	3	BM426270	pgf2n.pk0	341	284	25.1	534	7	CK838233	4063591 B	CK838233
269	428	37.8	252	1	AA325145	EST28102	342	282	24.0	156	3	BQ331200	MR4-ET014	BQ331200
270	426	37.7	708	5	EX780010	EX780010	343	271	24.0	464	5	BU788428	1181g10.Y	BU788428
271	425	37.6	581	3	BP264149	BP264149	344	266	23.5	194	2	BF992138	QV3-GN020	BF992138
272	424.5	37.5	765	7	CN042095	vr1.p41 a	345	261.5	23.1	247	2	BF768814	PMO-IT001	BF768814
273	423	37.4	961	2	BI150788	602914879	346	260.5	23.0	354	2	CG949698	RC4-BT062	CG949698
274	422	37.3	735	7	CV480860	AGENCOURT	347	259	22.9	666	7	CN789130	4123550 B	CN789130
275	422	37.3	754	6	CD053018	LITHZF000	348	258	22.8	581	2	BI067896	pgf1n.pk0	BI067896
276	420	37.1	647	1	AA536734	vj88b09.r	349	249.5	22.1	625	6	CD807796	UI-M-GW0-	CD807796
277	418	37.0	313	2	BF992133	QV3-GN020	350	248	21.9	790	2	BG502867	602550426	BG502867
278	416	36.8	811	7	CK693033	ZF101-P00	351	245.5	21.7	524	1	AV383388	603539613	AV383388
279	408.5	36.1	648	1	AW321603	u036b06.Y	352	245	21.5	655	8	CK034936	BM576902	CK034936
280	408.5	36.1	836	8	CX135661	AGENCOURT	353	243.5	21.5	425	6	CB696073	AMGNNUC.N	CB696073
281	408	36.1	608	7	CK966606	4081935 B	354	243	21.5	504	5	BM576902	BM576902	BM576902
282	407	36.0	391	3	EM784919	im09c09.Y	355	243	21.5	547	1	AA476073	va26906.r	AA476073
283	405	35.8	352	5	BQ787387	AGENCOURT	356	239	21.1	781	7	CV480876	AGENCOURT	CV480876
284	404.5	35.8	816	7	CK806777	AGENCOURT	357	233.5	20.6	587	1	AM608908	RC3-PT002	AM608908
285	402	35.5	691	7	CK798310	AGENCOURT	358	233.5	20.6	587	1	AM608952	RC3-PT002	AM608952
286	400	35.4	347	5	BU7070378	im09c09.X	359	231	20.4	478	1	AA168965	H0A48-1.G	AA168965
287	394	34.8	749	2	BF130513	601818647	360	229	20.2	409	2	BG900023	PM1-MT014	BG900023
288	393	34.7	655	3	BI449441	de28e09.X	361	227.5	20.1	155	2	BF893164	PM1-MT014	BF893164
289	391	34.6	304	2	BF992144	QV3-GN020	362	222.5	19.7	1453	4	AY814979	Schietobo	AY814979
290	390	34.5	250	1	AM794660	PMO-OT001	363	222	19.6	482	5	BU072078	ims4a02.Y	BU072078
291	389	34.4	548	3	BI449373	de27d10.X	364	221	19.5	577	9	BZ858137	C0240-232	BZ858137
292	384	34.0	640	3	BI449373	de27d10.X	365	221	19.1	707	5	BU418830	603958346	BU418830
293	383.5	33.9	712	2	BB609556	BB609556	366	215	19.0	149	3	BQ336306	PM1-MT014	BQ336306
294	382.5	33.8	600	3	BI990829	4081-88 M	367	215	19.0	277	1	AA647383	vg77b12.s	AA647383
295	380.5	33.6	1046	6	CA976386	AGENCOURT	368	214	18.9	541	6	CD321260	STcPu538	CD321260
296	378.5	33.5	703	5	BY119852	BY119852	369	212	18.7	748	2	BI224035	602942947	BI224035
297	374.5	33.1	531	7	CN233559	RJA113P02	370	211.5	18.7	625	6	CB190354	1235e10.Y	CB190354
298	373.5	33.0	615	6	CB579756	AMGNNUC.N	371	211	18.7	154	10	CG887267	RRS512 Ba	CG887267
299	373	33.0	467	6	CF788416	860364 MA	372	208.5	18.4	472	5	BU073441	ik63a06.Y	BU073441

c 373	208	18.4	733	10	CE536187	CE536187 tigr-g88-	446	126.5	11.2	858	8	DR817985	DR817985 ZM_BFB005
c 374	206	18.2	666	7	CO050979	CO050979 Le.mx0_21	447	126	11.1	1353	10	CL977639	CL977639 OSIFCC030
c 375	204	18.0	198	1	AL869566	AL869566 AL869566	448	125	11.1	520	6	CB220518	CB220518 LAB023A09
c 376	202.5	17.9	475	6	CB728877	CB728877 AMGNNUC:C	449	125	11.1	614	6	CB375256	CB375256 rx04e05.Y
c 377	202	17.9	121	7	CV572057	CV572057 od20e01.Y	450	124	11.0	455	2	BG737174	BG737174 rk67g08.Y
c 378	199	17.6	274	6	CD699206	CD699206 EST15729	451	123.5	10.9	633	7	CV003096	CV003096 aam01-14m
c 379	199	17.6	315	9	BZ837985	BZ837985 CH240_236	452	123	10.9	841	8	DR537955	DR537955 rs02753.C
c 380	199	17.6	729	7	CN778287	CN778287 pgn2c_pk0	453	121.5	10.7	561	7	CK564432	CK564432 wswpb0_00
c 381	197.5	17.5	740	1	AW097171	AW097171 rs40f010.Y	454	121.5	10.7	924	8	DR924013	DR924013 EST111555
c 382	196.5	17.4	853	11	CR149458	CR149458 Forward S	455	119.5	10.6	631	3	BN066897	BN066897 KS07019D1
c 383	193	17.1	684	3	BJ879891	BJ879891 BJ879891	456	119.5	10.6	882	8	DR935568	DR935568 EST112710
c 384	189	16.7	137	2	BF892413	BF892413 PM1-WT014	457	117.5	10.4	559	3	BI747771	BI747771 rxm44b05.Y
c 385	189	16.7	992	9	CC216952	CC216952 CH261-110	458	115.5	10.2	532	6	CB387482	CB387482 OSTF081B1
c 386	188	16.6	159	2	BF364316	BF364316 RC1-NN106	459	115	10.2	442	8	DN091360	DN091360 JGI_CABE4
c 387	186	16.4	875	2	BG529201	BG529201 602558273	460	115	10.2	517	11	DE122996	DE122996 Oryzias 1
c 388	185.5	16.4	711	8	DR407274	DR407274 mhn33d09	461	113	10.0	626	10	CE592495	CE592495 tigr-g88-
c 389	185	16.4	519	2	BB867803	BB867803 BB867803	462	111.5	9.9	813	8	DR924566	DR924566 EST111610
c 390	184	16.3	744	7	CN155540	CN155540 942844 MA	463	111.5	9.9	860	7	CV694952	CV694952 SJS_016_0
c 391	183	16.2	744	9	CE158280	CE158280 tigr-g88-	464	111	9.8	715	8	DR816705	DR816705 ZM_BFB004
c 392	179	15.8	444	10	AG204589	AG204589 Pan trogl	465	111	9.8	720	5	BR313039	BR313039 BW313039
c 393	176.5	15.6	560	3	BI501881	BI501881 rm06c12.Y	466	111	9.8	741	7	CO517714	CO517714 3530_1_11
c 394	174	15.4	641	2	BG977003	BG977003 602845553	467	111	9.8	767	8	DR968669	DR968669 ZM_BFB009
c 395	173	15.3	623	2	BF045278	BF045278 BP250008A	468	111	9.8	786	7	CO523018	CO523018 3530_1_15
c 396	171	15.1	136	1	AA213865	AA213865 zrx3h08.r	469	111	9.8	827	7	CV482523	CV482523 AGENCOURT
c 397	170	15.0	153	2	BF992130	BF992130 QV3-GN020	470	110.5	9.8	639	6	CA112710	CA112710 SCEQB106
c 398	162.5	14.4	809	8	CR863267	CR863267 SJS_016_0	471	110.5	9.8	880	9	BH207435	BH207435 Sm1-45M4
c 399	161	14.2	759	7	CA429123	CA429123 EST02352	472	110	9.7	410	5	BU408003	BU408003 603482066
c 400	160	14.1	647	5	BW052866	BW052866 BW052866	473	109	9.6	431	7	CK695369	CK695369 ZF101-P00
c 401	160	14.1	673	5	BW035002	BW035002 BW035002	474	108.5	9.6	376	1	AV203791	AV203791 Tetraodon
c 402	160	14.1	696	5	BW031213	BW031213 BW031213	475	108.5	9.6	1729	4	CNS0FLGZ	DR935567 EST112710
c 403	156.5	13.8	757	10	BX198893	BX198893 Danio rer	476	107.5	9.5	839	8	DR935567	DR935567 AV951030
c 404	153	13.5	304	2	BE619103	BE619103 601472729	477	107	9.5	505	1	AV951030	AV951030 AV951030
c 405	153	13.5	312	3	BMI53309	BMI53309 TCBAPIQ14	478	106.5	9.4	566	6	CD472549	CD472549 nad01-1ms
c 406	153	13.5	580	6	CA777140	CA777140 ip03f10.Y	479	106	9.4	865	8	DR781329	DR781329 BAAC-PMP1
c 407	153	13.5	582	3	BP194502	BP194502 BP194502	480	105.5	9.3	863	7	CK175928	CK175928 EST765248
c 408	153	13.5	587	1	AU015298	AU015298 AU015298	481	105.5	9.3	890	8	DR593316	DR593316 WS02616.B
c 409	153	13.5	722	2	BF679649	BF679649 602154095	482	105	9.3	317	1	AV413455	AV413455 AV413455
c 410	152	13.4	545	6	CB406887	CB406887 OSTR081B1	483	105	9.3	712	11	DE111858	DE111858 Oryzias 1
c 411	151.5	13.4	672	11	DE094838	DE094838 Oryzias 1	484	104.5	9.2	585	6	CB025685	CB025685 TGSTZYC8
c 412	149.5	13.2	456	1	AA839622	AA839622 vw97e06.r	485	104	9.2	311	7	CO539357	CO539357 ta31ze04.
c 413	149	13.2	684	5	BW033083	BW033083 BW033083	486	103.5	9.2	462	9	BH900556	BH900556 Octb00098
c 414	148	13.1	546	6	CB600618	CB600618 AGENCOURT	487	103.5	9.2	494	9	BR900557	BR900557 Octb00099
c 415	148	13.1	550	2	BG667432	BG667432 DRACLE09	488	103.5	9.2	584	3	BJ524578	BJ524578 BJ524578
c 416	146	12.9	1030	5	BU235217	BU235217 603791177	489	103.5	9.2	596	9	BH650868	BH650868 BOMIG54TF
c 417	145	12.8	537	7	CR774766	CR774766 DKF2p469A	490	103.5	9.2	651	5	BQ852542	BQ852542 QGB18E23.
c 418	144	12.7	570	6	CB188959	CB188959 ks27b06.Y	491	103.5	9.2	711	5	BQ995001	BQ995001 QGF8M14.Y
c 419	143	12.6	226	8	H34653	H34653 EST111757 R	492	103	9.1	367	5	BY067359	BY067359 BY067359
c 420	142	12.6	750	5	BU370465	BU370465 603595629	493	103	9.1	522	3	BJ882055	BJ882055 BJ882055
c 421	142	12.6	1282	4	CNS0ADRP	EX813905 Arabidops	494	103	9.1	533	3	BJ006584	BJ006584 BJ006584
c 422	141	12.5	1464	4	CNS0AAVU	EX815384 Arabidops	495	103	9.1	540	3	BJ001515	BJ001515 BJ001515
c 423	140	12.4	524	3	BP263000	BP263000 BP263000	496	103	9.1	600	3	BJ009618	BJ009618 BJ009618
c 424	139.5	12.3	746	2	BF140146	BF140146 601786704	497	103	9.1	615	3	BJ002736	BJ002736 BJ002736
c 425	138	12.2	743	5	BU337201	BU337201 603515540	498	103	9.1	617	3	BJ003192	BJ003192 BJ003192
c 426	137	12.1	563	8	DR003404	DR003404 TC114160	499	103	9.1	633	3	BJ005134	BJ005134 BJ005134
c 427	137	12.1	682	2	BE310128	BE310128 601092780	500	103	9.1	658	3	BJ010466	BJ010466 BJ010466
c 428	136.5	12.1	352	6	CB780491	CB780491 AMGNNUC:N							
c 429	136.5	12.1	730	7	CV756544	CV756544 sj16-010							
c 430	136	12.0	510	9	BH900534	BH900534 Octb00076							
c 431	134.5	11.9	672	1	AJ500568	AJ500568 AJ500568							
c 432	134	11.8	297	2	BF170990	BF170990 PCL1883 M							
c 433	134	11.8	545	9	BH900879	BH900879 Octb00221							
c 434	133.5	11.8	1497	10	CL979153	CL979153 OSIFCC032							
c 435	132	11.7	134	3	BJ061261	BJ061261 BJ061261							
c 436	132	11.7	750	3	BI559000	BI559000 603241366							
c 437	130	11.5	915	3	BP135431	BP135431 BP135431							
c 438	130	11.5	934	5	BA22490	BA22490 BX422490							
c 439	128	11.3	646	7	CO525830	CO525830 3530_1_17							
c 440	128	11.3	723	7	CV740501	CV740501 SJAL_027							
c 441	128	11.3	735	8	DR823742	DR823742 ZM_BFB006							
c 442	128	11.3	738	8	DR817895	DR817895 ZM_BFB005							
c 443	128	11.3	848	8	DR811846	DR811846 ZM_BFB004							
c 444	127.5	11.3	808	8	DN932266	DN932266 AGENCOURT							
c 445	126.5	11.2	844	7	CV698876	CV698876 SJS_041_7							

ALIGNMENTS

RESULT 1

CX166335

LOCUS

DEFINITION

HES2C_39_B09_gl_A035 NIH_MGC_258 Homo sapiens CDNA clone

IMAGE:7469923 5', mRNA sequence.

ACCESSION

CX166335

VERSION

CX166335.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1 (bases 1 to 810)

810 bp mRNA linear EST 23-DEC-2004

HES2C_39_B09_gl_A035 NIH_MGC_258 Homo sapiens CDNA clone

IMAGE:7469923 5', mRNA sequence.

CX166335

CX166335.1

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 810)

Alignment Scores:

Pred. No.: 3,59e-124 Length: 883
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x BU179107 (1-883)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
DB 18 ATGGAAGGGCTCTGAATCTCTACTTCGAGCCTCCGGTGGAGGAGCGCTTGGAAAGC 77
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
DB 78 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 137
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnAsnGlySerMet 60
DB 138 GATTCACCATCTCTAATACGCCCATCTGAAGTACTCAGCAGAAATATGGCAGCATG 197
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 198 TTCTCTCTCATTTACCTGGAATATTGATGATTAGATCTAAACAATCTGTGACAGAGGCT 257
QY 81 ArgGlyValCysSerTyrIleuAlaLeuTyrSerProAspValIlePheLeuGlnVal 100
DB 258 CGAGGGGTGTGTTCTCTACTTGTACAGCCAGATGTGATATTTCTACAGGAAGTT 317
QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleThrGly 120
DB 318 ATCCCCCATATTATAGCTTACCTAAGAGAGATCAAGTAATTATGAGATTATACAGT 377
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
DB 378 CATGAAGAAGGATATTTACACGCTATATGTTGAAGAAATCAAGAGTGAATTAAGAAAGC 437
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysValHisVal 160
DB 438 CAAGAGATTATTTCTCTTCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 497
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerArgGlyHis 180
DB 498 AACGTGTACGAAATAGAGCTTTGCTTATGACATCCATTTGAGAGACACAGAGGCTAT 557
QY 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
DB 558 GCTGCGGAACGAATGAATCAGTTAAATGTTTAAAGAAATGCAAGAGGCTCCAGAG 617
QY 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
DB 618 TCAGCTACAGTTATATTTGACGAGATACAAATCTAAGGGATCGAGAGGTACCAAGATGT 677

RESULT 3

BM468826
LOCUS BM468826 972 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOURT 6445782 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5587154
5', mRNA sequence.

ACCESSION BM468826
VERSION BM468826.1 GI:18517868
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 972)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: L1AM12356 row: d column: 03
High quality sequence stop: 707.

FEATURES

source Location/Qualifiers

1..972
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/clone="IMAGE:5587154"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"

/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 4,14e-124 Length: 972
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x BM468826 (1-972)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
DB 55 ATGGAAGGGCTCTGAATCTCTACTTCGAGCCTCCGGTGGAGGAGCGCTTGGAAAGC 114
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
DB 115 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 174
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnAsnGlySerMet 60
DB 175 GATTCACCATCTCTAATCAAGTACTCAGCAGAAATATGGCAGCATG 234
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 235 TTCTCTCTCATTTACCTGGAATATTGATGATTAGATCTAAACAATCTGTGACAGAGGCT 294
QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
DB 295 CGAGGGGTGTGTTCTCTACTTACAGTGTGATGATGATGATGATGATGATGATGATGAT 354
QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleThrGly 120
DB 355 ATTCCTCCATATTATAGCTTACCTAAGAAAGAGATCAAGTAATTATGAGATTATTACAGGT 414
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
DB 415 CATGAAGAAGGATATTTCAAGCTATATGTTGAAGAAATCAAGAGTGAATTAAGAAAGC 474
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysValHisVal 160
DB 475 CAAGAGATTATTTCTCTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 534
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
DB 535 AACGTGTACGAAATAGAGCTTTGCTTATGACATCCCATTTGGAGAGACACAGAGGCTAT 594
QY 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200

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Db      595 GCTCGGAACGAATGATCAGTTAAAAATGGTTTTGAAGAAAAATGCAAGAGGCTCCAGAG 654
Qy      201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db      655 TCAGCTACAGTTATATTTCGAGGAGATACAAATCTTAAGGGATCGAGAGGTTACCAAGATGT 714

RESULT 4
LOCUS   BX338160
DEFINITION BX338160 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1056YC23 5-PRIME, mRNA sequence.
ACCESSION BX338160
VERSION   BX338160.2 GI:46283046
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 981)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 2, 2003 this sequence version replaced gi:30345671.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1056AB12QP1&c=3474.r.

FEATURES
Source Location/Qualifiers
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/db_xref="taxon:9606"
/clone="CS0D1056YC23"
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/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 4.2e-124 Length: 981
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x BX338160 (1-981)
Qy      1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db      173 ATGGAAAGGGCTCTGAATCTCTACTTCGAGCTCCGGTGGAGGAGCGCTTGGAAACGC 232
Qy      21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db      233 CGACCTGAACACCATCTCTGAGCCCAACAGCCTATGTTGACCTTACCATGAGAAACAACT 292
Qy      41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db      293 GATTCCACCACTTCTAAATACAGCCCATCTGAAGATACCTCAGCAAGAAAATGGCAGCATG 352
Qy      61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
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Db      353 TTCTCTCTCAATTACCTGGAATATTGATGGATTAGATCTAAACAATCTGTGCAGAGGGCT 412
Qy      81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db      413 CGAGGGGGTGTGTCTTACTTACCTTGTACAGCCAGATGTGATATTTCTACAGGAAGTT 472
Qy      101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db      473 ATTCCCCCATATTATAGCTACTTAAGAAGAGATCAAGTAAATTATGAGATTTATTACAGGT 532
Qy      121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db      533 CATGAAGAAGGATATTTCACAGCTATAATTGTTGAAGAAAATCAAGAGTGAATAATAAAGC 592
Qy      141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db      593 CAAGAGATTTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGCAATGTG 652
Qy      161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db      653 AATGTGTACGGAATAGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCACCAGAGGCGCAT 712
Qy      181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db      713 GCTCGGGAACGAATGAATCAGTTAAAAATGGTTTAAAGAAAATGCAAGAGGCTCCAGAG 772
Qy      201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db      773 TCAGCTACAGTTATATTTTCAGGAGATACAAATCTAAGGGATCGAGAGGTTACCAAGTGT 832
RESULT 5
LOCUS   DQ049205
DEFINITION Homo sapiens TTRAP gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ049205
VERSION   DQ049205.1 GI:66902404
KEYWORDS GSS.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1089)
AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civallo, D.,
White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 1089)
AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civallo, D.,
White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
FEATURES
Source Location/Qualifiers
1..1089
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
<1..>1089
/genes="TTRAP"
/locus_tag="HC17203"

ORIGIN
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Alignment Scores:

Pred. No.: 4_91e-124 Length: 1089
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x DQ049205 (1-1089)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 160 ATGGAAGGGCTCTGAACCTCTTACCTTCGAGCCTCGGTGGAGGAGCGCTTGGAAAGC 219
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 220 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAAC 279
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnAsnGlySerMet 60
Db 280 GATTCACACACTTCTAAATACGCCCTCTGAAGATACTCAGCAAGAAAATGGCAGCATG 339
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 340 TTCTCTCTCATTTACCTGGAATATTGATGGATTAGATCTTAAACAATCTCTCAGAGAGG 399
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 400 CGAGGGGTGTGTTCTCTACTTACCTTGTACAGCCAGATGTGATATTTCTACAGGAAG 459
Qy 101 IleProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 460 ATTCCCATATTATAGCTACTCTAAGAAGAGATCAAGTAATATGAGATTTATACAGGT 519
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLeuLysSer 140
Db 520 CATGAAGAAGGATATTTCACAGCTATATGTTGAAGAAATCAAGAGTGAATTTAAAGAG 579
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db 580 CAAGAGATATTCTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 639
Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 640 AACGTGTGAGGAATAGAGCTTTGCCCTTTATGACATCCCATTTGGAGAGCACCAGAGG 699
Qy 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 700 GCTGCGGAACGAATCAATCAGTTAAATAATGGTTTTTAAAGAAAATGCAAGAGGCTCC 759
Qy 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 760 TCAGCTACAGTTATATTTGCAGGAGATACAAATCTTAAGGGATCGAGAGGTTACCAGAT 819

RESULT 6

LOCUS CR601303 1168 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSODN005YN02 of Adult brain of Homo sapiens (human).

ACCESSION CR601303

VERSION CR601303.1 GI:50482110

KEYWORDS HTC; CNSLT; cDNA.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 1168)

REFERENCE

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600

REFERENCE

AUTHORS 2 (bases 1 to 1168)

TITLE Genoscope.

JOURNAL Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)

COMMENT - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES

source

1..1168 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODN005YN02"
/tissue_type="Adult brain"
/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:

Pred. No.: 5_46e-124 Length: 1168
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x CR601303 (1-1168)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 185 ATGGAAGGGCTCTGAACCTCTTACCTTCGAGCCTCGGTGGAGGAGCGCTTGGAAAGC 244
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 245 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAAC 304
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnAsnGlySerMet 60
Db 305 GATTCACACACTTCTAAATACGCCCTCTGAAGATACTCAGCAAGAAAATGGCAGCATG 364
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 365 TTCTCTCTCATTTACCTGGAATATTGATGGATTAGATCTTAAACAATCTCTCAGAGAG 424
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 425 CGAGGGGTGTGTTCTCTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAG 484
Qy 101 IleProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 485 ATTCCCATATTATAGCTACTCTTAAAGAAGAGATCAAGTAATATGAGATTTATACAGGT 544
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLeuLysSer 140
Db 545 CATGAAGAAGGATATTTTACAGCTATAATGTTGAAGAAAATCAAGAGTGAATTTAAAGAG 604
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db 605 CAAGAGATATTCTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 664
Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 665 AACGTGTGAGGAATAGAGCTTTGCCCTTATGATCATCCCATTTGGAGAGCACCAGAGG 724
Qy 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 725 GCTGCGGAACGAATGAATCAGTTAAAAATGGTTTTTAAAGAAAATGCAAGAGGCTCCAG 784
Qy 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220


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Db 785 TCAGCTACAGTTATATTCGAGGAGATACAAATCTTAGGGATCGAGAGGTTACCAAGTCT 844
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RESULT 7
CR592636 1620 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DM007YE11 of Fetal liver of Homo sapiens
DEFINITION (human).
ACCESSION CR592636
VERSION 1 GI:50473443
KEYWORDS HTC; CNSLT.CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1620)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1620)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES Location/Qualifiers
source 1..1620
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM007YE11"
/tissue_type="Fetal liver"
/plasmid="pCMVSPORT_6"
ORIGIN
Alignment Scores: 8.91e-124 Length: 1620
Pred. No.: 1131.00 Matches: 220
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 4
US-10-757-745-2_COPY_54_273 (1-220) x CR592636 (1-1620)
Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 103 ATGGAAGGGCTCTGAATCTCTACTTCGAGCTCCGGTGGAGGAGCGCTTGGAAACG 162
Qy 21 ArgProGluThrIleSerGluProValGluThrTyrValAspLeuThrAsnGluGluThr 40
Db 163 CGACCTGAAACCACTCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACT 222
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 223 GATTCACCACTTCTAAATCAGCCCATCTGAAGATACTCAGCAAGAAATGGCAGCATG 282
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 283 TTCTCTCTACCTGGAATATTGATGGATTAGATCTAAACAATCTGTCTCAGAGAGGGCT 342
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 343 CGAGGGGTGTGTTCTTACTTACGCTTTGTACAGCCCAAGATGATATTCTTACAGGAAGTT 402
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Qy 101 IleProProTyrTyrSerTyrLeuLysLysValSerSerAsnTyrGluIleIleThrGly 120
Db 403 ATTCCCCCATATATAGCTACCTAAGAAGAGAGATCAAGTAATATGAGATTATTACAGGT 462
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 463 CATGAAGAAGAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAAGAAC 522
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db 523 CAAGAGATTATTCTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTG 582
Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 583 AACTGTCTAGGAATAGAGCTTTGCCTTATGACATCCATTTGGAGAGCACCAGAGGGCAT 642
Qy 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 643 GCTGGGAACGAATGAATCAGTTAAAAATGGTTTTAAAGAAATGCAAGAGGCTCCAGAG 702
Qy 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspGluValThrArgCys 220
Db 703 TCAGCTACAGTTATATTTTCAGGAGATACAAATCTTAAGGATCGAGAGGTTACCAAGTGT 762
RESULT 8
CR597293 1894 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DK007YK05 of Hela cells Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR597293
VERSION 1 GI:50478100
KEYWORDS HTC; CNSLT.CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1894)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1894)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES Location/Qualifiers
source 1..1894
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK007YK05"
/tissue_type="Hela cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Alignment Scores: 1.13e-123 Length: 1894
Pred. No.: 1131.00 Matches: 220
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 4
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US-10-757-745-2_COPY_54_273 (1-220) x CR597293 (1-1894)

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QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluSerAlaLeuGluArg 20
Db 178 ATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCGGTGGAGAGAGCGCTTGAAGCG 237
QY 21 ArgProGluThrIleSerGluProLysThrValAspLeuThrAsnGluThrThr 40
Db 238 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 297
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 298 GATTCACACCTCTCTAAAATCAGCCCATCTGAAGTACTCAGCAAGAAATGCGACGATG 357
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 358 TTCTCTCTCATTTACCTGGGAATATTGATGATTTAGATCTAAACAATCTGTGACAGAGGG 417
QY 81 ArgGlyValCysSerTyrIleuAlaLeuTyrSerProAspValIlePheIleuGlnGluVal 100
Db 418 CGAGGGGTGTCTCTACTTGTACAGCCAGATGTCATATTCTTACAGGAAGTT 477
QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 478 ATTCCTCCCATNTATATAGCTTACCTAAGAAGAGATCAAGTAATATGAGATTTACAGGT 537
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 538 CATGAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAGC 597
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysValHisVal 160
Db 598 CAAGAGATTTATTCCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTGATG 657
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 658 AACGTGTGAGGAATAGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCACAGAGGGCAT 717
QY 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 718 GCTGGGAACGAATGAATCAGTTAAAAATGGTTTAAAGAAATGCAAGAGGCTCCAGAG 777
QY 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 778 TCAGCTACAGTTATATTTCAGAGATACAAATCTAAGGGATCGAGAGGTTACAGATGT 837
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RESULT 9
CR595644LOCUS full-length cDNA clone CS0D1052YN13 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).

ACCESSION CR595644

VERSION CR595644.1 GI:50476451

KEYWORDS HTC; CNSLT; cDNA.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 1909)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Paradise Avenue

2 (bases 1 to 1909)

Genoscope.

REFERENCE

AUTHORS

TITLE Direct Submission

JOURNAL

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- web : www.genoscope.cns.fr)

COMMENT

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ScaI V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

Location/Qualifiers

source

1..1909
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1052YN13"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:

Pred. No.: 1.14e-123 Length: 1909

Score: 1131.00 Matches: 220

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x CR595644 (1-1909)

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QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluSerAlaLeuGluArg 20
Db 184 ATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCGGTGGAGAGAGCGCTTGAAGCG 243
QY 21 ArgProGluThrIleSerGluProLysThrValAspLeuThrAsnGluThrThr 40
Db 244 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 303
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 304 GATTCACACCTCTCTAAAATCAGCCCATCTGAAGTACTCAGCAAGAAATGCGACGATG 363
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 364 TTCTCTCTCATTTACCTGGGAATATTGATGATTTAGATCTAACAATCTGTGACAGAGGG 423
QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 424 CGAGGGGTGTCTCTACTTACAGTCTTGTACAGCCAGATGTCATATTCTTACAGGAAGTT 483
QY 101 IleProProTyrTyrSerTyrIleuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 484 ATTCCTCCCATNTATATAGCTTACCTAAGAAGAGATCAAGTAATATGAGATTTACAGGT 543
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 544 CATGAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAGC 603
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysValHisVal 160
Db 604 CAAGAGATTTATTCCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTGATG 663
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 664 AACGTGTGAGGAATAGAGCTTTGCCCTTATGACATCCCATTTTGGAGAGCACAGAGGGCAT 723
QY 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 724 GCTGGGAACGAATGAATCAGTTAAAAATGGTTTAAAGAAATGCAAGAGGCTCCAGAG 783
QY 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 784 TCAGCTACAGTTATATTTCAGAGATACAAATCTAAGGGATCGAGAGGTTACAGATGT 843
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RESULT 10

BX337905

LOCUS

DEFINITION

Homo sapiens PLACENTA Cot 25-NORMALIZED Homo sapiens cDNA
BX337905 mRNA linear EST 07-APR-2004
BX337905

clone CS0D1052YN13 5-PRIME, mRNA sequence.

ACCESSION BX337905
VERSION BX337905.2 GI:46273926
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1067)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 2, 2003 this sequence version replaced gi:30339657.
Contact: Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1052CG07QP1&c=3474.r.

FEATURES
source
1. .1067
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1052YN13"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 1,09e-123 Length: 1067
Score: 1128.00 Matches: 219
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.55% Mismatches: 0
Query Match: 99.73% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x BX337905 (1-1067)

Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 184 ATGAAAGGGCTCTGAACCTCTACTCGAGCCTCCGGTGGAGGAGCGCTTGGAAACGC 243
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAenGluGluThr 40
Db 244 CGACCTGAAACCACTCTCTGAGCCCAACACCTATGTCCTAACCAATGAGAAACAACT 303
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAenGlySerMet 60
Db 304 GATTCCACCACTTCTTAATTCAGCCCATCTGAAGATACTCAGCAAGAAATGGCAGCATG 363
Qy 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAenAenLeuSerGluArgAla 80
Db 364 TTCTCTCTCATTCCTGGAATATTGATTAGATCTAAACAATCTGTCTCAGAGGGCT 423
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 424 CGAGGGGTGTCTCTCTACTTACCTTTGTACAGCCCGAGATGTGATATTCTACAGGAAGTT 483
Qy 101 IleProTyrTyrSerTyrLeuLysIleArgSerSerAenTyrGluIleIleThrGly 120
Db 484 ATTCCCCCATATTATAGTCTACCTAAAGAAGAGATCAAGTATTATGATTATTACAGGT 543

QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 544 CATGAAGAGGATATTTTCACGCTATAATGTTTGAAGAAATCAAGAGTGAATTTAAAGAGC 603
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db 604 CAAGAGATTATTTCTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCATGTG 663
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 664 AATGTGTGAGGAATGAGCTTTGCCCTTATGACATCCATTTGGAGAGCACCAGAGGGCAT 723
QY 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysMetGlnGluAlaProGlu 200
Db 724 GCTCGGAACGAATGAATCAGTTAAAAATGGTTTAAAGAAATGGAAGAGGCTCCAGAG 783
QY 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 784 TCAGCTACAGTTATATTTCAGGAGATACAAATCTAAGGGATCGAGAGGTTACCAGATGT 843

RESULT 11

BX444691 1081 bp mRNA linear EST 04-MAY-2004
LOCUS BX444691 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
DEFINITION CS0DN005YN02 5-PRIME, mRNA sequence.
ACCESSION BX444691
VERSION BX444691.2 GI:47009162
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 1081)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 15, 2003 this sequence version replaced gi:30780264.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DN005DG01QP1&c=3474.r.

FEATURES
source
1. .1081
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DN005YN02"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Alignment Scores:
Pred. No.: 1,11e-123 Length: 1081
Score: 1128.00 Matches: 219
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.55% Mismatches: 0
Query Match: 99.73% Indels: 0

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DB: 5 Gaps: 0
US-10-757-745-2_COPY_54_273 (1-220) x BX444691 (1-1081)
QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
DB 186 ATGGAAGGGCTCTGAACCTCTTACCTTCGAGCCCTCGGTGGAGGAGCGCTTGGAAACGC 245
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
DB 246 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 305
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 306 GATTCACACCTCTTAAATCATGCCCCATCTGAAGATACCTCAGCAGAAAATGGCAGCAIG 365
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 366 TTCTCTCTCATTCACCTGGAATATTGATGATTAAGATCTAAACAATCTGTGAGAGGGCT 425
QY 81 ArgGlyValCysSerTyrIleuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
DB 426 CGAGGGGTGTGTTCTTACTTGTACAGCCAGATGTGATATTCTTACAGGAAGTT 485
QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleThrGly 120
DB 486 ATTCCCCCATATTATAGCTTACCTTAAGAAGAGATCAAGTAATTATGAGATTATTACAGGT 545
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
DB 546 CATGAAGAAGGATATTTCACAGCTATATGTTGAAGAAATCAAGAGTGAATTAAGAAC 605
QY 141 GlnGluIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
DB 606 CAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 665
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
DB 666 AATGTGTGAGGAATATGAGCTTTGCTTATGACATCCCATTTGGAGAGCACCAGAGGGCAT 725
QY 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
DB 726 GTCTGGGAACGATGATGATCAATCAATGATGATGATGATGATGATGATGATGATGATG 785
QY 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
DB 786 TCAGCTACAGTTATATTTGCAGGAGATACAAATCTTAAGGGATCGAGAGGTTACCAAGATGT 845

RESULT 12
BX358707 942 bp mRNA linear EST 08-APR-2004
LOCUS BX358707 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSOD1042YL19 5-PRIME, mRNA sequence.
ACCESSION BX358707
VERSION BX358707.2 GI:46306560
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 942)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30378261.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefgenoscope.cns.fr, web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
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was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3474.r

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?b=CSOD1042CF10QPI&c=3474.r>.

Location/Qualifiers
1. 942
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1042YL19"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 3.58e-123 Length: 942
Score: 1123.00 Matches: 218
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.54% Mismatches: 0
Query Match: 99.29% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x BX358707 (1-942)

QY 2 GluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 21
DB 32 CAGAGGGCTCTGAACCTCTTACTTCGAGCTCGGTGGAGGAGCGCTTGGAAACCGCA 91
QY 22 ProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThrAsp 41
DB 92 CCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACATGAT 151
QY 42 SerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPhe 61
DB 152 TCCACCACTTCTAAATCAGCCCATCTGAAGATACTCAGCAAGAAAATGGCAGCATGTC 211
QY 62 SerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArg 81
DB 212 TCTCTCATCTGGAATATTGATGATTAAGATTAATCTTAACAATCTGTGAGAGGGCTCGA 271
QY 82 GlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIle 101
DB 272 GGGGTGTGTCTCTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATT 331
QY 102 ProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGlyHis 121
DB 332 CCCCATTATTTAGCTACCTAAAGAGAGATCAAGTAATTTATGAGATTATTACAGGTCA 391
QY 122 GluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGln 141
DB 392 GAAGAAGGATATTTCAGACTATAATGTTGAAGAAATCAAGATGGAATTAAGAAAGCCNA 451
QY 142 GluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsn 161
DB 452 GAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTAAT 511
QY 162 ValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAla 181
DB 512 GTGTGAGAAATGAGCTTTTGCCTTATGACATCCCCATTTGGAGAGCACCAGAGGGCATGCT 571
QY 182 AlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGluSer 201
DB 572 GCGGAACGAATGAATCAGTTAAAAATGGTTTTTAAAGAAAATGCAAGAGGCTCCAGAGTCA 631
QY 202 AlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
DB 632 GCTACAGTTATATTTCAGGAGAGATACAAATCTTAAGGGATCGAGAGGTTTACCAGATGT 688

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RESULT 13
BX337141
LOCUS
DEFINITION
  BX337141 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
  clone CS0D1036VJ02 5-PRIME, mRNA sequence.
ACCESSION
  BX337141
VERSION
  BX337141.2 GI:462711144
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homiidae; Homo.
REFERENCE
  1 (bases 1 to 1018)
  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  Full-length cDNA libraries and normalization
  Unpublished (2001)
COMMENT
  On May 2, 2003 this sequence version replaced gi:30337585.
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
  Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
  1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
  end enriched, double-strand cDNA was digested with Not I and cloned
  into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
  was normalized. Library was constructed by Life Technologies, a
  division of Invitrogen. This sequence belongs to sequence cluster
  3474.r
  For more information about this cluster, see
  http://www.genoscope.cns.fr/cdna?s=CS0D1036VJ02&p1&c=3474.r.
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    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0D1036VJ02"
    /tissue_type="PLACENTA COT 25-NORMALIZED"
    /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
    /notes="1st strand cDNA was primed with a NotI-oligo(dT)
    primer. Five prime end enriched, double-strand cDNA was
    digested with Not I and EcoR V sites of the pCMVSPORT 6
    vector. Library was normalized."
ORIGIN
Alignment Scores:
Pred. No.: 4,02e-123 Length: 1018
Score: 1123.00 Matches: 218
Percent Similarity: 99.55% Conservative: 1
Best Local Similarity: 99.09% Mismatches: 1
Query Match: 99.29% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x BX337141 (1-1018)

Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluSerAlaLeuGluArg 20
Db 150 ATGGAAAGGGCTCTGAATCTCTACTTCGAGCTCCGGTGGAGGAGCGCTTGGAAACG 209

Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
Db 210 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTACCATTGAGAAACAACT 269

Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 270 GATTCACCACTCTTAAATCAGCCCATCTGAGATATCTCAGCAAGAAATGGCAGCATG 329

Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 330 TTCTCTCTCAATACCTGAATATTGATGATTAATCTAAACAACTTGTCTGAGAGGGCT 389

Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 390 CGAGGGGTGTGTTCTTACTTACCTTTGTACAGCCAGCATGTGATATTCTTACAGGAATT 449

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Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 450 ATTCCCCCATATTATAGCTTACCTAAGAAGAGAGATCAAGTAATATGAGATTATTACAGGT 509

Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 510 CATGAAGAGAGATATTTCACAGCTATAATGTTTGAAGAAATCAAGAGTGAATTAAGAACG 569

Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db 570 CAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTG 629

Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 630 AATGTGTCAAGAAATGAGCTTTGCTTATGACATCCATTTGAGAGAGCAACAGAGGCGCAT 689

Qy 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 690 GCTCGGAAGAATGAATCAGTTAAATGGTTTAAAGAAATGGAAGAGGCTCCAGAG 749

Qy 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 750 TCAGCTACAGTTATATTTCAGAGAGATACAAATCTAAGGATCGAGAGGTTTACCATGT 809

RESULT 14
CR602029 1743 bp mRNA linear HTC 21-JUL-2004
LOCUS
DEFINITION
  full-length cDNA clone CS0D1042YL19 of Placenta Cot 25-normalized
  of Homo sapiens (human) .
ACCESSION
  CR602029
VERSION
  CR602029.1 GI:50482836
KEYWORDS
  HTC; CNSLT cDNA.
SOURCE
  Homo sapiens
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homiidae; Homo.
REFERENCE
  1 (bases 1 to 1743)
  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  Full-length cDNA libraries and normalization
  Unpublished
JOURNAL
  Contact : Feng Liang Email : fliang@lifetech.com URL :
  http://fulllength.invitrogen.com/Invitrogen Corporation 1600
  Faraday Avenue
  Redwood City, CA 94061
REFERENCE
  2 (bases 1 to 1743)
  Genoscope.
  Direct Submission
  Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
  BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
  - Web : www.genoscope.cns.fr)
COMMENT
  1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
  end enriched, double-strand cDNA was digested with Not I and EcoR V
  sites of the pCMVSPORT 6 vector. Library was constructed by Life
  Technologies, a division of Invitrogen.
FEATURES
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    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CS0D1042YL19"
    /tissue_type="Placenta Cot 25-normalized"
    /plasmid="pCMVSPORT_6"
ORIGIN
Alignment Scores:
Pred. No.: 9e-123 Length: 1743
Score: 1123.00 Matches: 218
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.54% Mismatches: 0
Query Match: 99.29% Indels: 0
DB: 4 Gaps: 0

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US-10-757-745-2_COPY_54_273 (1-220) x CR602029 (1-1743)

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QY 2 GluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 21
Db 32 CAGAGGCTCTGAATCTCTACTTCAGAGCCTCGGTGGAGAGGCGCTTGGACGCGA 91
QY 22 ProGluThrIleSerGluProlyThrTyrValAspLeuThrAsnGluGluThrAsp 41
Db 92 CTTGAACCATCTCTGAGCCCAAGACCTATGTGTGACCTAACCAATGAAGAACAACATGAT 151
QY 42 SerThrThrSerLysIleSerProSerGluAspThrGlnGlnGlnGlnGlnGlnGln 61
Db 152 TCCACCACCTCTTAATCAGCCCATCTGAAGATCTCAGCAGAAAATGGCAGCATGTC 211
QY 62 SerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArg 81
Db 212 TCTCTCATTCACCTGGAATATTGATGATTAGATCTAAACAATCTGTCTCAGAGAGGCTCGA 271
QY 82 GlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheIleGlnGluValIle 101
Db 272 GGGGTGTGTCTCTACTTGTGACCTTGTACAGCCAGATGTGATATTCTCAGAGAGTATT 331
QY 102 ProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGlyHis 121
Db 332 CCCCATTATATAGTACCTTAAGAGAGATCAAGTAAATTATGAGATTATTACAGGTCTAT 391
QY 122 GluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGln 141
Db 392 GAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAGACCAA 451
QY 142 GluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsn 161
Db 452 GAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAAC 511
QY 162 ValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAla 181
Db 512 GTGTGAGGAATGAGCTTTCCTTATGATCATCCATTTGGAGAGCACCAGAGGCGATGCT 571
QY 182 AlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGlnAlaProGluSer 201
Db 572 CGCGAACGAATGAATCAGTTAAATGTTTAAAGAAAATGCAAGAGGCTCCAGAGTCA 631
QY 202 AlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 632 GCTACAGTTATATTGTCAGGAGATCAAAATCTAAGGGATCGAGAGGTACCAGATGT 688
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RESULT 15

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CR765451
LOCUS DKF2p469E2434_r1 846 bp mRNA linear EST 23-SEP-2004
DEFINITION DKF2p469E2434 5', mRNA sequence.
ACCESSION CR765451
VERSION CR765451.1 GI:52605526
KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pongo.
1 (bases 1 to 846)
Ottawaelder, B., Obermaier, B., Deutschenbaier, S., Schaipp, A.,
Mewes, H.W., Wall, B., Amd, C., Osanger, A., Fobo, G., Han, M. and
Wiemann, S.
Pongo pygmaeus mRNA (Ottawaelder, B., Obermaier, B.,
Contact: MIPS
Unpublished (2004)
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix
```

(Martinried/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKF2p469E2434) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneId=DKF2p469E2434
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.

FEATURES

source

1..846

Location/Qualifiers
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKF2p469E2434"
/tissue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"

ORIGIN

Alignment Scores:

Pred. No.: 6,96e-123 Length: 846
Score: 1120.00 Matches: 218
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.09% Mismatches: 1
Query Match: 99.03% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x CR765451 (1-846)

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QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 63 ATGGAAGGCTCTGAATCTCTACTTCAGAGCCTCGGTGGAGAGGCGCTTGGACGC 122
QY 21 ArgProGluThrIleSerGluProlyThrTyrValAspLeuThrAsnGluGluThr 40
Db 123 CGCCCTGAACCATCTCTGAGCCCAAGACCTATGTGTGACCTAACCAATGAAGAAACAAC 182
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGlnGlnGlnGln 60
Db 183 GATTCACCATCTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAAATGGCAGCATG 242
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 243 TTCTCTCTCATTCACCTGGAATATTGATGATGATAGTACTTAACAATCTCTCAGAGAGGCT 302
QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 303 CGAGGGGTGTGTCTCTACTTGTGACAGCCAGATGTGATATTCTACAGGAAGTT 362
QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 363 ATTCCCATATTATAGCTACCTAAAGAGAGTTCAGTAAATATATGAGATTATTACAGGT 422
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 423 CATGAAGAAGGGTATTTTTCACAGCTATCATGTTGAAGAAATCAAGAGTGAATTAAGAAGC 482
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db 483 CAAGAGATTATTCCTTTTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTG 542
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 543 AGTGTGTGAGAAATGAGCTTTCCTTATGACATCCCATTTTGGAGAGCACCAGAGGCGAT 602
QY 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 603 GCTCGGAACGAATGAATCAGTTAAAAATGGTTTTTAAAGAAAATGCAAGAGGCTCCAGAG 662
QY 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 663 TCAGCTACAGTTATATTGTCAGGAGATACAAATCTAAGGGATCGAGAGGTACCAGATGT 722
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RESULT 16
LOCUS BM926092 1046 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT_6649780 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5764440
5', mRNA sequence.
ACCESSION BM926092
VERSION BM926092.1 GI:19376471
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1. (bases 1 to 1046)
NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM12817 row: 0 column: 01
High quality sequence start: 4
High quality sequence stop: 632.
FEATURES
source
Location/Qualifiers
1..1046
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5764440"
/lab_host="DH10B"
/clone_lib="NIH_MGC_114"
Note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 9.57e-123 Length: 1046
Score: 1120.00 Matches: 217
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 99.09% Mismatches: 0
Query Match: 99.03% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_54_273 (1-220) x BM926092 (1-1046)
Qy 2 GluArgAlaLeuAenSerTyrPheGluProValGluSerAlaLeuGluArg 21
Db 36 CAGAGGGCTCTGAATCTCTACTTCGAGCTCCGGTGGAGGAGCGCTTGGACGCCGA 95
Qy 22 ProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrAsp 41
Db 96 CCTGAACCATCTCGAGCCCAAGACCTATGTGACCTAACCAATGAAGAAACCACTGAT 155
Qy 42 SerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAenGlySerMetPhe 61
Db 156 TCCACCACTTCTAAATCAGCCCATCTCAGATATCTCAGCAAGAAATGGCAGCATGTC 215
Qy 62 SerLeuIleThrProAsnIleAspGlyLeuAspLeuAenLeuSerGluArgAlaArg 81
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Db 216 TCTCTCATTACCTGGGAATATTGATGGATTAGATCTTAAACAATCTGTCCAGAGAGGGCTCGA 275
Qy 82 GlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIle 101
Db 276 GGGGTGTGTTCTTACCTTAGCTTTGTACGCCAGATGTGATATTTCTACAGGAAGTTATT 335
Qy 102 ProProTyrTyrSerTyrLeuLysLysAsgSerSerAsnTyrGluIleIleThrGlyHis 121
Db 336 CCCCCATATTATAGCTTACCTTAAAGAGAGATCAAGTAATATTATGAGATTATTACAGGTCAT 395
Qy 122 GluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValIleLysLysSerGln 141
Db 396 GAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAAGAAAGCAA 455
Qy 142 GluIleIleProPheProSerThrLysMetMetArgAenLeuLeuCysValHisValAsn 161
Db 456 GAGATTATTCCTTTTCAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTGAAT 515
Qy 162 ValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAla 181
Db 516 GTGTCCAGGAATGAGCTTTTGCTTATGACATCCCATTTGGAGAGACCAGAGGGCATGCT 575
Qy 182 AlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGluSer 201
Db 576 GCGGAACGATGATGAATCAGTTTAAATGGTTTAAAGAAATGGAAGAGGGCTCCAGAGTCA 635
Qy 202 AlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 636 GCTACAGTTATATTTCAGGAGATACAAATCTTAGGGATCGAGAGGTTCACGATGT 692
RESULT 17
LOCUS BG740396 870 bp mRNA linear EST 15-MAY-2001
DEFINITION 602634171F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4779449 5',
mRNA sequence.
ACCESSION BG740396
VERSION BG740396.1 GI:14051049
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1. (bases 1 to 870)
NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaaps-x@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM10636 row: m column: 18
High quality sequence stop: 826.
FEATURES
source
Location/Qualifiers
1..870
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4779449"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Skn3"
Note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Alignment Scores:
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Pred. No.: 1.26e-122 Length: 870
Score: 1118.00 Matches: 220
Percent Similarity: 99.55% Conservative: 0
Best Local Similarity: 99.55% Mismatches: 0
Query Match: 98.85% Indels: 1
DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x BG740396 (1-870)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 71 ATGGAAGGGCTCTGAATCTCTTACCTCGAGCCCTCGGTCGAGAGAGCGCTTGAAGCG 130
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
Db 131 CGACCTGAACCACTCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACA 190
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 191 GATTCACCACTCTTAATATCAGCCCACTGAAGATCTCAGCAAGAAATGGCAGCATG 250
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 251 TTCTCTCTCATTAACCTGGAATATTGATGATTAGATCTAAACAATCTGTCTGAGAGGGCT 310
QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 311 CGAGGGGTGTCTCTTACTTACTTGTACAGCCAGATGTGATATTCTACAGGAAGTT 370
QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 371 ATTCCTCCATATTATAGCTTACCTAAGAAGAGATCAAGTAATTATGAGATTATTACAGGT 430
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 431 CATGAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAAGAAAGC 490
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuValHisVal 160
Db 491 CAAGAGATTATTCTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 550
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 551 ATGTGTGAGGAATAGAGCTTTGCTTATGACATCCCATTTGAGAGACACAGAGGGCAT 610
QY 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 611 GCTGGCGAAGCAATGAATCAGTTAAATAATGGTTTAAAGAAATGCAAGAGGCTCCAGAG 670
QY 201 SerAlaThrValIle-PheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 671 TCAGCTACAGTTATAATTCGAGGAGATACAAATCTTAAGGGATCGAGAGGTTACCAAGTG 730
QY 220 s 220
Db 731 T 731

RESULT 18
AL555333 LOCUS
DEFINITION AL555333 Homo sapiens HELA-CELLS COT 25-NORMALIZED Homo sapiens
CDNA clone CSODK007YK05 5-PRIME, mRNA sequence.
ACCESSION AL555333
VERSION AL555333.3 GI:45960070
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 948)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
```

JOURNAL COMMENT

Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31277141.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of invitrogen. This sequence belongs to sequence cluster
3474.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?c=CSODK007AF03QPI&c=3474.r.

FEATURES

source

Location/Qualifiers

1..948
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK007YK05"
/cell_type="HELA"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 1.43e-122 Length: 948
Score: 1118.00 Matches: 218
Percent Similarity: 99.09% Conservative: 0
Best Local Similarity: 99.09% Mismatches: 2
Query Match: 98.85% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x AL555333 (1-948)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 179 ATGGAAGGGCTCTGAATCTCTTACCTCGAGCCCTCGGTCGAGAGAGCGCTTGAAGCG 238
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 239 CGACCTGAACCACTCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACA 298
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 299 GATTCACCACTCTTAAATCAGCCCACTGAAGATCTCAGCAAGAAATGGCAGCATG 358
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 359 TTCTCTCTCATTAACCTGGAATATTGATGATTAGATCTTAAACCAATCTGTCTGAGAGGGCT 418
QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 419 CGAGGGGTGTGTCTCTTACTTGTACAGCCAGATGTGATATTCTACAGGAAGTT 478
QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 479 ATTCCTCCATATTATAGCTTACCTAAGAAGAGATCAAGTAATTATGAGATTATTACAGGT 538
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 539 CATGAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAAGAAAGC 598
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuValHisVal 160
Db 599 CAAGAGATTATTCTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 658
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180


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Db      659 AATGTGTGAGAAATGAGCTTTGCTTATGACATCCCATTTGGAGAGCACCAGAGGGCAT 718
Qy      181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db      719 GCTGCGGAGCAATGATCATGTTAAATGTTTAAAGAAATGCAAGAGGCTCCAGAG 778
Qy      201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db      779 TCAGCTACAGTTATATTTCAGGAGATACAWATCTARGGGATCCAGAGGTTACCAAGATGT 838

RESULT 19
BUI69945
LOCUS   BUI69945
DEFINITION 883 bp mRNA linear EST 04-SEP-2002
5', mRNA sequence.
ACCESSION BUI69945
VERSION   BUI69945.1 GI:22683929
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 883)
AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: DCTD/DTP/Gazdar
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM13235 row: m column: 17
          High quality sequence stop: 413.

FEATURES
     source
     1..883
        location/Qualifiers
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:6024760"
            /tissue_type="large cell carcinoma"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_68"
            /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: Noti;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
            Average insert size 1.8 kb. Library constructed by Life
            Technologies."

ORIGIN
Alignment Scores:
Pred. No.:      2.94e-122      Length:      883
Score:          1115.00      Matches:      218
Percent Similarity: 99.54%      Conservative: 0
Best Local Similarity: 99.54%      Mismatches: 1
Query Match:     98.59%      Indels:      0
DB:              5          Gaps:      0

US-10-757-745-2_COPY_54_273 (1-220) x BUI69945 (1-883)

Qy      1 MetGluArgAlaLeuAsnSerThrPheGluProValGluGluSerAlaLeuGluArg 20
Db      40 ATGGAAGGGCTCTGAATCCTACTTCGAGCCTCGGTGGAGGAGCGCTTGGAAACG 99
Qy      21 ArgProGluThrIleSerGluProLysThrThrValAspLeuThrAsnGluGluThr 40
Db      100 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTCACCTAACCAATGAAGAAACAACT 159
Qy      41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGluAsnGlySerMet 60

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Db      160 GATTCCACCACCTCTTAAATTCAGCCCATCTGAAGATATCTCAGCAAGAAAATGCCAGCATG 219
Qy      61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db      220 TTCTCTCTCATTTACCTGGATATTGATGATTAGATCTAAACAATCTGTTCAGAGAGGGCT 279
Qy      81 ArgGlyValCysSerThrLeuAlaLeuThrSerProAspValIlePheLeuGlnGluVal 100
Db      280 CGAGGGGTGTGTTCTCTACTTAGCTTTGTACAGCCCATGTTGATATTTCTACAGGAAGTT 339
Qy      101 IleProProThrThrSerThrLeuLysLysArgSerSerAsnThrGluIleIleThrGly 120
Db      340 ATTCCCCCATATTATAGCTACCTTAAAGAAGAGATCAAGTAATTATGAGATTATTACAGGT 399
Qy      121 HisGluGluGlyThrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db      400 CATGAAGAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAGAGC 459
Qy      141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db      460 CAAGAGATTATTCTCTTTTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGTCATGTG 519
Qy      161 AsnValSerGlyAsnGlnLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db      520 AATGTGTCTAGAAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCACCAGAGGGCAT 579
Qy      181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db      580 GCTGCGGAGCAATGATCAGTTAAATGTTTAAAGAAATGCAAGAGGCTCCAGAG 639
Qy      201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArg 219
Db      640 TCAGCTACAGTTATATTTCAGGAGATACAAATCTAAGGATCGAGAGGGGTACCAGA 696

RESULT 20
BUI53049
LOCUS   BUI53049
DEFINITION 1192 bp mRNA linear EST 20-FEB-2002
5', mRNA sequence.
ACCESSION BUI53049
VERSION   BUI53049.1 GI:18791437
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 1192)
AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM12761 row: i column: 07
          High quality sequence stop: 747.

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        location/Qualifiers
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:5742798"
            /tissue_type="medulla"
            /lab_host="DH10B"
            /clone_lib="NIH_MGC_119"
            /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: Noti;
            Site 2: EcoRV (destroyed); RNA source normal medulla from

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Db      455 CATGAGAGGATATTTTACAGCTATATAATGTTGAAGAAATCAAGAGTGAATTTAAAGAGC 514
Qy      141 GlnGluIleProPheThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db      515 CAAGAGATTATCTCTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTGCATGTG 574
Qy      161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db      575 AATGTGTCCAGAAATGAGCTTTGCCCTATGACATCCCATTTGGAGAGCACCCAGGGCAT 634
Qy      181 AlaAlaGluArgMetAsnGlnLeuLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db      635 GCTGCGAACCAGATCAATCAATGTTAAAGAAATGCTTTTAAAGAAATGCAAGAGGCTCCAGAG 694
Qy      201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArg 219
Db      695 TCAGTACAGTATATTTTGCAGGAGATACAAATCTAAGGGATCGAGAGGTATCCCCAG 751

RESULT 22
LOCUS   BG740339 932 bp mRNA linear EST 15-MAY-2001
DEFINITION 602635289F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4780318 5',
mRNA sequence.
ACCESSION BG740339
VERSION   BG740339.1 GI:14050992
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

REFERENCE
AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
         Email: csapbs-remail.nih.gov
         Tissue Procurement: James Cleaver, M.D.
         cDNA Library Preparation: Life Technologies, Inc.
         cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
         Sequencing by: Incyte Genomics, Inc.
         Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
         Plate: LHAM10639 row: a column: 23
         High quality sequence stop: 759.
FEATURES
source   1..932
         /organism="Homo sapiens"
         /mol_type="mRNA"
         /db_xref="taxon:9606"
         /clone="IMAGE:4780318"
         /lab_host="DH10B (T1 phage-resistant)"
         /clone_lib="NCI_CGAP_Skn3"
         /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
         Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
         Average insert size 1.5kb. Library constructed by Life
         Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Alignment Scores:
Pred. No.: 7.28e-122 Length: 932
Score: 1112.00 Matches: 216
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.32% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x BG740339 (1-932)

Qy      5 LeuAsnSerTyrrPheGluProProValGluGluSerAlaLeuGluArgGluProGluThr 24
Db      3 CTGAATCTCTACTTCGAGGCTCCCGGTGGAGGAGAGCGCTTGGAAACCGCCGACCTGAAC 62

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Qy      25 IleSerGluProLysThrTyrrValAspLeuThrAsnGluGluThrThrAspSerThrThr 44
Db      63 ATCTCTGAGCCCAAGACCTTATGTTGACCTAACCAATGAAGAAACAACACTGATTCACCACT 122
Qy      45 SerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIle 64
Db      123 TCTAAATCAGGCCCATCTCTGAAGATACTCAGCAAGAAATGGCAGCATGTTCTCTCTCAT 182
Qy      65 ThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArgGlyValCys 84
Db      183 ACCTGGAATATTGATGGATTAGATCTTAAACAATCTCTGTCAGAGAGGGCTCGAGGGGTGTGT 242
Qy      85 SerTyrrLeuAlaLeuTyrrSerProAspValIlePheLeuGlnGluValIleProProFyr 104
Db      243 TCCTACTTACCTTTGTACAGCCAGATGATATTTCTACAGGAAGTTATTTCCCCCATAT 302
Qy      105 TyrrSerTyrrLeuLysLysArgSerSerAsnTyrrGluIleIleThrGlyHisGluGluGly 124
Db      303 TATAGCTACTCTAAGAGAGATCAAGTAATATTATGAGATTATTACAGGTCTATGAAGAAGGA 362
Qy      125 TyrrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGlnGluIleIle 144
Db      363 TATTTTACAGCTATATAATGTTGAAGAAATCAAGAGTGAATTTAAAGCCCAAGAGATTATT 422
Qy      145 ProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsnValSerGly 164
Db      423 CCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTGAATGTGTCTAGGA 482
Qy      165 AsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAlaGluArg 184
Db      483 AATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCACCCAGAGGGCATGTCGGGAACGA 542
Qy      185 MetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGluSerAlaThrVal 204
Db      543 ATGAATCAGTTAAAAATGGTTTAAAGAAATCAAGAGGCTCCAGAGTCCAGGTACAGTACAT 602
Qy      205 IlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db      603 ATATTTGCAGGAGATACAAATCTAAGGGATCGAGAGGTATACAGATGT 650

DQ049206 1089 bp DNA linear GSS 02-JUN-2005
Pan troglodytes TTRAP gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
DQ049206
DQ049206.1 GI:66902405
GSS.
SOURCE    Pan troglodytes (chimpanzee)
ORGANISM  Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Pan.
REFERENCE 1 (bases 1 to 1089)
AUTHORS  Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civallo,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE     A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED    15869325
REFERENCE 2 (bases 1 to 1089)
AUTHORS  Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civallo,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE     Direct Submission
JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
FEATURES  Location/Qualifiers

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Score:	1108.00	Matches:	216		
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Best Local Similarity:	98.18%	Mismatches:	4		
Query Match:	97.97%	Indels:	0		
DB:	11	Gaps:	0		
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DB	220	CGACCTGAACCATCTCTGAGCCCANNNNNNTGTGGACCTAACCAATGAAGAACAAC	279		
QY	41	AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet	60		
DB	280	GATTCACACACTCTTAAATCAGCCATCTGAAGATCTCAGCAAGAAATGGCAGCATG	339		
QY	61	PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerClnuArgAla	80		
DB	340	TTCTCTCTCATTAACCTGGGAATATTGATGATTAGATCTAAACAATCTGTCCAGAGGGCT	399		
QY	81	ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal	100		
DB	400	CGAGGGGTGTCTCTACTTACTAGCTTTGACGCCAGATGTGATATTCTACAGAGATT	459		
QY	101	IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly	120		
DB	460	ATTCCCCCATATTATAGCTTACCTAAGAAGAGATCAAGTAATTATGAGATTATTACAGT	519		
QY	121	HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer	140		
DB	520	CATGAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAAATTAAGAACG	579		
QY	141	GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysCysValHisVal	160		
DB	580	CAAGAGATTATTTCCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG	639		
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QY	181	AlaAlaGluArgMetAsnGlnIleLysMetValLeuLysLysMetGlnClnuIleProGlu	200		
DB	700	GCTGTGGACGCAATGAATCAGTTAAATAATGGTTTTTAAAGAAATGCAAGAGGCTCCAGAA	759		
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DB	760	TCAGCTACAGTTATTATTTCAGAGATACAAATCTAAGGGATCGAGAGGTTACCAAGTGT	819		
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LOCUS					
DEFINITION					
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CS0DM007YEL1 5-PRIME, mRNA sequence.					
ACCESSION					
BX422491.2 GI:46955237					
VERSION					
EST.					
KEYWORDS					
EST.					
SOURCE					
Homo sapiens (human)					
ORGANISM					
Homo sapiens					

REFERENCE		1 (bases 1 to 904)	
AUTHORS		Li, W.B., Gruber, C., Jessee, J. and Polayes, D.	
TITLE		Full-length cDNA libraries and normalization	
JOURNAL		Unpublished (2001)	
COMMENT		On May 15, 2003 this sequence version replaced gi:30766188.	
Contact: Genoscope			
Genoscope - Centre National de Sequencage			
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE			
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr			
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime			
end enriched, double-strand cDNA was digested with Not I and cloned			
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library			
was not normalized. Library was constructed by Life Technologies, a			
division of Invitrogen.			
This sequence belongs to sequence cluster 3474.r			
For more information about this cluster, see			
http://www.genoscope.cns.fr/cdna?s=CS0DM007AC06QP1&c=3474.r.			
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/clone="CS0DM007YEL1"			
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/clone_lib="Homo sapiens FETAL LIVER"			
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA			
was primed with a NotI-oligo(dT) primer. Five prime end			
enriched, double-strand cDNA was digested with Not I and			
cloned into the Not I and EcoRV sites of the pCMVSPORT 6			
vector. Library was not normalized."			
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Alignment Scores:			
Pred. No.:	1.09e-120	Length:	904
Score:	1102.00	Matches:	215
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Best Local Similarity:	97.73%	Mismatches:	4
Query Match:	97.44%	Indels:	0
DB:	5	Gaps:	0
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DB	103	ATGGAAGGGCTCTGAACCTCTCTACTTCGAGCCTCCGGTGGAGGAGCGCCTTGGAAACGC	162
QY	21	ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr	40
DB	163	CGACCTGAACCATCTCTGAGCCCAARACCTATGTTGACCTAACCAATGAAGAAACAAC	222
QY	41	AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet	60
DB	223	GATTCACACACTCTTAAATCAGCCCATCTGAAGATCTCAGCAARAAAAGGCGAGCATG	282
QY	61	PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla	80
DB	283	TTCTCTCTCATTAACCTGGGAATATTGATGATTAGATCTAAACAATCTGTCCAGAGGGCT	342
QY	81	ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal	100
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DB	403	ATTCCTCCATATTATAGCTTACCTAAGAAGAGATCAAGTAATTATGAGATTATTACAGGT	462
QY	121	HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer	140
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QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
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QY 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 643 GCTGCGGACCAATGAATCAGTTTAAAAATGGTTTAAAGAAAAATGGAAGAGGCTCCAGAG 702
QY 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
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RESULT 25
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LOCUS 17000424496911 GRN ES Homo sapiens cDNA 5', mRNA linear EST 16-MAY-2004
DEFINITION CN298924
ACCESSION CN298924
VERSION CN298924.1 GI:47315338
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 729)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 1514197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 729 Std Error: 0.00.
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/tissue_type="embryonic stem cells, cell lines H1, H7, and
H9"
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from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"

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Alignment Scores: 4.92e-119 Length: 729
Pred. No.: 1087.00 Matches: 212
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 96.11% Indels: 0
Query Match: 7 Gaps: 0
DB:

US-10-757-745-2_COPY_54_273 (1-220) x CN298924 (1-729)

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Db 94 ATGGAAAGGGCTCTGAATCCTCTACTTCGAGCCTCGGTGGAGGAGAGCGCCTTGGAAACG 153
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40

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Db 154 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGCTTAACCAATGAAGAAACAAC 213
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Db 214 GATTCCACCACTTCTAAAATACGCCCATCTGAAGATACCTCAGCAAGAAATGCGACATG 273
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 274 TTCTCTCTCATTTACCTGGATATTGATGGATTAGATCTAAACAATCTGTTCAGAGAGGCT 333
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Db 334 CGAGGGGTGTGTTCTCTACTTAGCTTTGTACAGCCAGATGTGATATTCTTACAGSAGTT 393
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Db 574 AACGTGTCAGAAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCACCAAGGGCAT 633
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QY 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeu 212
Db 694 TCAGCTACAGTTATATTTCAGGAGATACAAATCTA 729

RESULT 26
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DEFINITION ILLUMIGEN MCQ 5159 Katze MMR Macaca mulatta cDNA clone IBUM:5970
5' similar to Bases 11 to 990 highly similar to human TTRAP
(Hs.210628), mRNA sequence.
ACCESSION CN641671
VERSION CN641671.1 GI:47152691
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 1090)
AUTHORS Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
Prohl, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
Iadonato, S.P.
TITLE Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
JOURNAL Genome Biol. 6 (7), R60 (2005)
PUBMED 1599849
COMMENT Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2003.12.04. 732 Q20 bases.
PCR Primers
FORWARD: CCTCTACTAAAGGGAACAAA
BACKWARD: CACTATAGGGCGAATTGGGTA
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Alignment Scores:
Pred. No.:      2.71e-118      Length:      1090
Score:          1083.00      Matches:      210
Percent Similarity: 97.2%      Conservative:  4
Best Local Similarity: 95.45%      Mismatches:   6
Query Match:    95.76%      Indels:       0
DB:              7      Gaps:          0
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DB      92 CGCCCTGAAACCACTCTTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACCACT 151
QY      41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB      152 GATTCACCACTTCTTAAATCAGCCATCCTGAAGTACTCGAGCAAGAAATGACAGCATG 211
QY      61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB      212 TCTCTCTTCACTTACCTGGAATATTGATGATTAGATCTAAACAACTCTGTGAGAGGGCT 271
QY      81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
DB      272 CGAGGGGTGTGTTCTTACTTACGCTTGTACAGCCAGATGTGATATTCTACAGGAAGTT 331
QY      101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
DB      332 ATTCGCCCTTATTATAGCTTACCTAAAGAAGAGAGCAAGTGATTTATGAGATTATTACAGGT 391
QY      121 HisGluGluGlyTyrPheThrAlaIleMetIleLysLysSerArgValLysLeuLysSer 140
DB      392 CATGAAGAAGGATATTTTACAGCTATAATGTTGAAGAAATCAAGAGTCAAAATTAAGAGC 451
QY      141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
DB      452 CAAGAGATTATTCCTTTTCCAGTACCAAAATGATGAGAACTTTTATGTGTGATGTG 511
QY      161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
DB      512 AATGTGTGAGGAAATGAGCTTTGCCTTATGACATCCCATTTTGAGAGACCAAGAGGCGAT 571
QY      181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetClnGluAlaProGlu 200
DB      572 GCTGGGGAACGAATGAATCAGTTAAATAATGGTTTTTAAAGAAATCAAGAGGCTCCAGAG 631
QY      201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
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ACCESSION BI760756
VERSION    BI760756.1 GI:15752334
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ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1 (bases 1 to 757)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LHAM11462 row: m column: 15
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                stomachs, 62 yo male and 70 yo female. Library is
                oligo-dT primed and directionally cloned (EcoRV site is
                destroyed upon cloning). Average insert size 1.4 kb,
                insert size range 1-3 kb. Library is normalized and
                enriched for full-length clones and was constructed by C.
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                023. Note: this is a NIH_MGC Library."
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Score:          1077.00      Matches:      218
Percent Similarity: 99.09%      Conservative:  0
Best Local Similarity: 99.09%      Mismatches:   2
Query Match:    99.23%      Indels:       2
DB:              3      Gaps:          0
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QY      1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
DB      69 ATGGAAGGGCTCTGAACCTCTTACTTCGAGCCTCGGTGGAGGAGCGC-CTGGAAGCG 127
QY      21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
DB      128 CGACTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACCACT 187
QY      41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB      188 GATTCACCACTTCTTAAATCAGCCATCTGAAGTACTCAGCAAGAAATGCGCAGCATG 247
QY      61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
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Qy      101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db      367 ATTCCCCCATATATATAGCTTACCTAAAGAAGAGATCAAGTAATATGAGATATTATCAGGT 426
Qy      121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db      427 CATGAAGAAGATATTTTCAGCTATATGTTGAAGAAATCAAGAGTGAATTAAGAAGC 486
Qy      141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db      487 CAAGAGATTATTCCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTGCATGTG 546
Qy      161 AsnValSerGlyAsnGluLysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db      547 AACGTGTCCAGGAATCAGCTTTTGCCTTATGACATCCCATTTGGAGAGCACCGAGGGCAT 606
Qy      181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db      607 GCTGCCGAACGAATGATCAGTTAAATAATGGTTTAAAGAAATGCGAAGGGCTCCAGAG 666
Qy      201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
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RESULT 28

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BU661472      710 bp mRNA linear EST 30-SEP-2002
LOCUS      cl72d11.z1 Hembase; Erythroid Precursor Cells (LCB:cl library) Homo
DEFINITION      sapiens cDNA clone cl72d11 5', mRNA sequence.

```

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ACCESSION      BU661472.1 GI:23373654
VERSION      EST.
KEYWORDS
SOURCE

```

ORGANISM

```

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

```

REFERENCE

```

1 (bases 1 to 710)
Gubin,A.N., Lee,Y.T., Bouffard,G.G. and Miller,J.L.
Gene Expression in Human Erythroid Precursor Cells
Unpublished (2002)

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JOURNAL

```

COMMENT      Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
20892, USA

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Tel: 301 402 2373
Fax: 301 435 5148

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Email: jmf7@nih.gov

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The 'cl' library was constructed by Alexander Gubin, Ph.D. in the
Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing and/or
analyses by National Institutes of Health Intramural Sequencing
Center (NISC). More information available at:
http://hembase.nidk.nih.gov

```

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Plate: 72 row: d column: 11

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Seq primer: 5' lambda-Triplex2 Sequencing Primer.

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FEATURES

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Location/Qualifiers

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1..710

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/organism="Homo sapiens"

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/mol_type="mRNA"

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/db_xref="taxon:9606"

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/clone="cl72d11"

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/sex="unknown"

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/tissue_type="blood"

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/cell_type="Erythroid Precursor Cells"

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/cell_line="Primary Culture of Peripheral Blood

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Mononuclear Cells"
/dev stage="Precursor erythroblasts; GPA++"
/lab_host="DH5alpha"
/clone_lib="Hembase; Erythroid Precursor Cells (LCB:cl
library)"
/notes="Organ: blood; Vector: pTriplex2; Site_1: Sfil;
Site_2: Sfil; A complementary DNA (cDNA) library from
human erythroid precursor cells was constructed using
SMART PCR (polymerase chain reaction) cDNA library
Construction kit (Clontech, Palo Alto, CA) according to
the manufacturer's directions, but with slight
modifications. Briefly, reverse transcription was
performed in the presence of 1 umol/L peptide nucleic acid
(PNA) oligos
(N-terminal)-biotin-GTC-CAC-CCG-AAG-CTT-G- (C-terminal) and
(N-terminal)-biotin-C(T/C)T-GAA-GTT-CTC-AGG-A- (C-terminal)
. Synthesized cDNA was digested with Sfil and
size-selected on a 1% agarose gel (>800bp). Large-scale
sequencing of the library was performed by the NIH
Intramural Sequencing Center (NISC;
Http://www.nisc.nih.gov/)."

```

ORIGIN

```

Alignment Scores:
Pred. No.:      9,79e-118      Length:      710
Score:          1076.00      Matches:    210
Percent Similarity: 99.53%      Conservative: 0
Best Local Similarity: 99.53%      Mismatches: 1
Query Match:      95.14%      Indels:     0
DB:              5          Gaps:         0

US-10-757-745-2_COPY_54_273 (1-220) x BU661472 (1-710)

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Qy      1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluSerAlaLeuGluArg 20
Db      76 ATGGAAGAGGGCTCTGAACCTCTACTTCGAGCCCTCCGGTGGAGAGAGCCCTTGGAAACGC 135
Qy      21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db      136 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAGAAACAAC 195
Qy      41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db      196 GATTCACCCACCTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAAATGCGCAGCATG 255
Qy      61 PheSerLeuIleThrTyrPheThrAlaIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db      256 TTCTCTCTCATTTACCTGGAAATATTGATGGATTAGATCTAAACAATCTGTCCAGAGAGGGCT 315
Qy      81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db      316 CGAGGGGTGTGTTCTCTACTTGTACAGCCCAAGATGATGATTTCTTACAGGAAGTT 375
Qy      101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db      376 ATTCGCCCATATATATAGCTTACCTAAAGAAGAGATCAAGTAATTTATCAGATTTATTCAGGT 435
Qy      121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db      436 CATGAAGAAGAGATATTTCACAGCTATAATGTTTGAAGAAAATCAAGAGTGAATTAAGAAGC 495
Qy      141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db      496 CAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATAGAAACCCCTTTATGTGTGCATGTG 555
Qy      161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db      556 AACGTGTCCAGGAATGAGCTTTTGCCTTATGACATCCCATTTGGAGAGCACCGAGGGCAT 615
Qy      181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db      616 GCTGCCGAACGAATGAATCAGTTAAATAATGGTTTAAAGAAAATGCAAGAGGGCTCCAGAG 675

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Pred. No.:	1.56e-115	Length:	767
Score:	1058.00	Matches:	213
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Best Local Similarity:	96.38%	Mismatches:	4
Query Match:	93.55%	Indels:	2
DB:	2	Gaps:	0
US-10-757-745-2_COPY_54_273 (1-220) x BI258848 (1-767)			
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Db	157	CGACCTGAAACCACTCTCTGAGCCCAAGACCTATGTGTGACCTAACCAATGAAGAAACAACT	216
Qy	41	AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet	60
Db	217	GATTCACCACTTCTAAATACGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGCATG	276
Qy	61	PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla	80
Db	277	TTCTCTCTCATTACCTGGAATATTGATGGATTAGATCTAAACAATCTGTCTCAGAGGGCT	336
Qy	81	ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal	100
Db	337	CGAGGGGTGTGTTCTTACTTTAGCTTTGTACAGCCCAAGATGTGATATTTCTACAGGAAGTT	396
Qy	101	IleProProTyrTyrSerTyrLeuLysAspSerSerAsnTyrGluIleIleThrGly	120
Db	397	ATTCCCCCATTTATTAGCTTACCTTAAGAGAGATCAAGTAATTTATGAGATTATTACAGGT	456
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Qy	141	GlnGluIleIleProPheProSerThrLysMetMetMetArgAsnLeuLeuCysValHisVal	160
Db	517	CAAGAGATTATTCCTTTTCCAGTACCAGAAATGATGAGAAACCTTTTATGTGTGCATGTG	576
Qy	161	AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis	180
Db	577	AATGTGTCCAGAAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCACCAGAGGGCAT	636
Qy	181	Ala-AlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGl	200
Db	637	GCTTGGGAACGATGAATCAGTTACAACCTGGTTTAAAGACAATGCAAGAGGCTCCAGA	696
Qy	200	uSerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCy	220
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Qy	220	s 220	
Db	756	t 756	

Search completed: December 4, 2005, 15:32:07
Job time : 4700.12 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 3, 2005, 23:33:41 ; Search time 682.898 Seconds
(without alignments)
2147.074 Million cell updates/sec

Title: US-10-757-745-2_COPY_54_273

Perfect score: 1131

Sequence: 1 MERALNSYFEPVPEESALER.....SATVIFAGDTNLRDREVTTC 220

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO.spool/US10757745/runat_01122005_091747_10071/app_query.fasta_1.981
-DB=N_Geneseq -OFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNIT3=bits -START=1 -END=1 -MATRIX=blosom62 -TRANS=human40.cdi -LIST=500
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10757745 @CNC 1.1.1072 @runat_01122005_091747_10071 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
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8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1131	100.0	1920	3 AAZ47118	Aaz47118 Human CD4
2	1131	100.0	1936	10 ADD19013	Add19013 Human dis
3	1131	100.0	1936	13 ADP25361	Adp25361 PRO polyp
4	1131	100.0	1940	14 ADX06356	Adx06356 Cyclin-de

5	1131	100.0	1948	4 AAI58997	Aai58997 Human pol
6	1131	100.0	1948	5 ADQ99219	Adq99219 DNA encod
7	1131	100.0	1948	9 ADB48979	Adb48979 Novel hum
8	1131	100.0	1958	4 AAI60783	Aai60783 Human pol
9	1131	100.0	2499	2 AAX28153	Aax28153 Topoisome
10	1131	100.0	3152	9 ADA10970	Ada10970 Human cDN
11	1123	99.3	1296	3 AAC98160	Aac98160 Human col
12	1122	99.2	1898	4 AAH15146	Aah15146 Human cDN
13	904	79.9	752	4 AAH08073	Aah08073 Human cDN
14	765.5	67.8	1312	3 AAZ47119	Aaz47119 Mouse CD4
15	728	64.4	553	11 ADT95464	Adt95464 Colon can
16	728	64.4	553	11 ADX1946	Adx1946 Human cDN
17	726	64.2	625	11 ADT95512	Adt95512 Colon can
18	726	64.2	625	11 ADX1994	Adx1994 Human cDN
19	726	64.2	633	11 ADT95565	Adt95565 Colon can
20	726	64.2	633	11 ADX42047	Adx42047 Human cDN
21	723	63.9	644	11 ADT95551	Adt95551 Colon can
22	723	63.9	644	11 ADX42033	Adx42033 Human cDN
23	714.5	63.2	602	10 ADT34376	Adt34376 Mouse mit
24	713	63.0	674	11 ADT95548	Adt95548 Colon can
25	713	63.0	674	11 ADX42030	Adx42030 Human cDN
26	711	62.9	1079	2 AAX84209	Aax84209 DNA encod
27	711	62.9	1079	3 AAC79438	Aac79438 CDNA sequ
28	711	62.9	1079	6 ABK28982	Abk28982 Human bre
29	710	62.8	1088	5 AAS86254	Aas86254 DNA encod
30	708	62.6	625	11 ADT95029	Adt95029 Colon can
31	708	62.6	625	11 ADX41511	Adx41511 Human cDN
32	651	57.6	401	11 ADT95844	Adt95844 Colon can
33	651	57.6	401	11 ADX42326	Adx42326 Human cDN
34	559	49.4	483	2 AAX40590	Aax40590 Human sec
35	466	41.2	1227	5 AAS86255	Aas86255 DNA encod
36	465	41.1	774	10 ADD34375	Add34375 Mouse mit
37	414	36.6	391	11 ADT95307	Adt95307 Colon can
38	414	36.6	391	11 ADX41789	Adx41789 Human cDN
39	298	26.3	176	6 ABK27684	Abk27684 Human col
40	298	26.3	176	6 ABK59599	Abk59599 Human pan
41	298	26.3	179	6 ABL36461	Ab136461 Human col
42	182.5	16.1	444	4 AAI15311	Aai15311 Probe #52
43	182.5	16.1	691	4 AAI24484	Aai24484 Probe #14
44	154	13.6	525	13 ACN59762	Acn59762 Cotton gy
45	141	12.5	1566	3 AAC47239	Aac47239 Arabidops
46	141	12.5	1606	3 AAC41089	Aac41089 Arabidops
47	114	10.1	725	6 ABQ34465	Abq34465 Oligonucl
48	114	10.1	725	6 ABQ34464	Abq34464 Oligonucl
49	113	10.0	258	2 AAX41008	Aax41008 Human sec
50	107.5	9.5	110000	6 ABA03041_03	Continuation (4 of
51	106.5	9.4	5496	13 ADR46193	Adr46193 Retrotran
52	104.5	9.2	5496	13 ADR46200	Adr46200 Retrotran
53	104.5	9.2	9737	14 ADZ62001	Adz62001 Murine Cc
54	103.5	9.2	96960	8 ACF62734	Acf62734 Cancer ba
55	103.5	9.2	96960	10 ADB20849	Adb20849 MRP1 base
56	103.5	9.2	96960	10 ADB87938	Adb87938 Human UGT
57	103.5	9.2	96960	10 ADB96921	Adb96921 Human MDR
58	103.5	9.2	96960	10 ADB92112	Adb92112 Human MDR
59	103	9.1	37741	14 AEB47090	Aeb47090 Chimpanze
60	102.5	9.1	3532	10 ADE15671	Ade15671 Human str
61	102.5	9.1	3640	6 AAS99915	Aas99915 Polynucle
62	102.5	9.1	3640	12 ADL113159	Adl113159 Human ste
63	102.5	9.1	3875	13 ADR24178	Adr24178 Breast ca
64	102.5	9.1	3950	14 AEA19702	Aea19702 Novel hum
65	102.5	9.1	4058	14 AAI58478	Aai58478 Human pol
66	102.5	9.1	4061	4 ADQ98693	Adq98693 DNA encod
67	102.5	9.1	4061	5 ADB48453	Adb48453 Novel hum
68	102.5	9.1	4150	4 AAK51922	Aak51922 Human pol
69	102.5	9.1	4150	4 AAK52905	Aak52905 Human pol
70	102.5	9.1	4176	4 AAK52906	Aak52906 Human pol
71	102.5	9.1	4176	4 AAI60264	Aai60264 Human pol
72	102.5	9.1	4176	4 AEA20688	Aea20688 Novel hum
73	102.5	9.1	4176	14 AEA20689	Aea20689 Novel hum
74	102.5	9.1	4231	5 AAS87070	Aas87070 DNA encod
75	102.5	9.1	4258	4 AAK51921	Aak51921 Human pol
76	102.5	9.1	5048	14 ADX07700	Adx07700 Cyclin-de
77	102.5	9.1			

78	102.5	9.1	5077	14	ADZ49482	Adz49482 Insulin s	151	95	8.4	6009	12	ADJ12485	Adj12485 DNA fragm
79	102	9.0	110000	14	AEb39175_05	Continuation (6 of	152	95	8.4	8224	2	AAQ12261	Aaql12261 Versican
80	102	9.0	110000	14	AEb42401_05	Continuation (6 of	153	95	8.4	8224	6	ABT11088	Abt11088 Human bre
81	102	9.0	243335	14	AEb42735	Reb42735 L. pneumo	154	95	8.4	8224	8	ACC50121	Acc50121 Breast ca
82	102	9.0	295644	14	AEb35721	Reb35721 L. pneumo	155	95	8.4	8224	14	ADV70166	Adv70166 Tumor-ass
83	102	9.0	298667	14	AEb39173	Reb39173 L. pneumo	156	95	8.4	9647	11	ACN89856	Acn89856 Breast ca
84	101	8.9	60	6	ABN41860	Abn41860 Human spl	157	95	8.4	11185	6	ABL62702	Ab162702 Colon ade
85	100	8.8	2606	5	AA575832	AA575832 DNA encod	158	95	8.4	11185	6	ABN96814	Abn96814 Gene #331
86	99	8.8	2277	5	AA584982	AA584982 DNA encod	159	95	8.4	11185	11	ADN95527	Adn95527 Human BEC
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88	99	8.8	5130	5	AA572822	AA572822 DNA encod	161	95	8.4	11185	12	ADN04530	Adn04530 Antipsori
89	99	8.8	5130	5	AA574984	AA574984 DNA encod	162	95	8.4	11185	13	ADP23737	Adp23737 PRO polyp
90	99	8.8	5130	5	AA568166	AA568166 DNA encod	163	95	8.4	11185	14	ADW77698	Adw77698 Human cho
91	99	8.8	5130	5	AA585098	AA585098 DNA encod	164	95	8.4	11185	14	ADZ09721	Adz09721 Human bre
92	99	8.8	5130	5	AA566528	AA566528 DNA encod	165	95	8.4	11185	14	ADZ09676	Adz09676 Human bre
93	99	8.8	5130	5	AA589455	AA589455 DNA encod	166	95	8.4	11185	14	AEA04380	Aea04380 Human cDN
94	99	8.8	5130	5	AA567239	AA567239 DNA encod	167	95	8.4	11185	14	AEb17603	Aeb17603 Human CSP
95	99	8.8	5130	5	AA573825	AA573825 DNA encod	168	95	8.4	12319	6	AA594985	Aas94985 Human DNA
96	99	8.8	5130	5	AA570242	AA570242 DNA encod	169	94.5	8.4	5496	13	ADR46192	Adr46192 Retrotran
97	99	8.8	5130	5	AA570789	AA570789 DNA encod	170	94.5	8.4	5671	4	AA137390	Aal37390 Human mus
98	99	8.8	5130	5	AA584966	AA584966 DNA encod	171	94.5	8.4	5671	8	ABX60378	Abx60378 cDNA enco
99	99	8.8	5131	5	AA583326	AA583326 DNA encod	172	94.5	8.4	5671	12	ADJ31128	Adj31128 Human mus
100	99	8.8	5131	5	AA565594	AA565594 DNA encod	173	94.5	8.4	83698	6	ABN85767	Abn85767 Arabidops
101	99	8.8	5210	5	AA583526	AA583526 DNA encod	174	94.5	8.4	110000	13	ABD32923_4	Abd32923_4
102	99	8.8	5213	5	AA589597	AA589597 DNA encod	175	94	8.3	9487	13	ADR99037	Adr99037 Chondroit
103	99	8.8	5231	5	AA566699	AA566699 DNA encod	176	94	8.3	110000	6	ABQ69245_03	Abq69245_03
104	99	8.8	5450	5	AA565193	AA565193 DNA encod	177	93.5	8.3	3859	5	AA575201	Aas75201 DNA enco
105	99	8.8	5773	5	AA584049	AA584049 DNA encod	178	93.5	8.3	3859	5	AA576592	Aas76592 DNA enco
106	99	8.8	6028	10	ADE09776	Ad09776 Novel DNA	179	93.5	8.3	4823	5	AA571072	Aas71072 DNA enco
107	99	8.8	8065	5	AA578738	AA578738 DNA encod	180	93.5	8.3	5074	5	AA574241	Aas74241 DNA enco
108	99	8.8	10136	5	AA575390	AA575390 DNA encod	181	93.5	8.3	5548	5	AA571792	Aas71792 DNA enco
109	99	8.8	10136	10	ADF06156	Adf06156 Human con	182	93.5	8.3	5782	5	AA586650	Aas86650 DNA enco
110	99	8.8	10579	5	AA569831	AA569831 DNA encod	183	93.5	8.3	5976	5	AA569611	Aas69611 DNA enco
111	99	8.8	31952	4	AAK89370	AAK89370 Human dig	184	93.5	8.3	5976	5	AA572816	Aas72816 DNA enco
112	98.5	8.7	54493	11	ACN45086	Acn45086 Human gen	185	93.5	8.3	5976	5	AA574900	Aas74900 DNA enco
113	98.5	8.7	110000	9	ACH03408_2	ACH03408_2	186	93.5	8.3	5976	5	AA574241	Aas74241 DNA enco
114	98.5	8.7	110000	14	ADZ13747_1	ADZ13747_1	187	93.5	8.3	5976	5	AA570240	Aas70240 DNA enco
115	98.5	8.7	110000	14	ADZ13747_2	ADZ13747_2	188	93.5	8.3	5976	5	AA574982	Aas74982 DNA enco
116	98.5	8.7	127098	10	ADL13649	Adl13649 Osteoarth	189	93.5	8.3	5976	5	AA579076	Aas79076 DNA enco
117	98.5	8.7	347814	12	ADQ59440	Adq59440 Human can	190	93.5	8.3	5976	5	AA573823	Aas73823 DNA enco
118	98	8.7	1644	8	ACA49305	ACA49305 Prokaryot	191	93.5	8.3	5976	10	ADE09929	Ade09929 Novel DNA
119	97.5	8.6	10789	12	ADJ12524	Adj12524 DNA fragm	192	93.5	8.3	5984	5	AA566494	Aas66494 DNA enco
120	97	8.6	2928	12	ADQ97808	Adq97808 Mouse can	193	93.5	8.3	6007	8	ACA64808	ACA64808 Human L1
121	96.5	8.5	3060	13	ADR07698	Adr07698 Full leng	194	93.5	8.3	6024	5	AA571536	Aas71536 DNA enco
122	96.5	8.5	4863	8	ABX56504	ABX56504 Human pro	195	93.5	8.3	6041	12	ADJ12584	Adj12584 DNA fragm
123	96.5	8.5	5446	4	AA104704	AA104704 Human rep	196	93.5	8.3	6094	5	AA566296	Aas66296 DNA enco
124	96.5	8.5	5446	4	ABL97611	Ab197611 Human tes	197	93.5	8.3	6128	5	AA577158	Aas77158 DNA enco
125	96.5	8.5	6059	13	ADR46194	Adr46194 Retrotran	198	93.5	8.3	6163	5	AA577502	Aas77502 DNA enco
126	96.5	8.5	6075	10	ADF985467	Adf985467 Human tra	199	93.5	8.3	6963	4	AAK86787	Aak86787 Human imm
127	96.5	8.5	6539	6	ABS52449	AB52449 Human lon	200	93.5	8.3	6963	12	ADJ12596	Adj12596 DNA fragm
128	96.5	8.5	32042	2	AAZ09252	Aaz09252 Human CAR	201	93.5	8.3	7804	5	AA576736	Aas76736 DNA enco
129	96.5	8.5	32042	4	AAF30011	Aaf30011 Human CAR	202	93.5	8.3	7838	4	AAK86788	Aak86788 Human imm
130	96.5	8.5	32042	6	ABK89285	ABk89285 Human cas	203	93.5	8.3	7838	4	AAK86789	Aak86789 Human imm
131	96.5	8.5	32042	6	AA140765	AA140765 Genomic D	204	93.5	8.3	7838	12	ADJ12597	Adj12597 DNA fragm
132	96.5	8.5	32042	12	ADH01055	Adh01055 Human cas	205	93.5	8.3	7838	12	ADJ12576	Adj12576 DNA fragm
133	96.5	8.5	34001	9	ABT44144	ABt44144 Complemen	206	93.5	8.3	8177	5	AA578799	Aas78799 DNA enco
134	96.5	8.5	42048	4	AAK71918	AAK71918 Human imm	207	93.5	8.3	8181	5	AA570763	Aas70763 DNA enco
135	96.5	8.5	42299	4	AAK68932	AAK68932 Human imm	208	93.5	8.3	8214	5	AA577257	Aas77257 DNA enco
136	96.5	8.5	50196	4	AAK79598	AAK79598 Human imm	209	93.5	8.3	8907	5	AA568193	Aas68193 DNA enco
137	96.5	8.5	68571	12	ADH56913	Adh56913 Human CAR	210	93.5	8.3	8979	5	AA576713	Aas76713 DNA enco
138	96.5	8.5	90435	12	ADQ59524	Adq59524 Human can	211	93.5	8.3	11087	5	AA574637	Aas74637 DNA enco
139	96.5	8.5	90537	14	ADZ13905	Adz13905 Human can	212	93.5	8.3	11220	5	AA587868	Aas87868 DNA enco
140	96.5	8.5	98825	10	ADZ13905	ADZ13905 Human can	213	93.5	8.3	12364	5	AA570817	Aas70817 DNA enco
141	96.5	8.5	123785	14	ABX77171	ABx77171 DNA sequ	214	93.5	8.3	24861	12	ADQ97272	Adq97272 Human can
142	96.5	8.5	168828	14	ADZ13592	Adz13592 Human can	215	93.5	8.3	36783	12	ADJ12543	Adj12543 DNA fragm
143	96.5	8.5	185371	6	ABT10718	ABt10718 Human bre	216	93.5	8.3	49375	12	ADJ12449	Adj12449 DNA fragm
144	96	8.5	1650	8	ACA51704	ACA51704 Prokaryot	217	93.5	8.3	52746	14	AEa61129	Ea61129 Human FLJ
145	96	8.5	1650	8	ACA51704	ACA51704 Prokaryot	218	93.5	8.3	110469	12	ADQ97337	Adq97337 Human can
146	96	8.5	110000	8	AEQ83210_2	AEQ83210_2	219	93.5	8.3	160274	14	AEb32377	Eb32377 Human gen
147	95.5	8.4	3300	12	ADQ67381	Adq67381 Novel hum	220	93.5	8.3	160300	14	AEb32388	Eb32388 Human gen
148	95.5	8.4	10322	14	ACL64526	ACL64526 M. xanthu	221	93	8.2	59446	10	AAAD47904	Aad47904 Human tra
149	95.5	8.4	59001	12	ADH54712	Adh54712 Human VEG	222	93	8.2	89210	14	ADZ13911	Adz13911 Human can
150	95.5	8.4	70708	12	ADQ97605	Adq97605 Human can	223	92.5	8.2	1350	4	ABL08315	Ab108315 Drosophil

224	92.5	8.2	6102	4	AAK84540	AAK84540 Human imm	297	89.5	7.9	104644	6	ABQ99653	Abq99653 Human MS4
225	92.5	8.2	7172	4	AAK84541	AAK84541 Human imm	c 298	89.5	7.9	110000	12	ADQ97138_2	Continuation (3 of
226	92.5	8.2	37437	4	AAK84541	AAK84541 Human imm	c 299	89.5	7.9	152048	10	ADL13855	Adl13855 Osteoarthritis
227	92.5	8.2	58226	14	ADZ13229	ADZ13229 Human can	c 300	89.5	7.9	178825	11	ACN45144	Acn45144 Mouse gen
228	92.5	8.2	108359	9	ADAI13316	ADAI13316 Human can	c 301	89.5	7.9	221600	14	ADX80720	Adx80720 Human neu
229	92.5	8.2	110000	2	ADAI13316	ADAI13316 Human can	c 302	89	7.9	762	13	ADS59554	Ads59554 Bacterial
230	92.5	8.2	194534	12	ADQ97481	ADQ97481 Human can	c 303	89	7.9	768	13	ADS62764	Ads62764 Bacterial
231	92	8.1	6053	4	ABK43057	ABK43057 Genomic s	c 304	89	7.9	768	13	ADS63243	Ads63243 Bacterial
232	92	8.1	6053	9	ADBE1213	ADBE1213 Connectiv	c 305	89	7.9	66494	6	ABQ88140	Abq88140 Human ost
233	92	8.1	32313	5	ABE82912	ABE82912 DNA encod	c 306	89	7.9	110000	12	ADQ97331_0	Adq97331 Human can
234	91.5	8.1	1877	6	ABL90668	ABL90668 Human pol	c 307	88.5	7.8	829	10	ADE76279	Ade76279 Human BSK
235	91.5	8.1	2080	12	ADQ80905	ADQ80905 Streptomy	c 308	88.5	7.8	2781	10	ADBE62847	Adbe62847 Human .CDN
236	91.5	8.1	3828	14	ADCA31152	ADCA31152 Human ORF	c 309	88.5	7.8	3196	4	AALO4311	Aalo4311 Human .rep
237	91.5	8.1	3335	5	AASe6938	AASe6938 DNA encod	c 310	88.5	7.8	3593	4	AASe36134	Aase36134 Human car
238	91.5	8.1	3847	5	AASe76068	AASe76068 DNA encod	c 311	88.5	7.8	3593	4	AASe46828	Ade46828 Human car
239	91.5	8.1	3859	5	AASe76893	AASe76893 DNA encod	c 312	88.5	7.8	3593	13	ADJ08246	Adj08246 Human car
240	91.5	8.1	4354	5	AASe70274	AASe70274 DNA encod	c 313	88.5	7.8	3834	5	AASe71283	Aas71283 DNA encod
241	91.5	8.1	4354	5	AASe81832	AASe81832 DNA encod	c 314	88.5	7.8	3852	5	AASe79043	Aas79043 DNA encod
242	91.5	8.1	5377	5	AASe69665	AASe69665 DNA encod	c 315	88.5	7.8	4014	5	AASe74322	Aas74322 DNA encod
243	91.5	8.1	6042	5	AASe74914	AASe74914 DNA encod	c 316	88.5	7.8	4167	5	AASe78979	Aas78979 DNA encod
244	91.5	8.1	6042	10	ADQ9755	ADQ9755 Novel DNA	c 317	88.5	7.8	4819	4	AAK87359	Aak87359 Human imm
245	91.5	8.1	6111	9	ADB83173	ADB83173 Human cDN	c 318	88.5	7.8	6181	4	AASe26700	Aas26700 Human gen
246	91.5	8.1	7383	5	AASe73854	AASe73854 DNA encod	c 319	88.5	7.8	6181	8	ADAs98599	Ada98599 Human sec
247	91.5	8.1	7383	5	AASe73854	AASe73854 DNA encod	c 320	88.5	7.8	6181	8	ABX74049	Abx74049 Human nov
248	91.5	8.1	8446	6	ADG79370	ADG79370 Human sec	c 321	88.5	7.8	6181	8	ADA44324	Ada44324 Human sec
249	91.5	8.1	11538	4	AAK64949	AAK64949 Human imm	c 322	88.5	7.8	6181	10	ADC20713	Adc20713 Human sec
250	91.5	8.1	22713	4	AAK64950	AAK64950 Human imm	c 323	88.5	7.8	6181	10	ADF10882	Adf10882 Human sec
251	91.5	8.1	25220	12	ADJ12510	ADJ12510 DNA fragm	c 324	88.5	7.8	8551	5	AASe72883	Aas72883 DNA encod
252	91.5	8.1	32199	4	AAK90296	AAK90296 Human dig	c 325	88.5	7.8	13845	12	ADJ12531	Adj12531 DNA fragm
253	91.5	8.1	32199	4	AAK90296	AAK90296 Human dig	c 326	88.5	7.8	32178	5	AASe34500	Aas34500 Human DNA
254	91.5	8.1	32199	6	ABSe99850	ABSe99850 Genomic D	c 327	88.5	7.8	47040	12	ADQ97807	Adq97807 Mouse can
255	91.5	8.1	32199	10	ADB933003	ADB933003 Human col	c 328	88.5	7.8	90043	11	ACN44608	Acn44608 Mouse gen
256	91.5	8.1	69648	12	ADQ97934	ADQ97934 Human can	c 329	88.5	7.8	110000	6	ABSe90193_3	Abse90193_3
257	91.5	8.1	85859	11	ACN44222	ACN44222 Human gen	c 330	88.5	7.8	110000	6	ABQ69245_23	Abq69245_23
258	91.5	8.1	190276	14	ADY94258	ADY94258 BRAF prot	c 331	88.5	7.8	110000	6	ABQ87681_3	Abq87681_3
259	91.5	8.1	214019	10	ADL13809	ADL13809 Osteoarthritis	c 332	88.5	7.8	110000	8	ABX33717_3	Abx33717_3
260	91.5	8.1	302603	11	ADP75187	ADP75187 Osteoarthritis	c 333	88.5	7.8	181257	12	ADF69677	Adf69677 Human SLC
261	90.5	8.0	529	14	ADZ77221	ADZ77221 L-1 retro	c 334	88.5	7.8	213251	6	ABQ67193	Abq67193 Listeria
262	90.5	8.0	1647	8	ACA35703	ACA35703 Prokaryot	c 335	88.5	7.8	222880	10	ADC87622	Adc87622 Human GPC
263	90.5	8.0	1782	11	ACH95643	ACH95643 Klebsiell	c 336	88	7.8	1632	8	ACA32119	ACA32119 Prokaryot
264	90.5	8.0	2166	6	ABQ14591	ABQ14591 Oligonucl	c 337	88	7.8	1767	12	ADBE43923	Adbe43923 Human DP1
265	90.5	8.0	2166	6	ABQ14590	ABQ14590 Oligonucl	c 338	88	7.8	1769	12	ADQ97811	Adq97811 Human can
266	90.5	8.0	3850	4	AAK64888	AAK64888 Human imm	c 339	88	7.8	1971	14	ADZ49510	Adz49510 Insulin s
267	90.5	8.0	5676	4	AAK37391	AAK37391 Human mus	c 340	88	7.8	8718	6	ABL33273	Ab133273 Human imm
268	90.5	8.0	5676	8	ABX60379	ABX60379 cDNA enco	c 341	88	7.8	13188	2	AAV52203	Aav52203 Streptoco
269	90.5	8.0	5676	11	ADJ31129	ADJ31129 Human mus	c 342	88	7.8	74828	12	ADQ97992	Adq97992 Human can
270	90.5	8.0	16351	11	ADM77461	ADM77461 Human fib	c 343	88	7.8	110000	10	ABSe56454_16	Abse56454_16
271	90.5	8.0	110000	4	AAK95240_07	Continuation (8 of	c 344	88	7.8	110000	12	ADQ97138_3	Adq97138_3
272	90.5	8.0	110000	4	AAK96733_07	Continuation (8 of	c 345	87.5	7.7	727	3	AAZ97418	Aaz97418 Human pro
273	90.5	8.0	110000	6	ABT00010_07	Continuation (8 of	c 346	87.5	7.7	748	3	AASe87500	Aas87500 DNA encod
274	90.5	8.0	110000	6	ABT01503_07	Continuation (8 of	c 347	87.5	7.7	1589	5	AASe87499	Aas87499 DNA encod
275	90.5	8.0	110000	11	ADW70291_07	Continuation (8 of	c 348	87.5	7.7	2228	5	AASe87499	Aas87499 DNA encod
276	90.5	8.0	110000	12	ADH77486_07	Continuation (8 of	c 349	87.5	7.7	2717	5	AASe82908	Aas82908 DNA encod
277	90.5	8.0	116297	12	ADQ97587	ADQ97587 Human can	c 350	87.5	7.7	4002	5	AASe75995	Aas75995 DNA encod
278	90.5	8.0	208700	13	ABD32688	ABD32688 Human can	c 351	87.5	7.7	4890	5	AASe87489	Aas87489 DNA encod
279	90.5	8.0	228139	11	ACN44002	ACN44002 Human gen	c 352	87.5	7.7	5863	12	ADJ12580	Adj12580 DNA fragm
280	90	8.0	2649	4	AAK81646	AAK81646 Human imm	c 353	87.5	7.7	6002	4	AAK73672	Aak73672 Human ner
281	90	8.0	9592	13	ADQ38686	ADQ38686 Human SNP	c 354	87.5	7.7	6042	5	ABAI18816	Abai18816 Human ner
282	90	8.0	9659	13	ADQ38684	ADQ38684 Human SNP	c 355	87.5	7.7	6042	5	ABAI18816	Abai18816 Human ner
283	90	8.0	12553	13	ADQ38681	ADQ38681 Human SNP	c 356	87.5	7.7	6448	5	AASe82911	Aas82911 DNA encod
284	90	8.0	12620	13	ADQ38682	ADQ38682 Human SNP	c 357	87.5	7.7	7197	5	AASe87485	Aas87485 DNA encod
285	90	8.0	24132	4	AAK68729	AAK68729 Human imm	c 358	87.5	7.7	7556	5	AASe82893	Aas82893 DNA encod
286	90	8.0	24132	4	AASe82827	AASe82827 Genomic s	c 359	87.5	7.7	7731	5	AASe87486	Aas87486 DNA encod
287	90	8.0	24132	4	AASe82827	AASe82827 Genomic s	c 360	87.5	7.7	7731	5	AASe87486	Aas87486 DNA encod
288	90	8.0	24132	10	ADG41423	ADG41423 Human res	c 361	87.5	7.7	9339	3	AAA34840	Aaa34840 Human ade
289	90	8.0	24132	11	ADQ97197	ADQ97197 Human res	c 362	87.5	7.7	9339	10	ABZ96656	Abz96656 Human low
290	89.5	7.9	118544	12	ADQ97100	ADQ97100 Human can	c 363	87.5	7.7	9339	11	ABD20506	Abd20506 Human pul
291	89.5	7.9	5853	12	ADJ12575	ADJ12575 DNA fragm	c 364	87.5	7.7	9479	5	AASe66388	Aase66388 DNA encod
292	89.5	7.9	6410	12	ADJ12562	ADJ12562 DNA fragm	c 365	87.5	7.7	11742	5	AASe87514	Aas87514 DNA encod
293	89.5	7.9	7207	5	AAI99054	AAI99054 Human exc	c 366	87.5	7.7	12036	5	AASe75996	Aas75996 DNA encod
294	89.5	7.9	7207	5	AAI63404	AAI63404 Human exc	c 367	87.5	7.7	22421	3	AAA34844	Aaa34844 DNA encod
295	89.5	7.9	8553	9	ADB83218	ADB83218 Human cDN	c 368	87.5	7.7	22421	3	AAF20966	Aaf20966 Human low
296	89.5	7.9	76406	12	ADQ59203	ADQ59203 MSI-H car	c 369	87.5	7.7	22421	10	ABZ96660	Abz96660 Human nuc

370	87.5	7.7	22421	11	ABD20510	Abd20510 Human pul	443	86	7.6	8493	8	ACA03930	ACA03930 cDNA down
371	87.5	7.7	22977	4	AAK77120	AAk77120 Human imm	444	86	7.6	8503	4	AAI58253	AAi58253 Human pol
372	87.5	7.7	23157	5	AAK75998	AAk75998 DNA encod	445	86	7.6	8503	5	ADQ98460	ADq98460 DNA encod
c 373	87.5	7.7	37442	4	AAK84166	AAk84166 Human imm	446	86	7.6	8503	9	ADB48220	ADb48220 Novel hum
c 374	87.5	7.7	77781	10	ADL15049	ADl15049 Human mel	c 447	86	7.6	8527	4	AAI60039	AAi60039 Human pol
c 375	87.5	7.7	110000	10	ACF42745_1	Continuation (2 of	448	86	7.6	10769	12	ADP79308	ADp79308 Human muc
c 376	87.5	7.7	143239	12	ADQ17729	Continuation (2 of	c 449	86	7.6	50885	4	AAK70336	AAk70336 Human imm
c 377	87.5	7.7	163321	11	ACN43898	ACn43898 Human gen	c 450	86	7.6	108182	11	ACN44926	ACn44926 Human gen
c 378	87.5	7.7	198073	11	ACN44302	ACn44302 Human gen	c 451	86	7.6	110000	10	ACP67367_13	Continuation (14 o
c 379	87.5	7.7	310268	13	ADB32548	ADb32548 Human can	c 452	86	7.6	110000	10	ACB42401_21	Continuation (22 o
c 380	87	7.7	826	10	ADD34445	ADd34445 Mouse mit	c 453	86	7.6	175338	11	ACN45088	ACn45088 Mouse gen
381	87	7.7	990	14	ACL68201	ACL68201 M. xanthu	c 454	86	7.6	182624	10	ACF65379	ACf65379 Photorhab
382	87	7.7	1314	5	AAK65571	AAk65571 DNA encod	455	86	7.6	201986	11	ACN44430	ACn44430 Human gen
383	87	7.7	3061	12	ADQ35771	ADq35771 Novel mou	456	85.5	7.6	1765	4	ABL15691	ABl15691 Drosophil
384	87	7.7	3321	3	AAK81290	AAk81290 Mouse apo	c 457	85.5	7.6	3765	4	ABL15690	ABl15690 Drosophil
385	87	7.7	6763	3	AAK81309	AAk81309 Mouse FLA	458	85.5	7.6	4413	4	ABL09135	ABl09135 Drosophil
c 386	87	7.7	29384	14	ACL64766	ACL64766 M. xanthu	459	85.5	7.6	5956	12	ADJ12493	ADj12493 DNA fragm
387	87	7.7	39949	12	ADF31997	ADf31997 Full leng	460	85.5	7.6	6766	4	ABK42991	ABk42991 Genomic s
388	87	7.7	48200	12	ADF31998	ADf31998 Cosmid 2A	461	85.5	7.6	6766	4	AAK78681	AAk78681 Human imm
389	87	7.7	110000	6	ABX08336_03	Continuation (4 of	462	85.5	7.6	6766	9	ADB61147	ADb61147 Connectiv
390	87	7.7	110000	12	ADJ25985_03	Continuation (4 of	c 463	85.5	7.6	7190	4	ABL09134	ABl09134 Drosophil
391	87	7.7	110000	12	ADN97989_03	Continuation (4 of	464	85.5	7.6	7576	12	ADJ12479	ADj12479 DNA fragm
392	87	7.7	110000	12	ADO50281_03	Continuation (4 of	465	85.5	7.6	11002	12	ADJ12474	ADj12474 DNA fragm
393	87	7.7	110000	14	ABE85185_03	Continuation (4 of	c 466	85.5	7.6	11378	5	AAK87396	AAk87396 DNA encod
c 394	87	7.7	136328	6	ABZ35015	ABz35015 Human gen	467	85.5	7.6	11661	12	ADJ12491	ADj12491 DNA fragm
395	86.5	7.6	1077	13	ADS46222	ADs46222 Bacterial	468	85.5	7.6	13234	5	AAK82685	AAk82685 DNA encod
396	86.5	7.6	1644	13	ADS45761	ADs45761 Bacterial	469	85.5	7.6	49999	2	AAZ23901	AAz23901 Human LOB
397	86.5	7.6	2955	5	AAK71125	AAk71125 DNA encod	c 470	85.5	7.6	67253	14	AEA61178	AEa61178 Human GPR
398	86.5	7.6	3090	5	AAK79829	AAk79829 DNA encod	471	85.5	7.6	110000	12	ADQ97331_2	Continuation (3 of
399	86.5	7.6	3235	5	AAK66519	AAk66519 DNA encod	472	85.5	7.6	192427	10	ADL13825	ADl13825 Osteoarth
400	86.5	7.6	3235	5	AAK70247	AAk70247 DNA encod	473	85.5	7.6	330973	11	ACN44846	ACn44846 Human gen
401	86.5	7.6	3235	5	AAK70793	AAk70793 DNA encod	474	85.5	7.6	342748	14	ADZ13793	ADz13793 Human can
402	86.5	7.6	3235	5	AAK73829	AAk73829 DNA encod	475	85	7.5	1005	13	ADT43625	ADt43625 Bacterial
403	86.5	7.6	3235	5	AAK74990	AAk74990 DNA encod	476	85	7.5	1454	10	ABT42485	ABt42485 Toxicity
404	86.5	7.6	3316	5	AAK75000	AAk75000 DNA encod	477	85	7.5	1454	13	ADW41811	ADw41811 Rat card
405	86.5	7.6	3316	5	AAK70804	AAk70804 DNA encod	478	85	7.5	1951	4	ABL07583	ABl07583 Drosophil
406	86.5	7.6	3316	5	AAK70259	AAk70259 DNA encod	479	85	7.5	2328	9	ADA31682	ADa31682 DNA encod
407	86.5	7.6	3316	5	AAK73840	AAk73840 DNA encod	480	85	7.5	3018	6	ABK86166	ABk86166 Human ino
408	86.5	7.6	3588	5	AAK68192	AAk68192 DNA encod	481	85	7.5	3042	9	ABK54540	ABk54540 Human pho
409	86.5	7.6	3779	5	AAK81522	AAk81522 DNA encod	482	85	7.5	3157	8	ABX72211	ABx72211 Human NOV
410	86.5	7.6	4107	5	AAK71251	AAk71251 DNA encod	483	85	7.5	4026	4	ABD63144	ABd63144 Human cdn
411	86.5	7.6	4458	5	AAK72084	AAk72084 DNA encod	484	85	7.5	4036	4	ABL07582	ABl07582 Drosophil
412	86.5	7.6	5403	7	AD531026	ADg31026 Human gen	c 485	85	7.5	8739	4	AAK77090	AAk77090 Human imm
413	86.5	7.6	5403	7	ADY36414	ADy36414 HIRA geno	486	85	7.5	48727	4	AAK67375	AAk67375 Human imm
414	86.5	7.6	6038	12	ADJ12454	ADj12454 DNA fragm	c 487	85	7.5	99916	6	ADIO3931	ADi03931 Human enz
415	86.5	7.6	6152	12	ADJ12537	ADj12537 DNA fragm	c 488	85	7.5	110000	6	ABA90521_07	Continuation (8 of
c 416	86.5	7.6	6153	12	ADJ12511	ADj12511 DNA fragm	c 489	85	7.5	110000	13	ABD32806_1	Continuation (2 of
c 417	86.5	7.6	6984	6	ABN80135	ABn80135 Human che	490	85	7.5	110000	14	AEA61120_4	Continuation (5 of
c 418	86.5	7.6	7643	5	AAK79148	AAk79148 DNA encod	491	85	7.5	110000	14	AEA61102_2	Continuation (3 of
c 419	86.5	7.6	7769	5	AAK92381	AAk92381 DNA encod	492	85	7.5	157090	12	ADO47194	ADo47194 DNA seque
c 420	86.5	7.6	9330	8	AAK51996	AAk51996 Mouse Cyp	493	85	7.5	238484	11	ACN44210	ACn44210 Human gen
c 421	86.5	7.6	12275	8	AAK51995	AAk51995 Mouse Cyp	494	85	7.5	240000	8	ACD13446	ACd13446 Human DNA
c 422	86.5	7.6	30515	4	ABK42321	ABk42321 Genomic s	495	84.5	7.5	2637	3	AAA79729	AAa79729 Pinus rad
c 423	86.5	7.6	30515	4	AAK68732	AAk68732 Human imm	496	84.5	7.5	3756	5	AAK67699	AAk67699 DNA encod
c 424	86.5	7.6	30515	4	AAK85029	AAk85029 Human imm	497	84.5	7.5	3950	12	ADQ67308	ADq67308 Novel hum
c 425	86.5	7.6	30515	9	ADJ66477	ADj66477 Connectiv	c 498	84.5	7.5	5794	5	ABA16849	ABa16849 Human ner
c 426	86.5	7.6	42595	12	ADJ12615	ADj12615 DNA fragm	c 499	84.5	7.5	6069	5	ABA16851	ABa16851 Human ner
427	86.5	7.6	49355	12	ADQ97810	ADq97810 Human can	500	84.5	7.5	6172	12	ADJ12453	ADj12453 DNA fragm
428	86.5	7.6	100543	6	ABE52816	ABe52816 Genomic D	ALIGNMENTS						
c 429	86.5	7.6	116592	8	ABX15519	ABx15519 Human tyr	RESULT 1						
c 430	86.5	7.6	116592	10	AAK47900	AAk47900 Human tra	AAZ47118	AAZ47118 standard; cDNA; 1920 BP.					
c 431	86.5	7.6	116592	14	ABE47448	ABe47448 Human sul	XX	AAZ47118;					
c 432	86.5	7.6	116792	11	ACN44574	ACn44574 Human gen	DT	15-MAR-2000 (first entry)					
c 433	86.5	7.6	207542	14	ABE32385	ABe32385 Human gen	XX	Human CD40 receptor associated protein gene.					
c 434	86.5	7.6	207557	11	ABE32371	ABe32371 Human gen	DE	Human CD40 receptor associated protein gene.					
c 435	86.5	7.6	276820	14	ADP75188	ADp75188 Human ADA	XX	Antiarteriosclerotic; antiarthritic; neuroprotective; dermatological;					
c 436	86.5	7.6	349901	10	ADC86940	ADc86940 Human GPC	XX						
437	86	7.6	1053	10	ACF68579	ACf68579 Photorhab	KW						
438	86	7.6	2844	4	ABL09237	ABl09237 Drosophil							
439	86	7.6	3732	3	AAZ60932	AAz60932 Nucleotid							
440	86	7.6	4844	4	ABL09236	ABl09236 Drosophil							
441	86	7.6	6052	12	ADJ12542	ADj12542 DNA fragm							
442	86	7.6	6203	12	ADJ12521	ADj12521 DNA fragm							

KW immunosuppressive; antiinflammatory; immunosuppressive; antiallergic;
 KW human; CD40 receptor associated protein; CRAP; cytoplasmic domain;
 KW tumour necrosis factor; TNF; receptor; superfamily; CD30; homology;
 KW TNF receptor associated factor; TRAF; modulator; signalling pathway;
 KW diagnosis; NF-kappaB; Jun; kinase; atherosclerosis; multiple sclerosis;
 KW arthritis; systemic lupus erythematosus; graft rejection; allergy;
 KW graft versus host disease; autoimmune disease; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO9955859-A2.
 XX
 XX 04-NOV-1999.
 PD
 XX 28-APR-1999; 99WO-EP003025.
 XX
 XX 29-APR-1998; 98EP-00201392.
 XX
 XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 XX
 XX Pype SMC, Remacle JEFJG, Huylebroeck DFE;
 XX
 XX WPI; 2000-062029/05.
 DR
 XX P-PSDB; AAY56019.
 DR
 XX Novel proteins used to treat inflammatory diseases, NF-kappaB related
 PT diseases and for improvement of anti-tumor treatments.
 PT
 XX
 PS Claim 9; Page 37-39; 48pp; English.
 XX
 CC This sequence represents the gene encoding human CD40 receptor associated
 CC protein (CRAP). CRAP is a functional protein capable of interacting with
 CC the cytoplasmic domain of CD40 and/or other receptors of the tumour
 CC necrosis factor (TNF) receptor superfamily such as CD30 and TNF receptor
 CC 1, where the protein has no homology to TNF receptor associated factor
 CC (TRAF) proteins. The CD40 binding proteins can be used as modulators of
 CC the CD40 signalling pathway, especially to diagnose and treat TRAF-
 CC related, CD40-related, NF-kappaB related and/or Jun (kinase)-related
 CC diseases, and for the improvement of anti-tumour diseases. Diseases which
 CC may be treated include atherosclerosis, arthritis, multiple sclerosis,
 CC systemic lupus erythematosus, graft rejection, graft versus host disease,
 CC allergy, and autoimmune disease. The proteins can be used to sensitize
 CC tumour cells to anti-tumour treatments and to screen for compounds which
 CC interfere with the interaction of the proteins with other protein
 CC components of the TRAF, CD40 or NF-kappaB related pathway
 XX
 XX Sequence 1920 BP; 599 A; 327 C; 435 G; 557 T; 0 U; 2 Other;
 SQ
 Alignment Scores:
 Pred. No.: 9.08e-124 Length: 1920
 Score: 1131.00 Matches: 220
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps:
 US-10-757-745-2_COPY_54_273 (1-220) x AAZ47118 (1-1920)
 QY 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
 DB 179 ATGGAAGGCTCTGAACTCTACTTCTGAGCTCCGGTGGAGGAGCGCTTGGACGC 238
 QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAenGluThrThr 40
 DB 239 CGACCTGAACCATCTCTGAGCCAGACCTATGTTGACCTAACCAATGAAGAAACAAC 298
 QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAenGlySerMet 60
 DB 299 GAITCCACCACTTCTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGCGACATG 358
 QY 61 PheSerLeuIleThrTyrAenIleAspGlyLeuAspLeuAenLeuSerGluArgAla 80
 DB 359 TTCTCTCATTAACCTGGAATATGATGGATTAGATCTAAACAATCTCTCAGAGAGGCT 418

QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
 DB 419 CGAGGGGTGCTCTCTACTTACCTTGTACAGCCAGATGTGATATTTCTACAGGAAGTT 478
 QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAenTyrGluIleIleThrGly 120
 DB 479 ATTCCCCCATATTATAGCTACCTAAAGAGAGATCAAGTAAATTATGATATTATACAGT 538
 QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
 DB 539 CATGAAGAAGGATATTTCCAGCTATAATGTTGAAGAAATCAAGAGTGAATATAAAGC 598
 QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAenLeuLeuCysValHisVal 160
 DB 599 CAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 658
 QY 161 AenValSerGlyAenGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
 DB 659 AATGTGTCAGGAATGAGCTTTGCTTATGATCATCCCATTTTGGAGAGACCAAGAGGGCAT 718
 QY 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
 DB 719 GCTCGGAACGAATGAATCAGTTAAATGCTTTTAAAGAAATGCAAGAGGCTCCAGAG 778
 QY 201 SerAlaThrValIlePheAlaGlyAspThrAenLeuArgAspArgGluValThrArgCys 220
 DB 779 TCAGTACAGTTATATTTGCAGGAGATACAAATCTAAGGGATCGAGAGGTTACCAGATGT 838
 RESULT 2
 ADD19013
 ID ADD19013 standard; DNA; 1936 BP.
 XX
 AC ADD19013;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human disease related protein DNA sequence SeqID502.
 XX
 KW human; disease state; cytostatic; antiinflammatory; ophthalmological;
 KW antiarteriosclerotic; vulnery; gene therapy; angiogenesis; apoptosis;
 KW hypoxia-regulated condition; tumorigenesis; gluconeogenesis;
 KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
 KW glucose transportation; catecholamine synthesis; iron transport;
 KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
 KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
 KW inflammatory condition; wound healing; Gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO2003018621-A2.
 PN
 XX 06-MAR-2003.
 PD
 XX 23-AUG-2002; 2002WO-GB003892.
 PF
 XX 23-AUG-2001; 2001GB-00020558.
 PR
 XX 05-OCT-2001; 2001GB-00024037.
 XX
 XX (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX
 XX Kingeman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
 PI
 XX WPI; 2003-290046/28.
 XX
 DR P-PSDB; ADD19012.
 DR
 XX New substantially purified polypeptide, useful for diagnosing or treating
 PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
 PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
 PT wound healing.
 XX
 XX Claim 27; SEQ ID NO 502; 424pp; English.
 PS
 XX

CC This invention relates to novel human genes and gene product which are
CC implicated in certain disease states. Compounds which modulate the
CC proteins of the invention may have cytostatic, antiinflammatory, the
CC ophthalmological, antiarteriosclerotic or vulnerary activities. The
CC sequences of the invention may be useful for gene therapy. The invention
CC may be useful for diagnosing or treating a hypoxia-regulated condition,
CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
CC erythropoiesis, or the biological response to hypoxia conditions
CC including processes such as glycolysis, gluconeogenesis, glucose
CC transportation, catecholamine synthesis, iron transport or nitric oxide
CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
CC inflammatory conditions or wound healing. The present sequence is that of
CC a disease related protein encoding DNA sequence of the invention.
XX

SQ Sequence 1936 BP; 617 A; 330 C; 431 G; 558 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.18e-124 Length: 1936
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x ADD19013 (1-1936)

Qy 1 MetGluArgAlaLeuAasnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 176 ATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCCGGTGGAGGAGCGCCTTGGAAAGC 235
Qy 21 ArgProGluThrIleSerGluProIysThrTyrValAspLeuThrAsnGluGluThr 40
Db 236 CGACCTGAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACCAACT 295
Qy 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAasnGlySerWet 60
Db 296 GATTCACCACTTCTAAATCAGCCCATCTGAAAGATCTCAGCAAGAAATGGCAGCATG 355
Qy 61 PheSerIleuThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 356 TTCTCTCTCAATACCTGGAATATTGATGATTAGATTAGATCTAAACAATCTGTACAGAGGGCT 415
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 416 CGAGGGGTGTCTCTACTTACCTTGTACAGCCAGATGTGATATTCTACAGGAAGTT 475
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 476 ATTCCTCCCATATTATAGCTACTTAAGNAGAGATCAAGTAATTATGAGATTATTACAGGT 535
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuSer 140
Db 536 CATGAAGAAGGATATTTACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAAGAGC 595
Qy 141 GlnGluIleIleProPheProSerThrIysMetMetArgAsnLeuLeuCysValHisVal 160
Db 596 CAAGAGATATTATCTCTTTTCCAAGTACCACCAATGATGAGAAACCTTTTATGTGTGTCATGTG 655
Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 656 AACGTGTGAGGAATAGCTTTGTCTTATGATCATCCATTTGGAGAGCACCAGAGGGCAT 715
Qy 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 716 GCTCGGAACGAATGAATCAGTTAAATAATGTTTTTAAAGAAATGCAAGAGGCTCCAGAG 775
Qy 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 776 TCAGCTCAGTTATATTTCAGGAGATACAAATCTAAGGGATCGAGAGGTTTACCAGATGT 835
RESULT 3
ADP25361

ID ADP25361 standard; cDNA; 1936 BP.
XX
AC ADP25361;
XX
DT 18-NOV-2004 (first entry)
XX
DE PRO polypeptide encoding cDNA SEQ ID NO:475.
XX
KW ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antiporiatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
XX
OS Unidentified.
XX
FN WO2004041170-A2.
XX
PD 21-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-US034312.
XX
PR 01-NOV-2002; 2002US-0423394P.
XX
PA (GETH) GENENTECH INC.
XX
PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WJ;
PI Wu TD;
XX
DR WPI; 2004-419628/39.
DR P-PSDB; ADP25362.
XX
PT New PRO polypeptides and polynucleotides, useful for treating e.g. erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral nervous system.
XX
PS Claim 1; SEQ ID NO 475; 2940pp; English.
XX
CC The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antirheumatic, immunosuppressive, osteopathic, antidiabetic, dermatological, antiporiatic, antiallergic, antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjogren's syndrome, autoimmune vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polynuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polynuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence encodes a PRO protein of the invention.
XX
SQ Sequence 1936 BP; 617 A; 330 C; 431 G; 558 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9.18e-124 Length: 1936
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-10-757-745-2_COPY_54_273 (1-220) x ADP25361 (1-1936)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
DB 176 ATGGAAGGGCTCTGAACCTCTTCTGAGCGCTCCGGTGGAGGAGCGCTTGGAGCGC 235

QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
DB 236 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAAGAAACAAC 295

QY 41 AspSerThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 296 GATTCACACCTCTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATG 355

QY 61 PheSerLeuIleThrTyrPheThrAlaLeuAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 356 TTCTCTCTCATTTACCTGGGAATATTGATGATTAGATCTAAACAATCTGTACAGAGGGCT 415

QY 81 ArgGlyValCysSerTyrLeuAlaLeuThrSerProAspValIlePheLeuGlnGluVal 100
DB 416 CGAGGGGTGTCTCTTCTTCTGATGCTTGTACAGCCAGATGTGATATTCTACAGGAAGTT 475

QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
DB 476 ATTCCCCCATATTATAGCTTACCTAAAGAGAGATCAAGTAATTATGAGATTATTACAGGT 535

QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
DB 536 CATGAAGAAGGATATTTCACAGCTATTATGTTGAAGAAATCAAGAGTGAATTAAGAAC 595

QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
DB 596 CAAGAGATTATCTCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 655

QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
DB 656 AACGTGTCAAGAAATGAGCTTTTCCCTTATGACATCCCATTTGGAGAGCCAGAGGGCAT 715

QY 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
DB 716 GCTGCGGAACGAATGAATCAGTTAAATATGTTTTTAAAGAAATGCAAGAGGCTCCAGAG 775

QY 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
DB 776 TCAGCTACAGTTATATTTCAGGAGATACAAATCTAAGGGATCGAGAGGTTACAGATGT 835

RESULT 4
ADX06356
ID ADX06356 standard; DNA; 1940 BP.
AC ADX06356;
XX
XX 21-APR-2005 (first entry)
XX
XX Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 921.
DE
XX cytosstatic; cyclin-dependent kinase; cdk; biomarker; gene; ds.
XX Homo sapiens.
XX
XX WO2005012875-A2.
XX
XX 10-FEB-2005.
PD
XX
XX 29-JUL-2004; 2004WO-US024424.
XX
XX 29-JUL-2003; 2003US-0490890P.
PR
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
PA
XX

PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX WPI; 2005-163068/17.
DR P-PSDB; ADX06357.
XX
PT Biomarkers useful for predicting or determining the response of a mammal
PT to a cancer treatment comprising administration of a modulator of cyclin-
PT dependent kinase activity.
XX
XX Claim 5; SEQ ID NO 921; 141pp; English.
XX
CC This invention describes a novel method of predicting or determining
CC whether a mammal will respond or is responding to an anti-cancer agent
CC that modulates cyclin-dependent kinase (cdk) activity. The method
CC comprises measuring the level of one or more biomarkers selected from
CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the
CC invention is utilized in a kit for determining or predicting whether
CC patient would be susceptible or resistant to treatment by an agent
CC modulating cdk activity. The invention also describes a method for
CC utilizing individualized genetic profiles for treating diseases and
CC disorders based on patient's response and molecular level, specialized
CC against the biomarkers and a cell culture model to identify biomarkers.
CC The cdk modulator is preferably N-5-[(1,1-Dimethylethyl)-2-
CC oxazolyl)methyl]thiol-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
CC tartaric acid salt. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at fcp.wipo.int/pub/published_pct_sequences. This
CC sequence encodes a biomarker used in the method of the invention.
XX
SQ Sequence 1940 BP; 613 A; 330 C; 439 G; 558 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9,21e-124 Length: 1940
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-10-757-745-2_COPY_54_273 (1-220) x ADX06356 (1-1940)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
DB 185 ATGGAAGGGCTCTGAACCTCTTCTGAGCGCTCCGGTGGAGGAGCGCTTGGAGCGC 244

QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
DB 245 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 304

QY 41 AspSerThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 305 GATTCACACCTCTCTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGCGAGCATG 364

QY 61 PheSerLeuIleThrTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 80
DB 365 TTCTCTCTCATTTACCTGGGAATATTGATGATTAGATCTAAACAATCTGTTCAGAGGGCT 424

QY 81 ArgGlyValCysSerTyrLeuAlaLeuThrSerProAspValIlePheLeuGlnGluVal 100
DB 425 CGAGGGGTGTGTCTCTTCTTCTTCTGATGCTTGTACAGCCAGATGTGATATTCTTACAGGA 484

QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
DB 485 ATTCCCCCATATTATAGCTTACCTTAAAGAGAGATCAAGTAATTATGAGATTATTACAGGT 544

QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
DB 545 CATGAAGAAGGATATTTCACAGCTATTATGTTGAAGAAATCAAGAGTGAATTAAGAAC 604

QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160

Db 605 CAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTG 664
Qy 161 AsnValSerGlyAsnGluLeuGluMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 665 AACGTGTGAGGAAATGAGCTTTGCTTATGACATCCCATTTGGAGAGCACCAGAGGCGAT 724
Qy 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 725 GCTCGGGAACGAATGAATCAGTTTAAATGCTTTTAAAGAAATGCAAGAGGCTCCAGAG 784
Qy 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 785 TCAGCTACAGTTATATTGTCAGGAGATACAAATCTAAGGGATCGAGAGGTTTACCAGATGT 844
RESULT 5
AAI58997
ID AAI58997 standard; cDNA; 1948 BP.
XX
AC AAI58997;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 1200.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000MO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR P-PSDB; AAM39841.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Claim 1; SEQ ID NO 1200; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,

CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 1948 BP; 614 A; 335 C; 436 G; 563 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 9.27e-124 Length: 1948
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-757-745-2_copy_54_273 (1-220) x AAI58997 (1-1948)
Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 198 ATGGAAAGGGCTCTGAACCTCTACTTCGAGCCTCCGGTGGAGAGCGCTTGGAAACGC 257
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 258 CGACCTGAAACCATCTCTGAGCCAGACCTATGTTGACCTAACCATGAAAGAACACT 317
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 318 GATTCCACCACTTCTAAATTCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATG 377
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 378 TTCTCTCTCAATTACCTGGAATATTGATGGAATAGATCTAAACAATCTGTGAGAGGGCT 437
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 438 CGAGGGGTGTGTTCTTACTTAGCTTGTACAGCCAGATGTGATATTTCTACAGGAAGTT 497
Qy 101 IleProProTyrTyrSerTyrLeuLysLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 498 ATTCCCCCATATTATAGTACCTAAAGAGAGATCAAGTAATATATGAGATTATTACAGGT 557
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 558 CATGAAGARGGATATTTCACAGCTATATAATGTTGAAGAAATCAAGAGTGAATTAAGAAGC 617
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db 618 CAAGAGATTATTCTTTTCCAAAGTACCATAATGATGAGAAACCTTTTATGTGTCATGTG 677
Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 678 AATGTGTGAGGAAATGAGCTTTGCCTTATGACATCCCATTTGGAGAGCACCAGAGGCGAT 737
Qy 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 738 GCTGCGGAACGAATGAATCAGTTTAAATGCTTTTAAAGAAATGCAAGAGGCTCCAGAG 797
Qy 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 798 TCAGCTACAGTTATATTGTCAGGAGATACAAATCTAAGGGATCGAGAGGTTTACCAGATGT 857
RESULT 6
ADQ99219
ID ADQ99219 standard; cDNA; 1948 BP.
XX
AC ADQ99219;
XX
DT 23-SEP-2004 (first entry)
XX
DE DNA encoding human GPCR-like protein seqid 889.
XX
KW ophthalmological; immunomodulatory; cytostatic; antiatherosclerotic;

KW anti-diabetic; GPCR-like protein; ophthalmic disorder;
KW neurological disorder; immunological disorder; nephritic disorder;
KW hormonal dysfunction; cancer; atherosclerosis; diabetes;
KW molecular weight marker; food supplement; human; ss.
XX
OS Homo sapiens.
PN US6569662-B1.
XX
PD 27-MAY-2003.
XX
PF 19-JUL-2000; 2000US-00620312.
XX
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Zhou P, Drmanac RT;
XX WPI; 2001-442255/47.
DR
XX
XX New G-protein-coupled receptor-like polypeptides and polynucleotides,
PT useful for treating diseases of ophthalmic, neurological, immunological
PT and nephritic systems and hormonal dysfunction, cancer, atherosclerosis
PT and diabetes.
XX
PS Example 2; SEQ ID NO 889; 92pp; English.
XX
CC The invention describes an isolated polynucleotide (I) comprising a fully
CC defined (S1) of 749, 3188, 2484, 1169, 2936, 1467, 5773, 5714, 4041,
CC 1372, 3996, 3945, 2735, 1788, 585, 1782, 927, 5714 or 2282 nucleotides as
CC given in the specification, its translated or protein coding portion, its
CC extracellular portion or its active domain. The GPCR-like polypeptides
CC and polynucleotides are useful for the treatment of diseases of
CC ophthalmic, neurological, immunological and nephritic systems. They may
CC also be used to treat hormonal dysfunction, cancer, atherosclerosis and
CC diabetes. The antibodies are useful for detecting or quantitating the
CC polypeptide in tissue. The polypeptides can also be used as molecular
CC weight markers and as a food supplement. This sequence represents a human
CC polynucleotide of the invention.
XX
SQ Sequence 1948 BP; 614 A; 335 C; 436 G; 563 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9,278-124 Length: 1948
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x ADQ99219 (1-1948)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluSerAlaLeuGluArg 20
Db 198 ATGGAAGGGCTCTGAATCTCTACTTCGAGCCCTCGGTTGGAGAGCGCTTGGAAACGC 257
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
Db 258 CGACCTGGAACCACTCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAGAAACAAC 317
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 318 GATTCACCACTCTTAAATCAGCCATCTGAAGATACCTCAGCAAGAAATGCGCAGCATG 377
QY 61 PheSerLeuIleThrTrpAniIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 378 TTCTCTCTCATACCTGGAATATTGATGGATTAGATCTAAACAATCTGTCTGAGAGGGCT 437
QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 438 CGAGGGGGTGTGTCCTACTTAGCTTTGTACAGCCCAAGATGTGATATTCTTACAGGAAGTT 497

QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 498 ATTCCCCCATATTATAGCTACTCTAAAGAAAGAGATCAAGTAATATGAGATTATTACAGGT 557
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 558 CATGAAGAAGGATATTTTCCAGCTATAATGTTGAAGAAATCAAGAGTGAATTAAGAAAGC 617
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysValHisVal 160
Db 618 CAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTG 677
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 678 AATGTGTCCAGGAATGAGCTTTGCCTTATGACATCCCATTTGGAGAGCACCAGAGGGCAT 737
QY 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 738 GCTGCGGAACGAATGAATCAGTTAAATAATGTTTAAAGAAATCAAGAGAGGCTCCAGAG 797
QY 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 798 TCAGCTCAGATTATATTTGCGAGGAGATCAAAATCTAAGGATCGAGAGGTTACCATGAT 857
RESULT 7
ADB48979
ID ADB48979 standard; cDNA; 1948 BP.
XX
AC ADB48979;
XX
DT 04-DEC-2003 (first entry)
XX
DE Novel human cDNA SEQ ID NO 889.
XX
KW ss; cancer; neurodegenerative disease; human.
XX
OS Homo sapiens.
XX
PN US2003104529-A1.
XX
PD 05-JUN-2003.
XX
PF 04-JAN-2002; 2002US-00037270.
XX
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 19-JUL-2000; 2000US-00620312.
XX
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R T.
XX
XX Zhou P, Tang YT, Liu C, Asundi V, Drmanac RT;
XX WPI; 2003-678194/64.
XX
XX New polynucleotide, useful for treating diseases e.g., cancer or
PT neurodegenerative diseases.
XX
PS Claim 1; SEQ ID NO 889; 99pp; English.
XX
CC The invention relates to a polynucleotide comprising a sequence given in
CC the specification, or its mature protein-coding portion, or its
CC complement. The polynucleotide is useful for treating diseases e.g.,
CC cancer or neurodegenerative diseases and many others listed in the
CC specification. The present sequence represents a novel human cDNA. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=20030104529.

SQ	Sequence 1948 BP; 614 A; 335 C; 436 G; 563 T; 0 U; 0 Other;	
Alignment Scores:		
Pred. No.:	9.27e-124	Length: 1948
Score:	1131.00	Matches: 220
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	9	Gaps: 0
US-10-757-745-2_COPY_54_273 (1-220) x ADB48979 (1-1948)		
Qy	1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20	
Db	198 ATGGAAGGGCTCTGAACCTCTACTTCGAGCTCGGTGGAGGAGCGCTTGGACGC 257	
Qy	21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40	
Db	258 CGACCTGAACCACTCTGAGCCCAAGACCTATGTGACCTAACCAATGAAGAACCACT 317	
Qy	41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60	
Db	318 GATTCCACCACTTCTAAATCAGCCATCTCAAGATACTCAGCAAGAAATGCGCAGCATG 377	
Qy	61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80	
Db	378 TTCTCTCTCACTTACCTGGAATATTGATGGATTAGATCTAAACAATCTGTCAGAGGGCT 437	
Qy	81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100	
Db	438 CGAGGGGTGCTTCTACTTAGCTTTGTACAGCCAGATGTGATATTTCACAGGAGTT 497	
Qy	101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120	
Db	498 ATTCCCCATATTATAGCTACCTAAAGAAGAGATCAAGTAATTATGAGATTATTACAGGT 557	
Qy	121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140	
Db	558 CATGAAGAAGGATATTTCCAGCTGATATATGTGAAGAAATCAAGAGTGAATTTAAAGC 617	
Qy	141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160	
Db	618 CAAGAGATTATTCCTTTCCAGTACCCAAATGATGAGAAACCTTTTATGTGTGATGTG 677	
Qy	161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180	
Db	678 AATGTGTCCAGGAATGAGCTTTGCTTATGACATCCCATTTGGAGAGCACCAGAGGGCAT 737	
Qy	181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200	
Db	738 GCTCGGGAACGAATGAATCACTTAAATAATGTTTAAAGAAATGCAAGAGGCTCCAGAG 797	
Qy	201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220	
Db	798 TCAGCTACAGTTATATTTCAGAGGAGATACAATCTTAGGGATCGAGAGGTTTACCAGATGT 857	
RESULT 8		
AAI60783		
ID	AAI60783 standard; cDNA; 1958 BP.	
XX		
AC	AAI60783;	
XX		
DT	22-OCT-2001 (first entry)	
XX		
DE	Human polynucleotide SEQ ID NO 4772.	
XX		
KW	Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;	
KW	peripheral nervous system; neuropathy; central nervous system; CNS;	
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;	
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;	
KW	chemokinetic; thrombolytic; drug screening; arthritis; inflammation;	
KW	leukaemia; ss.	
XX		
OS	Homo sapiens.	
XX		
FN	WO200153312-A1.	
XX		
PD	26-JUL-2001.	
XX		
PF	26-DEC-2000; 2000WO-US034263.	
XX		
PR	23-DEC-1999; 99US-00471275.	
PR	21-JAN-2000; 2000US-00488725.	
PR	25-APR-2000; 2000US-0052317.	
PR	20-JUN-2000; 2000US-00598042.	
PR	19-JUL-2000; 2000US-00620312.	
PR	03-AUG-2000; 2000US-00653450.	
PR	14-SEP-2000; 2000US-00662191.	
PR	19-OCT-2000; 2000US-00693036.	
PR	29-NOV-2000; 2000US-00727344.	
XX	(HYSE-) HYSEQ INC.	
XX		
PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;	
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;	
PI	Zhou P, Goodrich R, Drmanac RT;	
XX		
DR	WPI; 2001-442253/47.	
DR	P-PSDB; AAM41627.	
XX		
PT	Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.	
PS	Claim 1; SEQ ID NO 4772; 10078pp; English.	
XX		
CC	The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nontropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification	
SQ	Sequence 1958 BP; 613 A; 339 C; 442 G; 564 T; 0 U; 0 Other;	
Alignment Scores:		
Pred. No.:	9.34e-124	Length: 1958
Score:	1131.00	Matches: 220
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	4	Gaps: 0
US-10-757-745-2_COPY_54_273 (1-220) x AAI60783 (1-1958)		
Qy	1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20	
Db	210 ATGGAAGGGCTCTGAACCTCTACTTCGAGCTCGGTGGAGGAGCGCTTGGACGC 269	
Qy	21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40	
Db	270 CGACCTGAACCACTCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAAGAACCACT 329	
Qy	41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60	
Db	330 GATTCCACCACTTCTAAATCAGCCATCTGAAGATACTCAGCAAGAAATGCGCAGCATG 389	
Qy	61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80	

PA (JONE/) JONES D A.
XX
PI Lasek AW, Jones DA;
XX
DR WPI; 2003-265756/26.
XX
PT New combination comprising cDNAs that are differentially expressed in
PT colon disorder, useful for diagnosing, treating, staging or monitoring
PT treatment for colon cancers.
XX
PS Claim 1; SEQ ID NO 88; 231pp; English.
XX
CC The invention relates to a combination comprising cDNAs that are
CC differentially expressed in colon disorder. The methods and compositions
CC of the present invention are useful for diagnosing, treating, staging or
CC monitoring treatment for colon cancer. They are also useful in high
CC throughput methods for using cDNAs to detect differential expression of
CC nucleic acids in a sample, screening molecules or compounds to identify a
CC ligand which specifically binds a cDNA and using a protein to screen
CC molecules or compounds to identify at least one ligand which specifically
CC binds the protein. The present sequence represents a human cDNA
CC differentially expressed in colon cancer.
XX
SQ Sequence 3152 BP; 875 A; 643 C; 707 G; 926 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 1.85e-123 Length: 3152
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x ADA10970 (1-3152)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
DB 1411 ATGGAAGGGCTCTGAATCTCTACTTCGAGCCTCCGGTGGAGAGCGCTTGGAAACGC 1470

QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 1471 CGACTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAGAACAACACT 1530

QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 1531 GATTCCACCCTTCTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGCATG 1590

QY 61 PheSerIleuThrThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 1591 TTCCTCTCATTACCTGGAAATATTGATGGATTAGATCTAAACAATCTGTACAGAGGGCT 1650

QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
DB 1651 CGAGGGGTGTCTCTACTTAGCTTGTACAGCCAGATGTGATATTTCTACAGGAAGTT 1710

QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerAsnTyrGluIleIleThrGly 120
DB 1711 ATTCCCCATATTATAGCTACTTAAGAAGAGATCAAGTAATATTAGATTATTACAGGT 1770

QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
DB 1771 CATGAAGAAGGATATTTCCACAGCTATATATGTTGAAGAAATCAAGAGTGAATTTAAAGC 1830

QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
DB 1831 CAAGAGATTATTCCTTTTCCAGTAGTACCAAAATGATGAGAAACCTTTTATGTGTCAGTGTG 1890

QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
DB 1891 AATGTGTGAGAAATGAGCTTTGCTTATGATCATCCCATTTGGAGAGCACCAGAGGGCAT 1950

QY 181 AlalaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200

Db 1951 GCTGCGGACGAATGAATCAGTTAAATGGTTTTAAAGAAATGCAAGAGCTCCAGAG 2010
Qy 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 2011 TCAGCTACAGTTATATTTGCAGGAGATACAAATCTAAGGGATCGAGAGTTTACCAGATGT 2070

RESULT 11
AAC98160
ID AAC98160 standard; cDNA; 1296 BP.
XX
AC AAC98160;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:170.
XX
DB Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW identification; cytostatic; cardioactive; neuroprotective; vulnerary;
KW immunomodulatory; muscular; gynaecological; gastrointestinal;
KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;
KW neural disorder; immune system disorder; muscular disorder;
KW reproductive disorder; gastrointestinal disorder; renal disorder;
KW infectious disease; cardiovascular disorder; ss.
XX
OS Homo sapiens.
XX
FN WO200055351-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005883.
XX
PR 12-MAR-1999; 99US-0124270P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587534/55.
XX
P-PSDB; AAB53403.
XX
FT Colon cancer associated gene sequences, referred to as colon cancer
FT antigens, useful for the treatment, prevention, and diagnosis of colon
FT disorders such as colon cancer.
XX
PS Claim 1; Page 597; 2104pp; English.
XX
CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
CC vulnerary, nephrotropic, antiinfective and antibacterial activities, and
CC can be used in gene therapy. The colon cancer antigen polynucleotides,
CC proteins and antibodies to the proteins are useful for the prevention,
CC treatment and diagnosis of colon disorders, such as colon cancer. The
CC polynucleotides may be used in diagnostics and research, such as for
CC chromosome identification, and as hybridisation probes. The proteins may
CC also be used to prevent diseases such as neural disorders, immune system
CC disorders, muscular disorders, reproductive disorders, gastrointestinal
CC disorders, wounds, renal disorders, infectious diseases and
CC cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 1296 BP; 376 A; 250 C; 326 G; 333 T; 0 U; 11 Other;

Alignment Scores:
Pred. NO.: 4.6e-123 Length: 1296
Score: 1123.00 Matches: 219
Percent Similarity: 99.55% Conservative: 0
Best Local Similarity: 99.55% Mismatches: 1
Query Match: 99.29% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x AAC98160 (1-1296)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluSerAlaLeuGluArg 20
DB 183 ATGGAAGGGCTCTGAACCTCTGAGCGCTCGGTTGGAGGAGCGCTTGGACGC 242

QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
DB 243 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAACT 302

QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnLeuAsnGlySerMet 60
DB 303 GATTCACCCACTTCTAAATCAGCCATCTGAAGATCTCAGCAAGAAAATGCCAGCATG 362

QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 363 TTCTCTCTCTATTAACCTGGAATATTGATGATTAGATCTAAACAATCTGTGACAGAGGGCT 422

QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
DB 423 CGAGGGGTGTGTTCTTACTTACTTGTACGCCAGATGATGATTTCTACAGAGATT 482

QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
DB 483 ATTCCCCCATATTATAGCTACCTAAAGAGAGATCAAGTAATTATGAGATTATTACAGT 542

QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
DB 543 CATGAAGAAGGAKATTTCACAGCTATAATGTTGAAGAAAATCAAGAGTGAATTAAGAGC 602

QY 141 GlnGluIleIleProPheProSerThrTyrMetMetArgAsnLeuLeuCysValHisVal 160
DB 603 CAAGAGATTATTCTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTG 662

QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
DB 663 AAYGTGTGAGGAATGAGCTTTGCTTATGACATCCATTTGGAGACACAGAGGCAT 722

QY 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
DB 723 GCTCGCGAAGCAATGAATCAGTTAAATAATGTTTAAAGAAAATGCAAGAGGCTCCAGAG 782

QY 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
DB 783 TCAGCTACAGTTATATTTCAGGAGATACAAATCTAAGGGATCGAGAGGTACCATGT 842

RESULT 12

AAH15146

ID AAH15146 standard; cDNA; 1898 BP.

AC AAH15146;

XX 26-JUN-2001 (first entry)

DT Human cDNA sequence SEQ ID NO:13209.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX Homo sapiens.

XX EPI074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-00116126.

XX 29-JUL-1999; 99JP-00248036.

XX 27-AUG-1999; 99JP-00300253.

XX 11-JAN-2000; 2000JP-00118776.

XX 02-MAY-2000; 2000JP-00183767.

XX 09-JUN-2000; 2000JP-00241899.

XX (HELI-) HELIX RES INST.

XX PA

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX Claim 8; SEQ ID NO 13209; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention

XX Sequence 1898 BP; 590 A; 327 C; 426 G; 555 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.05e-122 Length: 1898
Score: 1122.00 Matches: 219
Percent Similarity: 99.55% Conservative: 0
Best Local Similarity: 99.55% Mismatches: 1
Query Match: 99.20% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x AAH15146 (1-1898)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
DB 160 ATGGAAGGGCTCTGAACCTCTGAGCGCTCGGTTGGAGAGCGCTTGGACGC 219

QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
DB 220 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAACT 279

QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnLeuAsnGlySerMet 60
DB 280 GATTCACCCACTTCTAAATCAGCCATCTGAAGATCTAAGCAATCTGTGACAGAGGGCT 339

QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 340 TTCTCTCTCTATTAACCTGGAATATTGATGATTAGATCTAAACAATCTGTGACAGAGGGCT 399

QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
DB 400 CGAGGGGTGTGCTCTTACTTACTTGTACAGCCAGATGTTGATATTCTACAGGAAGTT 459

QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
DB 460 ATTCCCCCATATTATAGCTACCTAAAGAGAGATCAAGTAATTATGAGATTATTACAGGT 519

QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140

Db	520	CATGAAGAAGGATATTTT	CACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAAAGC	579
Qy	141	GlnGluIleileProPheProSerThrIysMetMetArgAsnLeuLeuCysValHisVal	160	
Db	580	CAAGAGATTATTCCTTTTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCATGTG	639	
Qy	161	AsnValSerGlyAsnGlnLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis	180	
Db	640	AACTGTGAGGAATAGAGCTTTGCCTTATGACATCCCATTTTGAGAGCACCAAGAGGGCAT	699	
Qy	181	AlaAlaGluArgMetAsnGlnLeuIysMetValLeuIysIysMetGlnGluAlaProGlu	200	
Db	700	GCTCGCGGAACGAATGAATCAGTFAAAATGTTTTAAAGAAAAATGCAAGAGGCTCCAGAG	759	
Qy	201	SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys	220	
Db	760	TCAGCTACAGTTATATTTTGCAGGAGATACAAATCTTAAGGATCGAGAGGTACCAAGTGT	819	

RESULT 13

AAH08073

ID AAH08073 standard; cDNA: 752 BP.

AC AAH08073:

DT 26-JUN-2001 (first entry)

Human cDNA clone (5'-primer) SEQ ID NO:4908.

Human; primer; detection; diagnosis; antisense therapy; qene therapy; ss.

OS Homo sapiens.

PN EP1074617-A2.

PD 07-FEB-2001.

28-JUL-2000; 2000EP-00116126.

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.
yy

PA (HELI-) HELIX RES INST.

DT	Ota E	Tsogai F	Nishikawa F	Havachi K	Saito K	Vamamoto T.
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PI Oka I, IBOYAI I, NISHIKAWA I, HAYASHI K, SAITO K,
PT Tshii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T:

WPT: 2001-318749/34

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

PS Claim 1: SEO ID NO 4908: 2537pp + Sequence Listing; English.

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, cDNA libraries, and the like.

CC antibody, or its antigen-binding fragment, which specifically binds to
CC the polypeptide, (iv) a method of detecting or determining the presence
CC of cancer in a patient, (v) a fusion protein comprising at least one of
CC the polypeptides, (vi) an oligonucleotide that hybridises to the
CC polynucleotide sequence under highly stringent conditions, and (vii) a
CC method of stimulating and/or expanding T cells specific for a tumour
CC protein. The polypeptide specifically comprises the amino acid sequence
CC of C634S, C635S, C637S, C640S, C636S or one of the potential open reading
CC frames (ORFs) of C636S. These polypeptides are encoded by the
CC polynucleotide sequences, where both are capable of eliciting a humoral
CC and/or cellular immune response. The polynucleotides, polypeptides, and
CC antibodies are useful for diagnosing, preventing or treating cancer,
CC particularly colon cancer. The polynucleotide and polypeptide sequences
CC are also useful in DNA strand invasion, antisense inhibition, mutational
CC analysis, nucleic acid purification, isolation of transcriptionally
CC active genes, blocking or transcription factor binding, genome cleavage
CC or in situ hybridisation, and as enhancers of transcription or
CC biomarkers. This sequence represents a human colon cancer associated
CC cDNA. Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at seqdata.uspto.gov
XX
SQ Sequence 553 BP; 181 A; 94 C; 125 G; 151 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.: 1.18e-76 Length: 553
Score: 728.00 Matches: 142
Percent Similarity: 97.93% Conservative: 0
Best Local Similarity: 97.93% Mismatches: 3
Query Match: 64.37% Indels: 0
DB: 11 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x ADT95464 (1-553)

Qy 76 LeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIle 95
Db 30 CTCTANATGCATGCTCGAGGGGTGTCTCTTACCTTAGCTTTGTACAGCCAGATGTGATA 89
Qy 96 PheLeuGlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyr 115
Db 90 TTTCTACAGGAAGTTATTCCCTCCCATATTATAGCTACCTTAAGAAGAGATCAAGTAATTAT 149
Qy 116 GluIleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArg 135
Db 150 GAGATTATTACAGTTCATGAGAGAGGATATTTCACAGCTATATATTGTAAGAAATCAAGA 209
Qy 136 ValLysLeuLysSerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeu 155
Db 210 GTGAAATTAATAAGCCAGAGATTATTCCTTTCCAAAGTACCAAAATGATGAGAAACCTT 269
Qy 156 LeuCysValHisValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGlu 175
Db 270 TTATGTGTGCATGTGAATGTGTGAGGAATAGAGCTTTGCCCTTATGACATCCCATTTGGAG 329
Qy 176 SerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMet 195
Db 330 AGCACCCAGAGGCATGCTCGAGACGATGTAATCAGTTAAATGTTTAAAGAAATG 389
Qy 196 GlnGluAlaProGluSerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArg 215
Db 390 CAAGAGGCTCCAGAGTCAGCTACAGTTATATTTCAGGAGATACAAATCTAAGGGATCGA 449
Qy 216 GluValThrArgCys 220
Db 450 GAGGTTACCATGT 464
RESULT 16
ID ADX41946
XX ADX41946 standard; cDNA; 553 BP.
AC ADX41946;
XX
DT 21-APR-2005 (first entry)
XX

DE Human cDNA encoding colon cancer protein SEQ ID NO 983.

XX Cytostatic; Immunostimulant; therapy; diagnosis; colon cancer; neoplasm;
KW ss; gene.

OS Homo sapiens.

XX W0200274156-A2.

XX 26-SEP-2002.

XX 01-FEB-2002; 2002WO-US002870.

XX 02-FEB-2001; 2001US-0267400P.

XX 07-FEB-2001; 2001US-0267382P.

XX 11-MAY-2001; 2001US-0290322P.

XX 12-JUL-2001; 2001US-0305265P.

XX 16-AUG-2001; 2001US-0313077P.

XX (CORI-) CORIXA CORP.

XX Jiang Y, Chenault RA, Xu J, Indirias CY, Lodes MJ, Secríst H;

PI Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;

XX WPI; 2003-040540/03.

XX New isolated nucleic acids and polypeptides capable of eliciting a
PT humoral and/or cellular immune response, useful for diagnosing,
PT preventing or treating cancer, particularly colon cancer.

XX Claim 1; SEQ ID NO 983; 244pp; English.

XX The invention relates to a new isolated nucleic acid. The nucleic acids,
CC polypeptides, antibodies are useful for diagnosing, preventing or
CC treating cancer, particularly colon cancer. The nucleic acid and
CC polypeptides are also useful in DNA strand invasion, antisense
CC inhibition, mutational analysis, nucleic acid purification, isolation of
CC transcriptionally active genes, blocking or transcription factor binding,
CC genome cleavage or in situ hybridization, and as enhancers of
CC transcription or biomarkers. The kits are useful for detecting antibody
CC binding. The present sequence represents a human cDNA encoding a colon
CC cancer protein.

XX SQ Sequence 553 BP; 181 A; 94 C; 125 G; 151 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.: 1.18e-76 Length: 553
Score: 728.00 Matches: 142
Percent Similarity: 97.93% Conservative: 0
Best Local Similarity: 97.93% Mismatches: 3
Query Match: 64.37% Indels: 0
DB: 11 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x ADX41946 (1-553)

Qy 76 LeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIle 95

Db 30 CTCTANATGCATGCTCGAGGGGTGTCTCTTACCTTAGCTTTGTACAGCCAGATGTGATA 89

Qy 96 PheLeuGlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyr 115

Db 90 TTTCTACAGGAAGTTATTCCCTCCCATATTATAGCTACCTTAAGAAGAGATCAAGTAATTAT 149

Qy 116 GluIleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArg 135

Db 150 GAGATTATTACAGTTCATGAGAGGATATTTCACAGCTATATATTGTAAGAAATCAAGA 209

Qy 136 ValLysLeuLysSerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeu 155

Db 210 GTGAAATTAATAAGCCAGAGATTATTCCTTTCCAAAGTACCAAAATGATGAGAAACCTT 269

Qy 156 LeuCysValHisValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGlu 175

Db 270 TTATGTGTGCATGTGAATGTGTGCAGAAATGAGCTTTCCTTATGACATCCCATTTGGAG 329
Qy 176 SerThrArgGlyHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMet 195
Db 330 AGCACCAGAGGGCATGCTGCGGAACGAATGAATCAGTTAAAAATGGTTTTAAAGAAATG 389
Qy 196 GlnGluAlaProGluSerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArg 215
Db 390 CAAGAGGCTCCAGATGACGTACAGTATATTTTGCAGGAGATACAAATCTAAGGATCGA 449
Qy 216 GluValThrArgCys 220
Db 450 GAGTTACCAGATGT 464
RESULT 17
ADT95512
ID ADT95512 standard; cDNA; 625 BP.
XX
AC ADT95512;
XX
DT 16-DEC-2004 (first entry)
XX
DE Colon cancer associated human cDNA sequence #1031.
XX
KW Colon cancer; T cell; tumour protein; C634S; C635S; C637S; C640S; C636S;
KW humoral immune response; cellular immune response; cytostatic;
KW immunostimulant; human; ss.
XX
OS Homo sapiens.
XX
PN US2003087818-A1.
XX
PD 08-MAY-2003.
XX
PF 01-FEB-2002; 2002US-00066543.
XX
PR 02-FEB-2001; 2001US-0267400P.
PR 07-FEB-2001; 2001US-0267382P.
PR 11-MAY-2001; 2001US-0290322P.
PR 12-JUL-2001; 2001US-0305265P.
PR 16-AUG-2001; 2001US-0313077P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Jiang Y, Chenault RA, Xu J, Indrias CV, Lodes MJ, Secretist H;
XX Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;
XX WPI; 2003-040540/03.
XX
XX New isolated nucleic acids and polypeptides capable of eliciting a
XX humoral and/or cellular immune response, useful for diagnosing,
XX preventing or treating cancer, particularly colon cancer.
XX
XX Claim 1; SEQ ID NO 1031; 87pp; English.
XX
XX The invention relates to polynucleotide and polypeptide sequences
XX associated with cancer, particularly colon cancer. Also disclosed are (i)
XX an expression vector comprising the polynucleotide, (ii) a host cell
XX transformed or transfected with the expression vector, (iii) an isolated
XX antibody, or its antigen-binding fragment, which specifically binds to
XX the polypeptide, (iv) a method of detecting or determining the presence
XX of cancer in a patient, (v) a fusion protein comprising at least one of
XX the polypeptides, (vi) an oligonucleotide that hybridises to the
XX polynucleotide sequence under highly stringent conditions, and (vii) a
XX method of stimulating and/or expanding T cells specific for a tumour
XX protein. The polypeptide specifically comprises the amino acid sequence
XX of C634S, C635S, C637S, C640S, C636S or one of the potential open reading
XX frames (ORFs) of C636S. These polypeptides are encoded by the
XX polynucleotide sequences, where both are capable of eliciting a humoral
XX and/or cellular immune response. The polynucleotides, polypeptides, and
XX antibodies are useful for diagnosing, preventing or treating cancer,
XX particularly colon cancer. The polynucleotide and polypeptide sequences
XX are also useful in DNA strand invasion, antisense inhibition, mutational

CC analysis, nucleic acid purification, isolation of transcriptionally
CC active genes, blocking or transcription factor binding, genome cleavage
CC or in situ hybridisation, and as enhancers of transcription or
CC biomarkers. This sequence represents a human colon cancer associated
CC cDNA. Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at seqdata.uspto.gov
XX
SQ Sequence 625 BP; 202 A; 104 C; 144 G; 174 T; 0 U; 1 Other;
Alignment Scores: 2.43e-76 Length: 625
Pred. No.: 726.00 Matches: 141
Score: 726.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 64.19% Gaps: 0
DB: 11
US-10-757-745-2_COPY_54_273 (1-220) x ADT95512 (1-625)
Qy 80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99
Db 42 GCTCGAGGGGTGTCTTCTACTTACGCTTTGTACAGCCAGATGTGATATTTCTACAGGAA 101
Qy 100 VallieProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThr 119
Db 102 GTTATTTCCCATATTTATAGCTACCTAAAGAAGAGATCAAGTAAATTATGAGATTATTACA 161
Qy 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgVallyLeuLys 139
Db 162 GGTCTATGAAGAAGGATATTTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAATA 221
Qy 140 SerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysValHis 159
Db 222 AGCCAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCAT 281
Qy 160 ValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGly 179
Db 282 GTGAATGTGTGAGGAAATGAGCTTTTGCCTTATGACATCCCATTTGAGAGACCAGAGGG 341
Qy 180 HisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaPro 199
Db 342 CATGCTGCGGAACGAATGAATCAAGTAAATGTTTAAAGAAATGCAAGAGGGCTCCA 401
Qy 200 GluSerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArg 219
Db 402 GAGTCAGCTACAGTTATATTTTGCAGGAGATACAAATCTTAAGGGATCGAGAGGTACCAGA 461
Qy 220 Cys 220
Db 462 TGT 464
RESULT 18
ADX41994
ID ADX41994 standard; cDNA; 625 BP.
XX
AC ADX41994;
XX
XX 21-APR-2005 (first entry)
XX
XX Human cDNA encoding colon cancer protein SEQ ID NO 1031.
XX
XX Cytostatic; Immunostimulant; therapy; diagnosis; colon cancer; neoplasm;
XX ss; Gene.
XX
XX Homo sapiens.
XX
XX WO200274156-A2.
XX
XX 26-SEP-2002.
XX
XX 01-FEB-2002; 2002WO-US002870.
XX
XX 02-FEB-2001; 2001US-0267400P.
XX

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PR 07-FEB-2001; 2001US-0267382P.
PR 11-MAY-2001; 2001US-0290322P.
PR 12-JUL-2001; 2001US-0305285P.
PR 16-AUG-2001; 2001US-0313077P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Jiang Y, Chenault RA, Xu J, Indirias CY, Lodes MJ, Secretist H;
XX Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;
XX
XX WPI; 2003-040540/03.
XX
XX New isolated nucleic acids and polypeptides capable of eliciting a
XX humoral and/or cellular immune response, useful for diagnosing,
XX preventing or treating cancer, particularly colon cancer.
XX
XX Claim 1; SEQ ID NO 1031; 244bp; English.
XX
XX The invention relates to a new isolated nucleic acid. The nucleic acids,
XX polypeptides, antibodies are useful for diagnosing, preventing or
XX treating cancer, particularly colon cancer. The nucleic acid and
XX polypeptides are also useful in DNA strand invasion, antisense
XX inhibition, mutational analysis, nucleic acid purification, isolation of
XX transcriptionally active genes, blocking or transcription factor binding,
XX genome cleavage or in situ hybridization, and as enhancers of
XX transcription or biomarkers. The kits are useful for detecting antibody
XX binding. The present sequence represents a human cDNA encoding a colon
XX cancer protein.
XX
XX Sequence 625 BP; 202 A; 104 C; 144 G; 174 T; 0 U; 1 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 2,43e-76 Length: 625
XX Score: 726.00 Matches: 141
XX Percent Similarity: 100.00% Conservativity: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 64.19% Indels: 0
XX DB: 11 Gaps: 0
XX
XX US-10-757-745-2_COPY_54_273 (1-220) x ADX41994 (1-625)
XX
Qy 80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99
Db 42 GCTCAGGGGTGTTCTTACTTACCTTGTGTACAGCCAGATGTGATATTTCTACAGGAA 101
Qy 100 ValIleProProTyrTyrSerTyrLeuLysLysArgSerAsnTyrGluIleThr 119
Db 102 GTTATTCCTCCATATATAGCTACCTTAAGAAGAGATCAAGTAATTATGAGATTATTACA 161
Qy 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLys 139
Db 162 GGTCAATGAAGAAGATATTTTCCAGCTATATATGTTGAAGAAATCAAGAGTGAATTTAAA 221
Qy 140 SerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysValHis 159
Db 222 AGCCAGAGATATTCCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTGCAT 281
Qy 160 ValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGly 179
Db 282 GTGAATGTGTGAGAAATGAGCTTTTGCCTTATGATCATCCCATTTGGAGAGCACCAGAGGG 341
Qy 180 HisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaPro 199
Db 342 CATGTCGGGAACGAATGAATCAGTTAAAAATGGTTTAAAGAAAAATGCAAGAGGCTCCA 401
Qy 200 GluSerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArg 219
Db 402 GAGTCAGCTACAGTTATATTTTGCAGGAGATACAAATCTAAGGGATCGAGAGGTTACCAGA 461
Qy 220 Cys 220
Db 462 TGT 464
```

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RESULT 19
ADT95565
ID ADT95565 standard; cDNA; 633 BP.
XX
XX AC ADT95565;
XX
XX 16-DEC-2004 (first entry)
XX
XX Colon cancer associated human cDNA sequence #1084.
XX
XX Colon cancer; T cell; tumour protein; C634S; C635S; C637S; C640S; C636S;
XX humoral immune response; cellular immune response; cytostatic;
XX immunostimulant; human; ss.
XX
XX Homo sapiens.
XX
XX US2003087818-A1.
XX
XX 08-MAY-2003.
XX
XX 01-FEB-2002; 2002US-00065543.
XX
XX 02-FEB-2001; 2001US-0267400P.
XX
XX 07-FEB-2001; 2001US-0267382P.
XX
XX 11-MAY-2001; 2001US-0290322P.
XX
XX 12-JUN-2001; 2001US-0305285P.
XX
XX 16-AUG-2001; 2001US-0313077P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Jiang Y, Chenault RA, Xu J, Indirias CY, Lodes MJ, Secretist H;
XX Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;
XX
XX WPI; 2003-040540/03.
XX
XX New isolated nucleic acids and polypeptides capable of eliciting a
XX humoral and/or cellular immune response, useful for diagnosing,
XX preventing or treating cancer, particularly colon cancer.
XX
XX Claim 1; SEQ ID NO 1084; 87bp; English.
XX
XX The invention relates to polynucleotide and polypeptide sequences
XX associated with cancer, particularly colon cancer. Also disclosed are (i)
XX an expression vector comprising the polynucleotide, (ii) a host cell
XX transformed or transfected with the expression vector, (iii) an isolated
XX antibody, or its antigen-binding fragment, which specifically binds to
XX the polypeptide, (iv) a method of detecting or determining the presence
XX of cancer in a patient, (v) a fusion protein comprising at least one of
XX the polypeptides, (vi) an oligonucleotide that hybridises to the
XX polynucleotide sequence under highly stringent conditions, and (vii) a
XX method of stimulating and/or expanding T cells specific for a tumour
XX protein. The polypeptide specifically comprises the amino acid sequence
XX of C634S, C635S, C637S, C640S, C636S or one of the potential open reading
XX frames (ORFs) of C636S. These polypeptides are encoded by the
XX polynucleotide sequences, where both are capable of eliciting a humoral
XX and/or cellular immune response. The polynucleotides, polypeptides, and
XX antibodies are useful for diagnosing, preventing or treating cancer,
XX particularly colon cancer. The polynucleotide and polypeptide sequences
XX are also useful in DNA strand invasion, antisense inhibition, mutational
XX analysis, nucleic acid purification, isolation of transcriptionally
XX active genes, blocking or transcription factor binding, genome cleavage
XX or in situ hybridization, and as enhancers of transcription or
XX biomarkers. This sequence represents a human colon cancer associated
XX cDNA. Note: The sequence data for this patent was obtained in electronic
XX format directly from the USPTO web site at seqdata.uspto.gov
XX
XX Sequence 633 BP; 205 A; 108 C; 144 G; 175 T; 0 U; 1 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 2,48e-76 Length: 633
XX Score: 726.00 Matches: 141
XX Percent Similarity: 100.00% Conservativity: 0
XX Best Local Similarity: 100.00% Mismatches: 0
```

Query Match:	64.19%	Indels:	0
DB:	11	Gaps:	0
US-10-757-745-2_COPY_54_273 (1-220) x ADT95565 (1-633)			
Qy	80	AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu	99
Db	34	GCTCAGGGGTGTCTCTACTTGTACAGCCCGAGATGTGATATTTCTACAGGA	93
Qy	100	ValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThr	119
Db	94	GTTATTTCCCATATATAGTACCTAAAGAAGAGATCAAGTAATATGAGATATTATTA	153
Qy	120	GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLys	139
Db	154	GCTCATGAAGAAGGATATTTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTA	213
Qy	140	SerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysValHis	159
Db	214	AGCCAAGAGATTTTCTTTTCCAGTACCAAAATGATGAGAACTTTTATGTGTCAT	273
Qy	160	ValAsnValSerGlyAsnGluLysCysLeuMetThrSerHisLeuGluSerThrArgGly	179
Db	274	GTGAATGTGTCAAGAAATGAGCTTTGCCTTATGACATCCATTTGGAGAGCACCAGGG	333
Qy	180	HisAlaAlaGluArgMetAsnGlnLysMetValLeuLysLysSerArgValLysLeuLys	199
Db	334	CATGCTGCGGAACGAATGAATCAAGTAAATGTTGAAGAAATCAAGAGTGAATTA	453
Qy	220	Cys 220	
Db	454	TGT 456	
RESULT 20			
ID	ADX42047	standard; cdna; 633 BP.	
XX	AC	ADX42047;	
XX	DT	21-APR-2005 (first entry)	
XX	DE	Human cDNA encoding colon cancer protein SEQ ID NO 1084.	
XX	KW	Cytostatic; Immunostimulant; therapy; diagnosis; colon cancer; neoplas;	
XX	KW	ss; Gene.	
XX	OS	Homo sapiens.	
XX	PN	WO200274156-A2.	
XX	PD	26-SEP-2002.	
XX	PF	01-FEB-2002; 2002WO-US002870.	
XX	PR	02-FEB-2001; 2001US-0267400P.	
XX	PR	07-FEB-2001; 2001US-0267382P.	
XX	PR	11-MAY-2001; 2001US-0290322P.	
XX	PR	12-JUL-2001; 2001US-0305265P.	
XX	PR	16-AUG-2001; 2001US-0313077P.	
XX	PA	(CORI-) CORIXA CORP.	
XX	PI	Jiang Y, Chenault RA, Xu J, Indrias CY, Lodes MJ, Secretist H;	
XX	PI	Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;	
XX	DR	WPI; 2003-040540/03.	
XX	PT	New isolated nucleic acids and polypeptides capable of eliciting a	
XX	PT	humoral and/or cellular immune response, useful for diagnosing,	
PT	preventing or treating cancer, particularly colon cancer.		
XX	Claim 1; SEQ ID NO 1084; 244pp; English.		
XX	The invention relates to a new isolated nucleic acid. The nucleic acids, polypeptides, antibodies are useful for diagnosing, preventing or treating cancer, particularly colon cancer. The nucleic acid and polypeptides are also useful in DNA strand invasion, antisense inhibition, mutational analysis, nucleic acid purification, isolation of transcriptionally active genes, blocking or transcription factor binding, genome cleavage or in situ hybridization, and as enhancers of transcription or biomarkers. The kits are useful for detecting antibody binding. The present sequence represents a human cDNA encoding a colon cancer protein.		
SQ	Sequence 633 BP; 205 A; 108 C; 144 G; 175 T; 0 U; 1 Other;		
Alignment Scores:			
Pred. No.:	2.48e-76	Length:	633
Score:	726.00	Matches:	141
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	64.19%	Indels:	0
DB:	11	Gaps:	0
US-10-757-745-2_COPY_54_273 (1-220) x ADX42047 (1-633)			
Qy	80	AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu	99
Db	34	GCTCAGGGGTGTCTCTACTTGTACAGCCCGAGATGTGATATTTCTACAGGA	93
Qy	100	ValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThr	119
Db	94	GTTATTTCCCATATATAGTACCTAAAGAAGAGATCAAGTAATATGAGATATTATTA	153
Qy	120	GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLys	139
Db	154	GCTCATGAAGAAGGATATTTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTA	213
Qy	140	SerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysValHis	159
Db	214	AGCCAAGAGATTTTCTTTTCCAGTACCAAAATGATGAGAACTTTTATGTGTCAT	273
Qy	160	ValAsnValSerGlyAsnGluLysCysLeuMetThrSerHisLeuGluSerThrArgGly	179
Db	274	GTGAATGTGTCAAGAAATGAGCTTTGCCTTATGACATCCATTTGGAGAGCACCAGGG	333
Qy	180	HisAlaAlaGluArgMetAsnGlnLysMetValLeuLysLysSerArgValLysLeuLys	199
Db	334	CATGCTGCGGAACGAATGAATCAAGTAAATGTTGAAGAAATCAAGAGTGAATTA	453
Qy	220	Cys 220	
Db	454	TGT 456	
RESULT 21			
ID	ADT95551	standard; cdna; 644 BP.	
XX	AC	ADT95551;	
XX	DT	16-DEC-2004 (first entry)	
XX	DE	Colon cancer associated human cDNA sequence #1070.	
XX	KW	Colon cancer; T cell; tumour protein; C634S; C635S; C637S; C640S; C636S;	
XX	KW	humoral immune response; cellular immune response; cytostatic;	
XX	KW	immunostimulant; human; ss.	

OS	Homo sapiens.		
XX	US2003087818-A1.	Db	152 GGTCAATGAAGAAGGATATTTTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATATAAA 211
XX	08-MAY-2003.	Qy	140 SerGlnGluIlelleProPheProSerThrIysMetMetArgAsnLeuLeuCysValHis 159
XX	01-FEB-2002; 2002US-00066543.	Db	212 AGCCAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCAT 271
XX	02-FEB-2001; 2001US-0267400P.	Qy	160 ValAsnValSerGlyAsnGluLeuLeuCysLeuMetThrSerHisLeuGluSerThrArgGly 179
XX	07-FEB-2001; 2001US-0267382P.	Db	272 GTGAATGTGCAGAAATAGCTTTTGCTTATGACATCCCATTTTGGAGAGACCAGAGGG 331
XX	11-MAY-2001; 2001US-0290322P.	Qy	180 HisAlaAlaGluArgMetAsnGlnLeuLeuMetValLeuLysLysMetGlnGluAlaPro 199
XX	12-JUL-2001; 2001US-0305265P.	Db	332 CATGCTCGGACGAATGAATCAAGTTAAATAATGCTTTTAAAGAAATGGAAGAGGCTCCA 391
XX	16-AUG-2001; 2001US-0313077P.	Qy	200 GluSerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArg 219
XX	(CORI-) CORIXA CORP.	Db	392 GAGTCAGCTACAGTTATATTTTGCAGGAGATACAAATCTAAGGGATCGAGAGGTTACCAGA 451
XX	Jiang Y, Chenault RA, Xu J, Indirias CY, Lodes MJ, Secretist H;		
XX	Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;		
XX	WPI; 2003-040540/03.		
XX	New isolated nucleic acids and polypeptides capable of eliciting a		
XX	humoral and/or cellular immune response, useful for diagnosing,		
XX	preventing or treating cancer, particularly colon cancer.		
XX	Claim 1; SEQ ID NO 1070; 87pp; English.		
XX	The invention relates to polynucleotide and polypeptide sequences		
XX	associated with cancer, particularly colon cancer. Also disclosed are (i)		
XX	an expression vector comprising the polynucleotide, (ii) a host cell		
XX	transformed or transfected with the expression vector, (iii) an isolated		
XX	antibody, or its antigen-binding fragment, which specifically binds to		
XX	the polypeptide, (iv) a method of detecting or determining the presence		
XX	of cancer in a patient, (v) a fusion protein comprising at least one of		
XX	the polypeptides, (vi) an oligonucleotide that hybridises to the		
XX	polynucleotide sequence under highly stringent conditions, and (vii) a		
XX	method of stimulating and/or expanding T cells specific for a tumour		
XX	protein. The polypeptide specifically comprises the amino acid sequence		
XX	of C634S, C635S, C637S, C638S, C639S, C640S, C641S, C642S, C643S,		
XX	polynucleotide sequences, where both are capable of eliciting a humoral		
XX	and/or cellular immune response. The polynucleotides, polypeptides, and		
XX	antibodies are useful for diagnosing, preventing or treating cancer,		
XX	particularly colon cancer. The polynucleotide and polypeptide sequences		
XX	are also useful in DNA strand invasion, antisense inhibition, mutational		
XX	analysis, nucleic acid purification, isolation of transcriptionally		
XX	active genes, blocking or transcription factor binding, genome cleavage		
XX	or in situ hybridisation, and as enhancers of transcription or		
XX	biomarkers. This sequence represents a human colon cancer associated		
XX	cDNA. Note: The sequence data for this patent was obtained in electronic		
XX	format directly from the USPTO web site at seqdata.uspto.gov		
XX	Sequence 644 BP; 206 A; 110 C; 148 G; 180 T; 0 U; 0 Other;		
XX	Alignment Scores:		
XX	Pred. No.:	5.78e-76	Length: 644
XX	Score:	723.00	Matches: 140
XX	Percent Similarity:	100.00%	Conservative: 1
XX	Best Local Similarity:	99.29%	Mismatches: 0
XX	Query Match:	63.93%	Indels: 0
XX	DB:	11	Gaps: 0
XX	US-10-757-745-2_COPY_54_273 (1-220) x ADR95551 (1-644)		
Qy	80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99		
Db	32 GCTCAGGGGTGTCTTACTAGCTTTGTACAGCCAGATGATATTTCTACAGAA 91		
Qy	100 ValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleThr 119		
Db	92 GTTATTCCTCCCATATATATAGCTACCTAAGAAGAGATCAAGTAATATGAGATTATTACA 151		
Qy	120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValIleLys 139		


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QY 100 ValIleProProTyrSerTyrLeuLysLysSerSerSerAenTyrGluIleThr 119
DB 252 GTTATCCCCCATCTGTGCTTACCTTAAGAAGAGAGAGCCAGTTCACAAATTATTACA 311
QY 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLys 139
DB 312 GGTAAATGAAGAAGATATTTCACAGCTATATACTATTGAAGAAAGGAGAGTGAATTTAAA 371
QY 140 SerGlnGluIleIleProPheProSerThrLysMetMetArgAenLeuLeuCysValHis 159
DB 372 AGTCAGGAGATATTCTCTTTCCAAATACCAAAATGATGAGAGCCTGCTATGCGTAAAT 431
QY 160 ValAenValSerGlyAenGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGly 179
DB 432 GTGAGTTTGGGTGAATGAATTTTGCCTTATGACATCCCAATTTGGAGAGCACCAGAGAA 491
QY 180 HisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaPro 199
DB 492 CATCTCGGGAACGAAATGAAGACAATTAATAAACTGTTCTTGGAAAAATGCAAGAGCTCCA 551
QY 200 GluSerAlaThrValIlePheAlaGlyAspThrAenLeuArgAspArgGlu 216
DB 552 GATTCAACACCGGTATATTTCGAGGAGATACAAATTTAAGAGATCAAGAA 602
RESULT 24
ADT95548
ID ADT95548 standard; cDNA; 674 BP.
AC ADT95548;
XX
DT 16-DEC-2004 (first entry)
DE
KW Colon cancer associated human cDNA sequence #1067.
KW Colon cancer: T cell; tumour protein; C634S; C635S; C637S; C640S; C636S;
KW humoral immune response; cellular immune response; cytostatic;
KW immunostimulant; human; ss.
XX
OS Homo sapiens.
XX
PN US2003087818-A1.
XX
PD 08-MAY-2003.
XX
PF 01-FEB-2002; 2002US-00066543.
XX
PR 02-FEB-2001; 2001US-0267400P.
XX
PR 07-FEB-2001; 2001US-0267382P.
XX
PR 11-MAY-2001; 2001US-0290322P.
XX
PR 12-JUL-2001; 2001US-0305265P.
XX
PR 16-AUG-2001; 2001US-0313077P.
XX
PA (CORI-) CORIXA CORP.
XX
XX Jiang Y, Chenault RA, Xu J, Indirias CY, Lodes MJ, Secretist H;
PI Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;
XX
XX WPI; 2003-040540/03.
XX
XX New isolated nucleic acids and polypeptides capable of eliciting a
PT humoral and/or cellular immune response, useful for diagnosing,
PT preventing or treating cancer, particularly colon cancer.
XX
PS Claim 1; SEQ ID NO 1067; 87pp; English.
XX
XX The invention relates to polynucleotide and polypeptide sequences
CC associated with cancer, particularly colon cancer. Also disclosed are (i)
CC an expression vector comprising the polynucleotide, (ii) a host cell
CC transformed or transfected with the expression vector, (iii) an isolated
CC antibody, or its antigen-binding fragment, which specifically binds to
CC the polypeptide, (iv) a method of detecting or determining the presence
CC of cancer in a patient, (v) a fusion protein comprising at least one of
CC the polypeptides, (vi) an oligonucleotide that hybridises to the
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CC polynucleotide sequence under highly stringent conditions, and (vii) a
CC method of stimulating and/or expanding T cells specific for a tumour
CC protein. The polypeptide specifically comprises the amino acid sequence
CC of C634S, C635S, C637S, C640S, C636S or one of the potential open reading
CC frames (ORFs) of C636S. These polypeptides are encoded by the
CC polynucleotide sequences, where both are capable of eliciting a humoral
CC and/or cellular immune response. The polynucleotides, polypeptides, and
CC antibodies are useful for diagnosing, preventing or treating cancer,
CC particularly colon cancer. The polynucleotide and polypeptide sequences
CC are also useful in DNA strand invasion, antisense inhibition, mutational
CC analysis, nucleic acid purification, isolation of transcriptionally
CC active genes, blocking or transcription factor binding, genome cleavage
CC or in situ hybridisation, and as enhancers of transcription or
CC biomarkers. This sequence represents a human colon cancer associated
CC cDNA. Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at seqdata.uspto.gov
XX
SQ Sequence 674 BP; 213 A; 114 C; 152 G; 191 T; 0 U; 4 Other;
Alignment Scores:
Pred. No.: 9.52e-75 Length: 674
Score: 713.00 Matches: 141
Percent Similarity: 99.30% Conservative: 0
Best Local Similarity: 99.30% Mismatches: 0
Query Match: 63.04% Indels: 1
DB: 11 Gaps: 0
US-10-757-745-2_COPY_54_273 (1-220) x ADT95548 (1-674)
QY 80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99
DB 18 GCTCGAGGGTGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGAA 77
QY 100 ValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAenTyrGluIleThr 119
DB 78 GTTATTTCCCATATATTATAGTACCTAAAGAGAGATCAAGTAATATGAGATTATTACA 137
QY 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLys 139
DB 138 GGTCAATGAAGAAGGATATTTTACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAA 197
QY 140 SerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHis 159
DB 198 AGCCAAGAGATTATTCCTTTCCAGTACCAGTAATGATGAGAAACCTTTTATGTGTGCAT 257
QY 160 ValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGly 179
DB 258 GTGAATGTGTGAGAAATGAGCTTTGCTTTATGACATCCCATTTGGAGAGCACCAGAGGG 317
QY 180 HisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaPro 199
DB 318 CATGCTCGGAACGAATGAATGAATGTTTAAAGAAATGCTTTTAAAGAAATGCAAGAGGCTCCN 377
QY 200 -GluSerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrAr 219
DB 378 TGAGTCAGCTACAGTTATATTTCGAGGAGATACAAATCTAAGGGATCGAGAGGTTACAG 437
QY 219 gCys 220
DB 438 ATGT 441
RESULT 25
ADX42030
ID ADX42030 standard; cDNA; 674 BP.
XX
XX AC ADX42030;
XX
XX DT 21-APR-2005 (first entry)
XX
XX DE Human cDNA encoding colon cancer protein SEQ ID NO 1067.
XX
XX KW Cytostatic; Immunostimulant; therapy; diagnosis; colon cancer; neoplasm;
XX ss; gene.
```


Qy 83 ValCysSerTyrLeuAlaLeuTyrSerProaspValIlePheLeuGlnGluValIlePro 102
Db 1077 GTGTGTTCTTACTTAGCTTTGTACAGCCACAGATGTGATATTCTACAGGAAGTTATTCC 1018
Qy 103 ProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGlyHisGlu 122
Db 1017 CCATATTATAGTACCTTAAGAAGAGATCAAGTAATTATGAGATTATTACAGGTCATGAA 958
Qy 123 GluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGlnGlu 142
Db 957 GAAGGATATTTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAATAAGCAAGAG 898
Qy 143 IleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsnVal 162
Db 897 ATTATTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCATGTGAATGTG 838
Qy 163 SerGlyAsnGlnLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAla 182
Db 837 TCAGGAATGAGCTTTGCTTTATGACATCCCATTTGGAGACACAGAGGCGATGCTGCG 778
Qy 183 GluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGluSerAla 202
Db 777 GAACGAATGAATCAGTTAAATAATGTTTTAAAGAAATGCAAGAGGCTCCAGAGTCAGCT 718
Qy 203 ThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 717 ACAGTTATATTTGCAGGAGATACAAATCTAAGGGATCGAGAGGTTACCAGATGT 664

RESULT 27
AAC79438/c
ID AAC79438 standard; cDNA; 1079 BP.
XX
AC AAC79438;
XX
DT 07-FEB-2001 (first entry)
XX
DE cDNA sequence of human breast tumour clone 1015D11.
XX
KW Human; breast tumour antigen; cytostatic; immunotherapy; breast cancer;
KW vaccine; ss.
XX
OS Homo sapiens.
XX
FN WO200061756-A2.
XX
PD 19-OCT-2000.
XX
PF 10-APR-2000; 2000WO-US009688.
XX
PR 09-APR-1999; 99US-00288950.
PR 02-JUL-1999; 99US-00346327.
XX
PA (CORI-) CORIXA CORP.
XX
PI Reed SG, Xu J, Dillon DC;
XX
DR WPI; 2000-638568/61.
XX

A novel isolated polypeptide comprising an immunogenic portion of a breast cancer protein useful in the detection and treatment of breast cancer.

Claim 4; Page 77; 95pp; English.

The present sequence was isolated from a breast tumour cDNA library. It is provided in a specification relating to compounds for immunotherapy and diagnosis of breast cancer. Breast tumour antigens and the polynucleotides that encode them may be used in the production of a pharmaceutical composition to be used in the treatment of breast cancer. Proliferated T cells and incubated antigen presenting cells are also required. The polypeptides and polynucleotides may also be used to produce a vaccine

SQ Sequence 1079 BP; 327 A; 229 C; 177 G; 346 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.24e-74 Length: 1079
Score: 711.00 Matches: 138
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 62.86% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x AAC79438 (1-1079)

Qy 83 ValCysSerTyrLeuAlaLeuTyrSerProaspValIlePheLeuGlnGluValIlePro 102
Db 1077 GTGTGTTCTTACTTAGCTTTGTACAGCCACAGATGTGATATTCTACAGGAAGTTATTCC 1018
Qy 103 ProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGlyHisGlu 122
Db 1017 CCATATTATAGTACCTTAAGAAGAGATCAAGTAATTATGAGATTATTACAGGTCATGAA 958
Qy 123 GluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGlnGlu 142
Db 957 GAAGGATATTTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAATAAGCAAGAG 898
Qy 143 IleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsnVal 162
Db 897 ATTATTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCATGTGAATGTG 838
Qy 163 SerGlyAsnGlnLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAla 182
Db 837 TCAGGAATGAGCTTTGCTTTATGACATCCCATTTGGAGACACAGAGGCGATGCTGCG 778
Qy 183 GluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGluSerAla 202
Db 777 GAACGAATGAATCAGTTAAATAATGTTTTAAAGAAATGCAAGAGGCTCCAGAGTCAGCT 718
Qy 203 ThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 717 ACAGTTATATTTGCAGGAGATACAAATCTAAGGGATCGAGAGGTTACCAGATGT 664

RESULT 28
ABK28982/c
ID ABK28982 standard; cDNA; 1079 BP.
XX
AC ABK28982;
XX
DT 23-APR-2002 (first entry)
XX
DE Human breast tumour polypeptide cDNA clone #11.
XX
KW Human; breast tumour polypeptide; gene; ss; breast cancer; cytostatic;
KW immunostimulant.
XX
OS Homo sapiens.
XX
FN WO200198339-A2.
XX
PD 27-DEC-2001.
XX
PF 12-JUN-2001; 2001WO-US019032.
XX
PR 22-JUN-2000; 2000US-00602877.
PR 12-OCT-2000; 2000US-00687507.
PR 06-FEB-2001; 2001US-00778381.
XX
PA (CORI-) CORIXA CORP.
XX
PI Reed SG, Xu J, Dillon DC, Retter MW, Harlocker SL;
XX
DR WPI; 2002-147792/19.
XX
PT Polynucleotides encoding breast tumor polypeptides, useful for treating breast cancer or stimulating an immune response.

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XX Claim 1; Page 131; 150pp; English.
XX The invention relates to polynucleotides encoding breast tumour
XX polypeptides. The sequences are useful for treating cancer, preferably
XX breast cancer, in a patient or for stimulating an immune response. The
XX polynucleotides and polypeptides are also useful in the diagnosis and
XX monitoring of breast cancer. A method for detecting the presence of a
XX cancer in a patient, comprises obtaining a biological sample from the
XX patient, contacting the biological sample with a binding agent that binds
XX to a breast tumour polypeptide, detecting in the sample an amount of
XX polypeptide that binds to the binding agent, and comparing the amount of
XX polypeptide to a predetermined cut-off value, therefore determining the
XX presence of a cancer in the patient. Sequences ABK28920-ABK29025
XX represent cDNA clones encoding human breast tumour polypeptides of the
XX invention
XX SQ Sequence 1079 BP; 327 A; 229 C; 177 G; 346 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.24e-74 Length: 1079
Score: 711.00 Matches: 138
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 62.86% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x ABK28982 (1-1079)
QY 83 ValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIlePro 102
Db 1077 GTGTGTTCTTACTAGCTTTGTGTACAGCCAGATGTGATTTCTACAGGAGTTATTCCTC 1018
QY 103 ProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGlyHisGlu 122
Db 1017 CCATATTATAGCTACCTAAAGAAGAGATCAAGTAATATGAGATTATTACAGGTCATGAA 958
QY 123 GluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValIleLysLysSerGlnGlu 142
Db 957 GAAGGATATTTCACAGCTATTAATGTTGAAGAAATCAAGAGTGAATTTAAAGAACCCAGAG 998
QY 143 IleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsnVal 162
Db 897 ATTATTCCTTTTCAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGATGATG 838
QY 163 SerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAla 182
Db 837 TCAGGAAATCAGCTTTGCTTTATGACATCCATTTGGAGAGCACCAGAGGCGATGCTGCG 778
QY 183 GluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGluSerAla 202
Db 777 GAACGAATGAATCAGTTAAAAATGGTTTAAAGAAAAATGCAAGAGGCTCCAGAGTCAGCT 718
QY 203 ThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 717 ACAGTTATATTTCAGGAGATACAAATCTAAGGGATCGAGAGGTTACCATGT 564

RESULT 29
AAS86254
ID AAS86254 standard; cDNA; 1088 BP.
XX
AC AAS86254;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #22058.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
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XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US008631.
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX P-PSDB; ABG22067.
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX Claim 1; SEQ ID NO 22058; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
XX coding sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1088 BP; 345 A; 182 C; 236 G; 325 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.31e-74 Length: 1088
Score: 710.00 Matches: 138
Percent Similarity: 98.58% Conservative: 1
Best Local Similarity: 97.87% Mismatches: 2
Query Match: 62.78% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x AAS86254 (1-1088)
QY 80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99
Db 1 GCTCGAGGGGTGTGTCTTACTAGCTTTGTACAGCCAGATGTGATTTCTTACAGGAA 60
QY 100 ValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThr 119
Db 61 GTTATTTCCCATTTATTTAGCTTACCTTAAGAGAGATCAAGTAATTTATGAGATTATACA 120
QY 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValIleLysLys 139
Db 121 GGTTCATGAAGAAGGATATTTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAACA 180
QY 140 SerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHis 159
Db 181 AGCCAAGAGATTATTCCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTGCAT 240
QY 160 ValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGly 179
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Db 241 GTGAATGTGTGAGGAATGAGCTTTCCTTATGACATCCATTTGGAGAGCACCAAGGG 300
Qy 180 HisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaPro 199
Db 301 CATGTGCGGAACGAATGAATCAGTTAAAAATGGGTTTAAAGAAAAATGCAAGAGGCTCCA 360
Qy 200 GluSerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArg 219
Db 361 GAGTCAGCTACAGTTATATTTGCAGGAGATACAAATCTAAGGGATCGAGAGGTACCAGA 420

Qy 220 Cys 220
Db 421 TGT 423

RESULT 30

ADT95029
ID ADT95029 standard; cDNA; 625 BP.

XX AC ADT95029;

XX DT 16-DEC-2004 (first entry)

XX DE Colon cancer associated human cDNA sequence #548.

XX KW Colon cancer; T cell; tumour protein; C634S; C635S; C637S; C640S; C636S;

XX KW humoral immune response; cellular immune response; cytostatic;

XX KW immunostimulant; human; ss.

XX OS Homo sapiens.

XX PN US2003087818-A1.

XX PD 08-MAY-2003.

XX PF 01-FEB-2002; 2002US-00066543.

XX PR 02-FEB-2001; 2001US-0267400P.

XX PR 07-FEB-2001; 2001US-0267382P.

XX PR 11-MAY-2001; 2001US-0290322P.

XX PR 12-JUL-2001; 2001US-0305265P.

XX PR 16-AUG-2001; 2001US-0313077P.

XX PA (CORI-) CORIXA CORP.

XX PI Jiang Y, Chenault RA, Xu J, Indirias CY, Lodes MJ, Secrlist H;

XX PI Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;

XX DR WPI; 2003-040540/03.

XX PT New isolated nucleic acids and polypeptides capable of eliciting a

XX PT humoral and/or cellular immune response, useful for diagnosing,

XX PT preventing or treating cancer, particularly colon cancer.

XX PS Claim 1; SEQ ID NO 548; 87pp; English.

XX The invention relates to polynucleotide and polypeptide sequences
CC associated with cancer, particularly colon cancer. Also disclosed are (i)
CC an expression vector comprising the polynucleotide, (ii) a host cell
CC transformed or transfected with the expression vector, (iii) an isolated
CC antibody, or its antigen-binding fragment, which specifically binds to
CC the polypeptide, (iv) a method of detecting or determining the presence
CC of cancer in a patient, (v) a fusion protein comprising at least one of
CC the polypeptides, (vi) an oligonucleotide that hybridises to the
CC polynucleotide sequence under highly stringent conditions, and (vii) a
CC method of stimulating and/or expanding T cells specific for a tumour
CC protein. The polypeptide specifically comprises the amino acid sequence
CC of C634S, C635S, C637S, C640S, C636S or one of the potential open reading
CC frames (ORFs) of C636S. These polypeptides are encoded by the
CC polynucleotide sequences, where both are capable of eliciting a humoral
CC and/or cellular immune response. The polynucleotides, polypeptides, and
CC antibodies are useful for diagnosing, preventing or treating cancer,
CC particularly colon cancer. The polynucleotide and polypeptide sequences

CC are also useful in DNA strand invasion, antisense inhibition, mutational
CC analysis, nucleic acid purification, isolation of transcriptionally
CC active genes, blocking or transcription factor binding, genome cleavage
CC or in situ hybridisation, and as enhancers of transcription or
CC biomarkers. This sequence represents a human colon cancer associated
CC cDNA. Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at seqdata.uspto.gov

XX SQ Sequence 625 BP; 200 A; 107 C; 144 G; 172 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.: 3.35e-74 Length: 625
Score: 708.00 Matches: 140
Percent Similarity: 98.59% Conservative: 0
Best Local Similarity: 98.59% Mismatches: 1
Query Match: 62.60% Indels: 1
DB: 11 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x ADT95029 (1-625)

Qy 80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99
Db 26 GCTCGAGGGGTGTTCCTACTTAGCTTTGTACAGCCAGATGTGNTATTTCACAGGAA 85
Qy 100 ValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleThr 119
Db 86 GTTATCCCCCATATATATAGTACCTTAAGAAGAGATCAAGTAATATGAGATTATTACA 145
Qy 120 -GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLy 139
Db 146 GGGTCATGAAGAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAA 205
Qy 139 sSerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuValHi 159
Db 206 AAGCCAAAGAGATTATTCCTTTTCCAGTACCAAAATGATGAGAAACCTTTATGTGTGCA 265
Qy 159 sValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGl 179
Db 266 TGTGAATGTGTGAGGAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGACCAGAGG 325
Qy 179 YHisAlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaPr 199
Db 326 GCATGCTGCGGAACGAATGAATCAGTTAAAAATGGTTTTAAAGAAAAATGCAAGAGGCTCC 385
Qy 199 oGluSerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrAr 219
Db 386 AGAGTCAGCTACAGTTATATTTTCAGGAGATACAAATCTAAGGGATCGAGAGGTTACCAG 445
Qy 219 qCys 220
Db 446 ATGT 449

Search completed: December 4, 2005, 09:03:30

Job time : 723.898 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: December 3, 2005, 23:34:21; Search time 5796.78 Seconds
(without alignments)
2157.330 Million cell updates/sec

Title: US-10-757-745-2_COPY_54_273

Perfect score: 1131

Sequence: 1 MERALNSFEPVBSALER.....SATVIFAGDTNLRDREVTTC 220

Scoring table: BLOSUM62

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Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Command line parameters:

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-Q/cgn2.1/USPTO spool/US10757745/runat_01122005_091748_10079/app_query.fasta_1.981
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-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=0.5 -FGAPOP=6
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Database :

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4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pr.*

9: gb.ro.*

10: gb.sts.*

11: gb.sy.*

12: gb.un.*

13: gb.vi.*

14: gb.htg.*

15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1131	100.0	1261	8	AF201687 Homo sapi
2	1131	100.0	1920	6	BD205490 CD40-Inte
3	1131	100.0	1920	6	AR594294 Sequence

4	1131	100.0	1920	6	AX011599 Sequence
5	1131	100.0	1921	8	HSA269473
6	1131	100.0	1936	8	AF223469 Homo sapi
7	1131	100.0	1948	6	AR333938 Sequence
8	1131	100.0	1952	8	BC017553 Homo sapi
9	1131	100.0	2499	6	E23195 Topoisomera
10	1131	100.0	2499	6	BD157138 Primer fo
11	1122	99.2	1898	6	BD157138 Sequence
12	1122	99.2	1898	6	AX878304 Sequence
13	971.5	85.9	2151	8	AX002168 Homo sapi
14	964	85.2	150344	14	AX002168 Homo sapi
15	904	79.9	752	6	AC152027
16	904	79.9	752	6	BD150065 Primer fo
17	766.5	67.8	1312	6	AX870003 Sequence
18	766.5	67.8	1312	6	BD205491 CD40-Inte
19	766.5	67.8	1312	6	AR594295 Sequence
20	766.5	67.8	1312	6	AX011601 Sequence
21	711	62.9	1079	6	AX011601 Sequence
22	711	62.9	1079	6	BD139846 Mus muscu
23	711	62.9	1079	6	BD139846 Mus muscu
24	711	62.9	1079	6	BD139846 Mus muscu
25	708	62.6	1236	5	BD139846 Mus muscu
26	681.5	60.3	858	6	BD139846 Mus muscu
27	583	51.5	1451	5	BD139846 Mus muscu
28	563	49.8	1455	5	BD139846 Mus muscu
29	559	49.4	483	6	BD139846 Mus muscu
30	355	31.4	176819	8	BD139846 Mus muscu
31	352.5	31.2	20938	8	BD139846 Mus muscu
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33	352.5	31.2	167847	8	BD139846 Mus muscu
34	333	29.4	201	10	BD139846 Mus muscu
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39	258	22.8	198752	5	BD139846 Mus muscu
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42	228	20.2	245394	14	BD139846 Mus muscu
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45	169.5	15.0	110000	14	BD139846 Mus muscu
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47	160	14.1	2036	2	BD139846 Mus muscu
48	145	12.8	379	6	BD139846 Mus muscu
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51	141	12.5	1326	15	BD139846 Mus muscu
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56	123.5	10.9	237211	8	BD139846 Mus muscu
57	118	10.4	33899	2	BD139846 Mus muscu
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61	115.5	10.2	159184	14	BD139846 Mus muscu
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65	115.5	10.2	225182	14	BD139846 Mus muscu
66	113	10.0	258	6	BD139846 Mus muscu
67	113	10.0	258	6	BD139846 Mus muscu
68	113	10.0	150354	8	BD139846 Mus muscu
69	111	9.8	6424	2	BD139846 Mus muscu
70	110.5	9.8	103566	8	BD139846 Mus muscu
71	109	9.6	176426	8	BD139846 Mus muscu
72	108.5	9.6	146610	8	BD139846 Mus muscu
73	108	9.5	10246	1	BD139846 Mus muscu
74	108	9.5	10412	1	BD139846 Mus muscu
75	108	9.5	124696	14	BD139846 Mus muscu
76	108	9.5	219366	8	BD139846 Mus muscu

77	107.5	9.5	7549	1	LMO012351	AJ012351 Listeria	150	102.5	9.1	3640	6	AR448205	AR448205 Sequence
78	107.5	9.5	10013	1	DQ073436	DQ073436 Thermotog	151	102.5	9.1	3640	6	AX301218	AX301218 Sequence
c 79	107.5	9.5	15962	8	AC099055	AC099055 Homo sapi	152	102.5	9.1	3875	6	AB020710	AB020710 Homo sapi
c 80	107.5	9.5	160050	1	AL591974	AL591974 Listeria	153	102.5	9.1	4061	6	AR338872	AR338872 Sequence
c 81	107.5	9.5	349980	6	AX638811	AX638811 Sequence	154	102.5	9.1	4818	6	BC067215	BC067215 Homo sapi
c 82	107.5	9.5	349980	6	AX641665	AX641665 Sequence	155	102.5	9.1	4911	6	AX027388	AX027388 Sequence
c 83	107	9.5	101179	8	AC018472	AC018472 Homo sapi	156	102.5	9.1	5077	8	AY331186	AY331186 Homo sapi
84	107	9.5	151778	8	AC021311	AC021311 Homo sapi	157	102.5	9.1	50714	8	AL511488	AL511488 Human DNA
85	107	9.5	168690	14	AC024043	AC024043 Homo sapi	c 158	102.5	9.1	110000	1	AE016853	Continuation (40 o
86	107	9.5	173958	14	AC087351	AC087351 Homo sapi	159	102.5	9.1	110000	14	BX276116	Continuation (7 of
87	106.5	9.4	5496	6	CQ859958	CQ859958 Sequence	c 160	102.5	9.1	116407	8	AC008613	AC008613 Homo sapi
88	106.5	9.4	102932	8	AC073112	AC073112 Homo sapi	161	102.5	9.1	185763	8	AF152363	AF152363 Homo sapi
89	106.5	9.4	151143	8	AC108714	AC108714 Homo sapi	162	102.5	9.1	185774	8	AC016562	AC016562 Homo sapi
90	106.5	9.4	159082	8	AF000940	AF000940 Homo sapi	c 163	102.5	9.1	186737	14	AC093207	AC093207 Homo sapi
c 91	106.5	9.4	302988	1	AE017176	AE017176 Porphyrom	164	102.5	9.1	196501	8	AC005908	AC005908 Homo sapi
92	106	9.4	110000	1	AP006841	Continuation (21 o	c 165	102.5	9.1	205329	8	AL354951	AL354951 Human DNA
93	105.5	9.3	42683	8	AC013456	AC013456 Homo sapi	166	102.5	9.1	302050	1	CR628336	CR628336 Nitrosomo
94	105.5	9.3	62795	14	AC022602	AC022602 Homo sapi	167	102	9.0	110000	1	CR628337	Continuation (6 of
c 95	105.5	9.3	73427	8	AC117496	AC117496 Homo sapi	168	102	9.0	110000	1	AE017354	Continuation (6 of
c 96	105.5	9.3	145390	8	AC092963	AC092963 Homo sapi	169	102	9.0	110000	1	AP006841	Continuation (16 of
97	105.5	9.3	152311	14	AC011571	AC011571 Homo sapi	c 170	102	9.0	110000	1	CP000084	Continuation (10 o
98	105.5	9.3	158739	14	AC027402	AC027402 Homo sapi	c 171	102	9.0	110000	1	AC009046	AC009046 Homo sapi
99	105.5	9.3	176277	14	AC025941	AC025941 Homo sapi	c 172	102	9.0	153562	8	AC023955	AC023955 Homo sapi
100	105.5	9.3	178975	14	AC032322	AC032322 Homo sapi	173	102	9.0	160905	8	AC023955	AC023955 Homo sapi
c 101	105.5	9.3	188873	14	AC019223	AC019223 Homo sapi	174	102	9.0	168172	8	AC010528	AC010528 Homo sapi
c 102	105.5	9.3	201451	8	AC073623	AC073623 Homo sapi	175	102	9.0	187559	8	AC067843	AC067843 Homo sapi
103	105	9.3	173902	14	AC024667	AC024667 Homo sapi	176	102	9.0	188557	14	AC106737	AC106737 Homo sapi
104	105	9.3	175517	8	AC096586	AC096586 Homo sapi	c 177	102	9.0	253694	14	AC084005	AC084005 Homo sapi
105	105	9.3	177112	8	AC002452	AC002452 Homo sapi	c 178	102	9.0	291073	8	AE017323	AE017323 Listeria
106	104.5	9.2	5496	6	CQ859965	CQ859965 Sequence	179	101.5	9.0	28026	8	AC093314	AC093314 Homo sapi
107	104.5	9.2	9737	9	WU070139	WU070139 Mus muscula	c 180	101.5	9.0	70626	8	AL356274	AL356274 Human DNA
108	104.5	9.2	141186	14	AC035578	AC035578 Homo sapi	181	101.5	9.0	79796	14	AC142388	AC142388 Homo sapi
c 109	104.5	9.2	158745	8	AL136456	AL136456 Human DNA	182	101.5	9.0	82457	8	AC093025	AC093025 Homo sapi
c 110	104.5	9.2	162030	14	AC018601	AC018601 Homo sapi	183	101.5	9.0	82472	8	AC092150	AC092150 Homo sapi
111	104.5	9.2	167024	14	BX571816	BX571816 Homo sapi	c 184	101.5	9.0	97357	8	AL360235	AL360235 Human DNA
112	104.5	9.2	176783	8	AL139281	AL139281 Human DNA	c 185	101.5	9.0	100000	8	AP000204	AP000204 Homo sapi
c 113	104.5	9.2	184848	14	AC009699	AC009699 Homo sapi	c 186	101.5	9.0	122208	8	AL583826	AL583826 Human DNA
114	104.5	9.2	192254	14	AP000914	AP000914 Homo sapi	c 187	101.5	9.0	134922	8	AC123909	AC123909 Homo sapi
115	104	9.2	2260	5	BC089295	BC089295 Xenopus l	c 188	101.5	9.0	143910	8	AC104454	AC104454 Homo sapi
116	104	9.2	6591	6	CQ716085	CQ716085 Sequence	c 189	101.5	9.0	149898	8	AP000244	AP000244 Homo sapi
117	104	9.2	100132	8	AL114813	AL114813 Homo sapi	190	101.5	9.0	152420	14	BX927200	BX927200 Danio rer
c 118	104	9.2	110000	1	AP006627	Continuation (3 of	191	101.5	9.0	153471	14	AC027076	AC027076 Homo sapi
119	104	9.2	142970	14	AL355811	AL355811 Homo sapi	c 192	101.5	9.0	155056	14	AC046138	AC046138 Homo sapi
120	104	9.2	144899	8	BS000532	BS000532 Pan trogl	c 193	101.5	9.0	155595	14	AC011880	AC011880 Homo sapi
121	104	9.2	156054	8	AC090141	AC090141 Homo sapi	c 194	101.5	9.0	159598	8	AP004386	AP004386 Homo sapi
122	104	9.2	175134	14	AL161623	AL161623 Homo sapi	c 195	101.5	9.0	162131	14	AC024906	AC024906 Homo sapi
123	104	9.2	176932	8	AL157884	AL157884 Human DNA	c 196	101.5	9.0	166521	8	AC013724	AC013724 Homo sapi
c 124	104	9.2	179780	14	AC021013	AC021013 Homo sapi	197	101.5	9.0	169939	14	AC069206	AC069206 Homo sapi
125	104	9.2	193163	8	AC147341	AC147341 Pan trogl	c 198	101.5	9.0	171721	8	AC022821	AC022821 Homo sapi
126	103.5	9.2	9392	15	EMESTCA	L39121 Emericella	c 199	101.5	9.0	172438	8	AP006587	AP006587 Homo sapi
c 127	103.5	9.2	59725	15	ENU34740	U34740 Emericella	c 200	101.5	9.0	173795	14	AC130336	AC130336 Homo sapi
c 128	103.5	9.2	87243	8	AC1117497	AC117497 Homo sapi	c 201	101.5	9.0	174387	8	AC092350	AC092350 Homo sapi
c 129	103.5	9.2	96960	6	AX706964	AX706964 Sequence	c 202	101.5	9.0	178316	8	AC098653	AC098653 Homo sapi
c 130	103.5	9.2	96960	6	AX707894	AX707894 Sequence	c 203	101.5	9.0	178521	8	AC112644	AC112644 Homo sapi
c 131	103.5	9.2	143872	8	AC091987	AC091987 Homo sapi	204	101.5	9.0	182556	8	AC016879	AC016879 Homo sapi
c 132	103.5	9.2	162738	8	AC083812	AC083812 Homo sapi	205	101.5	9.0	183164	14	AC025897	AC025897 Homo sapi
c 133	103.5	9.2	174832	8	AF280107	AF280107 Homo sapi	c 206	101.5	9.0	187464	5	AL929007	AL929007 Zebrafish
134	103.5	9.2	193001	14	AC032321	AC032321 Homo sapi	c 207	101.5	9.0	192044	8	AL590439	AL590439 Human DNA
135	103	9.1	924	2	AF034258	AF034258 Caenorhab	c 208	101.5	9.0	194106	9	AL671993	AL671993 Mouse DNA
136	103	9.1	3016	2	DDU31631	U11631 Dictyosteli	209	101.5	9.0	197873	14	AC147722	AC147722 Pongo pyg
137	103	9.1	110000	1	CR628927	Continuation (16 o	c 210	101.5	9.0	207345	8	AC005062	AC005062 Homo sapi
138	103	9.1	110000	1	CP000083	Continuation (40 o	c 211	101.5	9.0	208135	5	EX004778	EX004778 Zebrafish
c 139	103	9.1	126135	8	AC107058	AC107058 Homo sapi	c 212	101.5	9.0	211866	9	AL671991	AL671991 Mouse DNA
c 140	103	9.1	144474	8	AF051934	AF051934 Homo sapi	c 213	101.5	9.0	218866	9	AP001709	AP001709 Homo sapi
141	103	9.1	161514	8	AC079845	AC079845 Homo sapi	214	101	8.9	340000	6	CQ544973	CQ544973 Sequence
142	103	9.1	182314	14	AC013670	AC013670 Homo sapi	215	101	8.9	132790	8	HS167A14	Z94721 Human DNA s
c 143	103	9.1	302912	14	AC116378	AC116378 Homo sapi	216	101	8.9	171197	14	CT005231	CT005231 Pan trogl
c 144	103	9.1	340000	8	HS21C068	AL163268 Homo sapi	217	101	8.9	174304	8	AL450327	AL450327 Human DNA
145	103	9.1	348050	8	H8229042	AJ229042 Homo sapi	218	101	8.9	184548	14	AC023551	AC023551 Homo sapi
146	102.5	9.1	601	10	BV185140	BV185140 sqm14705	219	101	8.9	196591	9	AC125196	AC125196 Mus muscu
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149	102.5	9.1	3591	8	AY531390	AY531390 Homo sapi	222	101	8.9	227154	9	AC115121	AC115121 Mus muscu

C 223	101	8.9	232822	14	AC120204	AC120204 Pan trogl	236	99.5	8.8	173804	8	HS1030M6	AL035089 Human DNA
C 224	100.5	8.9	741	15	AV135641	AV135641 Solanum t	297	99.5	8.8	176253	14	AP001078	AP001078 Homo sapi
C 225	100.5	8.9	3586	5	BC073616	BC073616 Xenopus l	C 298	99.5	8.8	177251	8	AC109583	AC109583 Homo sapi
C 226	100.5	8.9	10155	8	AC133111	AC133111 Homo sapi	C 299	99.5	8.8	177802	14	AC090085	AC090085 Homo sapi
C 227	100.5	8.9	21376	8	AL142116	AL142116 Homo sapi	C 300	99.5	8.8	178430	14	AC022530	AC022530 Homo sapi
C 228	100.5	8.9	29851	8	AL596133	AL596133 Human DNA	C 301	99.5	8.8	180430	8	AC096768	AC096768 Homo sapi
C 229	100.5	8.9	47422	8	AC130414	AC130414 Homo sapi	C 302	99.5	8.8	185251	8	CNS01DTM	AL132800 Human chr
C 230	100.5	8.9	75214	8	AC093250	AC093250 Homo sapi	C 303	99.5	8.8	185308	8	AC118757	AC118757 Homo sapi
C 231	100.5	8.9	112830	14	AP002911	AP002911 Homo sapi	C 304	99.5	8.8	186951	8	AC104952	AC104952 Homo sapi
C 232	100.5	8.9	119119	8	AC008970	AC008970 Homo sapi	C 305	99.5	8.8	190902	8	AC104952	AC104952 Homo sapi
C 233	100.5	8.9	120567	8	AL356498	AL356498 Human DNA	C 306	99.5	8.8	191373	8	AC017067	AC017067 Homo sapi
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C 240	100.5	8.9	149578	14	AC079850	AC079850 Homo sapi	C 313	99.5	8.8	212055	14	AP000899	AP000899 Homo sapi
C 241	100.5	8.9	152731	9	AC144855	AL144855 Mus muscu	C 314	99.5	8.8	214025	8	AC026782	AC026782 Homo sapi
C 242	100.5	8.9	154979	8	AL590011	AL590011 Human DNA	C 315	99.5	8.8	216382	14	AC154728	AC154728 Mus muscu
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C 247	100.5	8.9	192053	8	AC090155	AC090155 Homo sapi	C 320	99	8.8	131691	8	AC096765	AC096765 Homo sapi
C 248	100.5	8.9	196363	14	AC113078	AC113078 Mus muscu	C 321	99	8.8	164380	8	AP001002	AP001002 Homo sapi
C 249	100.5	8.9	197877	8	AC090142	AC090142 Homo sapi	C 322	99	8.8	164953	8	AC016252	AC016252 Homo sapi
C 250	100.5	8.9	198176	14	AC069127	AC069127 Homo sapi	C 323	99	8.8	169562	8	AL136980	AL136980 Human DNA
C 251	100.5	8.9	199089	9	AC130836	AC130836 Mus muscu	C 324	99	8.8	176759	14	AC037464	AC037464 Homo sapi
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C 253	100.5	8.9	209483	8	CNS05TDV	AL357153 Human chr	C 326	99	8.8	210567	14	AC074215	AC074215 Homo sapi
C 254	100.5	8.9	211039	14	AC068555	AC068555 Homo sapi	C 327	99	8.8	220678	14	AC023857	AC023857 Homo sapi
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C 256	100.5	8.9	228434	14	AC012205	AC012205 Homo sapi	C 329	98.5	8.7	1407	1	AV335513	AV335513 Bacillus
C 257	100.5	8.9	233250	8	AC053527	AC053527 Homo sapi	C 330	98.5	8.7	2027	5	XL074761	U74761 Xenopus lae
C 258	100.5	8.9	233372	14	AC109433	AC109433 Rattus no	C 331	98.5	8.7	5057	2	AF037042	AF037042 Dictyoste
C 259	100.5	8.9	249979	14	AC161500	AC161500 Mus muscu	C 332	98.5	8.7	6020	8	HSU93565	U93565 Human L1 el
C 260	100	8.8	110000	1	CP000076	Continuation (55 o	C 333	98.5	8.7	27762	8	AL160001	AL160001 Human DNA
C 261	100	8.8	118492	14	AC020548	AC020548 Homo sapi	C 334	98.5	8.7	39359	8	HSU22357	Z79699 Human DNA s
C 262	100	8.8	146828	8	CNS07EER	AL445884 Human chr	C 335	98.5	8.7	55917	8	AC006002	AC006002 Homo sapi
C 263	100	8.8	155295	14	AC055859	AC055859 Homo sapi	C 336	98.5	8.7	71463	8	AC080088	AC080088 Homo sapi
C 264	100	8.8	156054	8	AC090141	AC090141 Homo sapi	C 337	98.5	8.7	88428	8	AL133388	AL133388 Human DNA
C 265	100	8.8	161054	8	AC104444	AC104444 Homo sapi	C 338	98.5	8.7	88948	14	AC008947	AC008947 Homo sapi
C 266	100	8.8	166518	8	AC078986	AC078986 Homo sapi	C 339	98.5	8.7	99441	8	AL391841	AL391841 Human DNA
C 267	100	8.8	174545	8	AC022257	AC022257 Homo sapi	C 340	98.5	8.7	101539	8	AC073980	AC073980 Homo sapi
C 268	100	8.8	191965	8	CNS05TDG	AL935676 Human chr	C 341	98.5	8.7	103158	8	AC107391	AC107391 Homo sapi
C 269	100	8.8	193256	9	AL935124	AL935124 Mouse DNA	C 342	98.5	8.7	105885	8	AC008860	AC008860 Homo sapi
C 270	100	8.8	200898	8	AC092058	AC092058 Homo sapi	C 343	98.5	8.7	110050	15	CR382134	Continuation (3 of
C 271	100	8.8	264395	9	AL713894	AL713894 Mouse DNA	C 344	98.5	8.7	110158	8	AC092663	AC092663 Homo sapi
C 272	99.5	8.8	6045	8	AF149422	AF149422 Homo sapi	C 345	98.5	8.7	118331	8	AL391336	AL391336 Human DNA
C 273	99.5	8.8	90462	8	AC105400	AC105400 Homo sapi	C 346	98.5	8.7	124557	8	AL390834	AL390834 Human DNA
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C 280	99.5	8.8	129226	8	HS960017	AL022166 Human DNA	C 353	98.5	8.7	154018	14	AC062019	AC062019 Homo sapi
C 281	99.5	8.8	139493	14	AC018537	AC018537 Homo sapi	C 354	98.5	8.7	155815	14	AC018774	AC018774 Homo sapi
C 282	99.5	8.8	141432	14	AC015699	AC015699 Homo sapi	C 355	98.5	8.7	156687	14	AC158133	AC158133 Mus muscu
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C 284	99.5	8.8	146985	8	BS000630	BS000630 Pan trogl	C 357	98.5	8.7	162170	8	AC110283	AC110283 Homo sapi
C 285	99.5	8.8	154272	8	AC025477	AC025477 Homo sapi	C 358	98.5	8.7	165304	8	AC112204	AC112204 Homo sapi
C 286	99.5	8.8	155863	8	AC021506	AC021506 Homo sapi	C 359	98.5	8.7	167358	8	AC007556	AC007556 Homo sapi
C 287	99.5	8.8	161838	8	AC023795	AC023795 Homo sapi	C 360	98.5	8.7	170156	14	AP002412	AP002412 Homo sapi
C 288	99.5	8.8	162997	8	AC092035	AC092035 Homo sapi	C 361	98.5	8.7	170279	14	AC027053	AC027053 Homo sapi
C 289	99.5	8.8	163448	9	AC116579	AC116579 Mus muscu	C 362	98.5	8.7	171367	8	AL355977	AL355977 Human DNA
C 290	99.5	8.8	166580	9	AC154584	AC154584 Mus muscu	C 363	98.5	8.7	172400	8	AC090883	AC090883 Homo sapi
C 291	99.5	8.8	166999	8	AC117402	AC117402 Homo sapi	C 364	98.5	8.7	173032	8	AC130364	AC130364 Homo sapi
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C 294	99.5	8.8	173639	8	AC068991	AC068991 Homo sapi	C 367	98.5	8.7	175053	14	AC023226	AC023226 Homo sapi
C 295	99.5	8.8	173722	9	AC154548	AC154548 Mus muscu	C 368	98.5	8.7	177102	8	HSU1069C8	AL078623 Human DNA

C 369	98.5	8.7	179513	8	AC016612	Homo sapi	AC016612 Homo sapi
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C 371	98.5	8.7	180718	8	AL596087	Human DNA	AL596087 Human DNA
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C 376	98.5	8.7	184685	8	AL513128	Human DNA	AL513128 Human DNA
C 377	98.5	8.7	186084	8	AF002768	Homo sapi	AF002768 Homo sapi
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C 391	98.5	8.7	212856	9	AL929062	Mouse DNA	AL929062 Mouse DNA
C 392	98.5	8.7	214419	14	AC026076	Homo sapi	AC026076 Homo sapi
C 393	98.5	8.7	224913	9	AC162857	Mus muscu	AC162857 Mus muscu
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C 416	98	8.7	188615	8	AL590410	Human DNA	AC092669 Homo sapi
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C 420	97.5	8.6	2031	5	CR926178	Xenopus t	AC109585 Homo sapi
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C 422	97.5	8.6	6029	8	HGU73E8	Human DNA	U93572 Human L1 el
C 423	97.5	8.6	48726	8	AL139106	Human DNA	Z73361 Human DNA
C 424	97.5	8.6	63324	8	AL590375	Human DNA	AL139106 Human DNA
C 425	97.5	8.6	63385	8	H5J74G15	Human DNA	AL590375 Human DNA
C 426	97.5	8.6	63749	8	AC004694	Homo sapi	AL132673 Human DNA
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C 428	97.5	8.6	87346	14	AL359978	3	AC138658 Homo sapi
C 429	97.5	8.6	94019	8	AL359971	Human DNA	Continuation (4 of
C 430	97.5	8.6	94042	8	AC011090	Homo sapi	AL359971 Human DNA
C 431	97.5	8.6	108175	8	AC068206	Homo sapi	AC011090 Homo sapi
C 432	97.5	8.6	109920	8	AL359851	Human DNA	AC068206 Homo sapi
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C 435	97.5	8.6	118226	8	H546618	Human DNA	Continuation (6 of
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C 437	97.5	8.6	124337	8	H5BA436C9	Human DNA	AC025459 Homo sapi
C 438	97.5	8.6	126698	8	AP005713	Homo sapi	AL121825 Human DNA
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C 440	97.5	8.6	132599	8	AC027345	Homo sapi	AC092289 Homo sapi
C 441	97.5	8.6	133226	14	AL512364	Homo sapi	AC027345 Homo sapi

ALIGNMENTS

RESULT 1	AF201687	1261 bp	mrna	linear	PRI 16-MAY-2003
LOCUS	AF201687				
DEFINITION	Homo sapiens ETS1-associated protein 2 (EAP2) mRNA, complete cds.				
ACCESSION	AF201687				
VERSION	AF201687.1				
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 1261)
Pei.H., Yordy.J.S., Leng.Q., Zhao.Q., Watson,D.K. and Li.R.
EAPII interacts with ETS1 and modulates its transcriptional
function

Oncogene 22 (18), 2699-2709 (2003)

JOURNAL

PUBMED

12743594

2 (bases 1 to 1261)

Li.R., Pei.H. and Papas.T.S.

Direct Submission

Submitted (03-NOV-1999) Center for Molecular and Structural
Biology, Department of Medicine, and Hollings Cancer Center,
Medical University of South Carolina, 86 Jonathan Lucas St.,
Charleston, SC 29425, USA

Location/Qualifiers

1. .1261

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SEDTQGSNYSITLWNIDGLNLSERAGVCSYLALISPDVIFLQEVIPPIYS

LKRSNYSIIITGHEGYFTAILMKSRVLRKSQEIIPFPSTKMRNLICVHVNVSGN

ELCLMTSHLESTYRHAERANOLKMLKMQBAPESATVIFAGDTNLRDREVTGCGL

PNNVDVWFLGPKPHCOYTWDTQNNSLGITAAACKLRDFRIFFRAAAECHIIIPRSL

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ORIGIN

Alignment Scores:
Pred. No.: 2,73e-102 Length: 1261
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x AF201687 (1-1261)

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Db 245 CGACCTGAAACCACTCTCGAGCCCAAGCACTATGTGTGACCTAACCAATGAAGAAACAACT 304
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QY 61 PheSerLeuIleThrTrpAenIleAspGlyLeuAspLeuAenLeuSerGluArgAla 80
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QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
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QY 101 IleProProTyrTyrSerTyrLeuLysValArgSerSerAenTyrGluIleIleThrGly 120
Db 485 ATTCCCCCATATTATAGCTACCTAAGAGAGATCAAGTAAATATTATGAGATTATTACAGGT 544

QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
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QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db 605 CAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCATGTG 664
QY 161 AenValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 665 AATGTGTGAGGAATAGAGCTTTTGCCTTATGACATCCATTTGAGAGACACGAGGCGCAT 724
QY 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 725 GCTCGGGAACGAATCAATCAATGTTTAAAGAAATGCAAGAGGCTCCAGAG 784
QY 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 785 TCAGCTACAGTTATATTTTCAGAGATACAAATCTAAGGGATCGAGAGGTTACCATGATGT 844

RESULT 2

BD205490 1920 bp DNA linear PAT 17-JUL-2003
LOCUS CD40-Interacting and TRAF-interacting protein.
DEFINITION
ACCESSION BD205490
VERSION BD205490.1 GI:33015260
KEYWORDS JP 2002512796-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 1920)
Pyper,S.M.C., Ghislaian,J.E.F.J., Remacle and Huylebroeck,D.F.E.
CD40-Interacting and TRAF-Interacting protein
Patent: JP 2002512796-A 1 08-MAY-2002;
VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE VZW
OS Homo sapiens (human)
PN JP 2002512796-A/1
PD 08-MAY-2002
PF 28-APR-1999 JP 2000546003
PR 29-APR-1998 EP 98201392.2
PI STEFAN MARIA CHRISTIAAN PYPER,
PI JACQUES EMILE FERNAND JOSTANE GHISLAIAN REMACLE, PI DANNY
FRANCOIS EVELINE HUYLEBROECK
PC C12N15/09,A61K38/00,A61P9/10,A61P19/02,A61P25/00,A61P35/00, PC
A61P37/02,
PC A61P37/06,A61P43/00,C07K14/47,C07K16/18,G01N33/15,G01N33/50,
PC G01N33/566,
PC C12N15/00,A61K37/02
CC CD40-Interacting and TRAF-interacting protein. FH Key
FT CDS Location/Qualifiers
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FEATURES

source

Alignment Scores:
Pred. No.: 4,4e-102 Length: 1920
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x BD205490 (1-1920)

QY 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluSerAlaLeuGluArg 20
Db 1131.00 Matches: 220
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

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Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
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Db 479 ATCCCCCATATTATAGCTACTTAAAGAAGAGATCAAGTAATTATGAGATTATTACAG 538
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Db 659 AATGTGTGAGAAATGAGCTTTGCTTATGACATCCCATTTGAGAGACCCAGAGGGCAT 718
Qy 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 719 GCTGGGAACGAATGAATCAGTTTAAATGTTTAAAGAAATGCAAGAGCTCCAGAG 778
Qy 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 779 TCAGCTACAGTTATATTTCGAGGAGATACAAATCTAAGGGATCGAGAGGTTTACCAGAT 838

RESULT 3
AR594294
LOCUS AR594294 1920 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 1 from patent US 6812203.
ACCESSION AR594294
VERSION AR594294.1 GI:56643900
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1920)
AUTHORS Pye,S.M.C., Remacle,J.E.F. and Huylebroeck,D.F.E.
TITLE CD40-interacting and TRAF-interacting proteins
JOURNAL Patent: US 6812203-A 1 02-NOV-2004;
Vlaams Interuniversitair Instituut voor Biotechnologie VZW;
Zwijnaarde;
WOX;
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source Location/Qualifiers
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Alignment Scores:
Pred. No.: 4 4e-102 Length: 1920
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db 239 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAACAAC 298
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 299 GATTCACCACTTCTTAAATCAGCCCTCTGAAATCTCTGAAATCTCTGAAATCTCTGAA 358
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
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Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 419 CGAGGGGTGTGTCTCTACTTACCTTGTACAGCCAGATGTGATATTCTACAGGAAGTT 478
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerAsnTyrGluIleThrGly 120
Db 479 ATCCCCCATATTATAGCTACTTAAAGAAGAGATCAAGTAATTATGAGATTATTACAG 538
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 539 CATGAAGAAGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAGA 598
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
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Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
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Qy 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 719 GCTGGGAACGAATGAATCAGTTTAAATGTTTAAAGAAATGCAAGAGCTCCAGAG 778
Qy 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 779 TCAGCTACAGTTATATTTCGAGGAGATACAAATCTAAGGGATCGAGAGGTTTACCAGAT 838

RESULT 4
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LOCUS AX011599 1920 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 1 from Patent WO9955859.
ACCESSION AX011599
VERSION AX011599.1 GI:9998123
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
Remacle,J.E., Huylebroeck,D.F. and Pype,S.M.
CD40-interacting and traf-interacting proteins
Patent: WO 9955859-A 1 04-NOV-1999;
REMACLE JACQUES EMILE FERNAND (BE); VLAAMS INTERUNIV INST BIOTECH
(BE); HUYLEBROECK DANNY FRANCOIS EVE (BE); PYPE STEFAN MARIA
CHRISTIAAN (BE)
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ORIGIN
Alignment Scores:
Pred. No.: 4,41e-102 Length: 1920
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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QY 21 ArgProGluThrIleSerGluProLysThrValAspLeuThrAsnGluThrThr 40
Db 239 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACACT 298
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 299 GATTCACCACCTCTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGCAGATG 358
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 359 TTCTCTCTCTATACCTGGAATATTGATGATTAGATCTAAACAATCTGTCAGAGAGGCT 418
QY 81 ArgGlyValCysSerTyrIleuAlaLeuTyrSerProAspValIlePheIleuGlnGluVal 100
Db 419 CGAGGGGTGTGTTCTTACTAGCTTTGTACAGCCCATGTTGATATTTCTACAGGAAGTT 478
QY 101 IleProProTyrTyrSerTyrLeuLysValAspGlySerSerAsnTyrGluIleThrGly 120
Db 479 ATTCCCCCATATTATAGCTACCTTAAGAGAGATCAAGTAATATTAGATATTACAGGT 538
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 539 CATGAGNAGGATATTTCACAGCTATAATGTTGAGAAATCAAGAGTGAAATTAAGAGC 598
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db 599 CAAGAGATTATTCCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTGCATGTG 658
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 659 AATGTGTGTCAGAAATAGCTTTTCCCTTATGACATCCATTTGGAGAGCACCGAGGGCAT 718
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QY 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 779 TCAGCTACAGTTATATTTCAGGAGATACAAATCTAAGGATCGAGAGGTACAGATGT 838

RESULT 5
HSA269473
LOCUS
DEFINITION
Homo sapiens mRNA for TRAF and TNF receptor associated protein
(trap gene).
ACCESSION
AJ269473
VERSION
AJ269473.1 GI:8247253
KEYWORDS
TRAF and TNF receptor associated protein; trap gene.

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS
Pype,S., Declercq,W., Ibrahim,A., Michiels,C., Van
Rietschoten,J.G., Dewulf,N., de Boer,M., Vandenaabeele,P.,
Huylebroeck,D. and Remacle,J.E.
TITLE
TRAP, a novel protein that associates with CD40, tumor necrosis
factor (TNF) receptor-75 and TNF receptor-associated factors
(TRAFs), and that inhibits nuclear factor-kappa B activation
J. Biol. Chem. 275 (24), 18586-18593 (2000)
JOURNAL
PUBMED 10764746
REFERENCE
2 (bases 1 to 1921)
AUTHORS
Pype,S.
TITLE
Direct Submission
JOURNAL
Submitted (08-SEP-1999) Pype S., VIB07, Dept. Cell Growth,
Differentiation and Development, Flanders Interuniversity Institute
for Biotechnology, CELGEN, K.U. Leuven, Gasthuisberg Campus,
Herestraat 49, B-3000 Leuven, BELGIUM
COMMENT
Related sequence: AL031775.
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Alignment Scores:
Pred. No.: 4,41e-102 Length: 1921
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x HSA269473 (1-1921)
QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluSerAlaLeuGluArg 20
Db 181 ATGGAAGGCTCTGAACCTCTACTTCGAGCCTCCGGTGGAGAGCGCTTGGAAAGC 240
QY 21 ArgProGluThrIleSerGluProLysThrValAspLeuThrAsnGluThrThr 40
Db 241 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACACT 300
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Db 301 GATTCACCACTTCTAAATCAGCCACTCTCAAGATCTCAGCAAGAAATGGCAGCATG 360

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Db 661 AACGTGTTCAGGAATAGCTTTTGCTTATGATCATCCCATTTTGGAGAGCACCAGAGGGCAT 720

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Db 781 TCAGCTACAGTTATATTTGCAGGAGATACAAATCTAAGGGATCGAGAGTTACCAGATGT 840

RESULT 6

AF223469

LOCUS Homo sapiens AD022 protein (AD022) mRNA, complete cds.

DEFINITION AF223469

ACCESSION AF223469.1 GI:7578788

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

Song,H., Gao,G., Peng,Y., Ren,S., Chen,Z. and Han,Z.

1 (bases 1 to 1936)

A novel gene expressed in human adrenal gland

Unpublished

2 (bases 1 to 1936)

Song,H., Gao,G., Peng,Y., Ren,S., Chen,Z. and Han,Z.

Direct Submission

Submitted (12-JAN-2000) Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, China

Location/Qualifiers

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17. .1105

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Alignment Scores: 4.44e-102 Length: 1936

Pred. No.: 1131.00 Matches: 220

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 8 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x AF223469 (1-1936)

Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20

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Db 236 CGACCTGAAACCAATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAAC 295

Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60

Db 296 GATTCCACCACTTCTAAAAATCAGCCCATCTGAAGATCTCAGCAAGAAATATGGCAGCATG 355

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Db 596 CAAGAGATTATTCCTTTTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 655

Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180

Db 656 AACGTGTGAGGAATGAGCTTTTGCTTATGACATCCCATTTGGAGAGCACCAGAGGGCAT 715

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Db 716 GCTCGGGAACGAATGAATCAGTTAAAAATGCTTTTAAAGAAATGCAAGAGGCTCCAGAG 775

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RESULT 7

AR339398

LOCUS Sequence 889 from patent US 6569662.

DEFINITION AR339398

ACCESSION AR339398

VERSION AR339398.1 GI:33726255

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unknown.

Unclassified.

1 (bases 1 to 1948)

Tang,Y.T., Zhou,P. and Drmanac,R.T.

Nucleic acids and polypeptides

JOURNAL	Patent: US 6569662-A 889 27-MAY-2003;
FEATURES	Hysq, Inc.; Sunnyvale, CA
source	Location/Qualifiers
ORIGIN	1..1948
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	/mol_type="genomic DNA"
Alignment Scores:	
Pred. No.:	4,48e-102
Score:	1131.00
Percent Similarity:	Length: 1948
Best Local Similarity:	Matches: 220
Query Match:	Conservative: 0
DB:	Mismatches: 0
	Indels: 0
	Gaps: 0
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Qy	21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
Db	258 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACT 317
Qy	41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db	318 GATTCACCACTCTTAAATCAGCCCATCTGAAGATACCTCAGCAGAAATGCGCAGCATG 377
Qy	61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db	378 TTCTCTCTCATACCTGGGAATATTGATGATTAGATCTAAACAATCTGTGACAGAGGGCT 437
Qy	81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db	438 CGAGGGGTGTCTCTTACTTACTTGTACAGCCAGATGTGATATTCTACAGGAGTT 497
Qy	101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db	498 ATTCCCCCATATTATAGCTACCTAAGAAGAGATCAAGTAATATTATGAGATTATTACAGT 557
Qy	121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db	558 CATGAAGAAGAGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAAGAGC 617
Qy	141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db	618 CAAAGATTATTCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTG 677
Qy	161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db	678 AATGTGTGAGAAATCAGCTTTGCTTATGACATCCATTTGGAGAGCACCAGAGGGCAT 737
Qy	181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db	738 GCTGCGGAACGAATGAATCAGTTAAATAATGGTTTTAAAGAAATGCAAGAGGCTCCAGAG 797
Qy	201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db	798 TCAGCTACAGTTATATTTCGAGGAGATACAAATCTTAAGGATCGAGAGGTTACCAAGTGT 857
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BC017553	
LOCUS	BC017553
DEFINITION	Homo sapiens TRAF and TNF receptor associated protein, mRNA (cdna
ACCESSION	clone MGC:9099 IMAGE:3920790), complete cds.
VERSION	BC017553
KEYWORDS	MGC.
SOURCE	BC017553.2 GI:34782842
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE	
AUTHORS	
1 (bases 1 to 1952)	
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,	
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,	
Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,	
Hopkins,R., Jordan,H., Moore,T., Max,S.I., Wang,J., Heideh,F.,	
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,	
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,	
Scheetz,T.E., Brownstein,M.J., Udwin,T.B., Toshiyuki,S.,	
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,	
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,	
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,	
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,	
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,	
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,	
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,	
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,	
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,	
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalilus,D.E.,	
Schmerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.	
Generation and initial analysis of more than 15,000 full-length	
human and mouse cDNA sequences	
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
12477932	
2 (bases 1 to 1952)	
Strausberg,R.	
Direct Submission	
Submitted (19-NOV-2001) National Institutes of Health, Mammalian	
Gene Collection (MGC), Cancer Genomics Office, National Cancer	
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	
USA	
NIH-MGC Project URL: http://mgc.nci.nih.gov	
On Sep 16, 2003 this sequence version replaced gi:17028464.	
Contact: MGC help desk	
Email: cgapbs-remail.nih.gov	
Tissue Procurement: ATCC/DCTD/DTF	
cDNA Library Preparation: Life Technologies, Inc.	
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
DNA Sequencing by: Genome Sequence Centre,	
BC Cancer Agency, Vancouver, BC, Canada	
info@bcgsc.bc.ca	
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,	
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth	
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,	
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,	
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lisea Frahbu,	
Parvaneh Saedi, JR Santos, Angeliqne Schnerch, Ursula Skalska,	
Duane Smalilus, Jeff Stott, Miranda Teai, George Yang, Jacqueie	
Schein, Asim Siddiqui, Rob Holt, Marco Marra.	
Clone distribution: MGC clone distribution information can be found	
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
Series: IRAP Plate: 15 Row: m Column: 16	
This clone was selected for full length sequencing because it	
passed the following selection criteria: matched mRNA gi: 23510347.	
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/lab_host="DH10B"	
/note="Vector: pCMV-SPORT6"	
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38..1126	
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CDS	

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ORIGIN

Alignment Scores:
Pred. No.: 4,49e-102 Length: 1952
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x BC017553 (1-1952)

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Qy	21	ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr	40
Db	257	CGACTGNAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAACAAC	316
Qy	41	AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet	60
Db	317	GATTCACCACTTCTAAATCAGCCATCTCAAGATACTCAGCAAGAAATGGCAGCATG	376
Qy	61	PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla	80
Db	377	TTCTCTCTCATTTACCTGGAATATTGATGGATTAGATCTAAACAATCTGTACAGAGGGCT	436
Qy	81	ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal	100
Db	437	CGAGGGTGTTTCTCTTACCTTACCTTTGTACAGCCCAAGATGATGATTTCTACAGAAAGTT	496
Qy	101	IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly	120
Db	497	ATTCCCCCATATTATAGTACTCTAAAGAAGAGATCAAGTAATTATGAGATTATTACAGGT	556
Qy	121	HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer	140
Db	557	CATGAAGAAGGATATTTTACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAGAAGC	616
Qy	141	GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal	160
Db	617	CAAGAGATTATTCCTTTTCCAAGTACCAAAATGATGAGAAACCTTTTATGTTGTCATGTG	676
Qy	161	AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis	180
Db	677	AATGTGTCAGGAATAGCTTTTGCTTATGATCATCCCATTTGGAGAGCACCAGAGGGCAT	736
Qy	181	AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu	200
Db	737	GCTGGGAACGAATGAATCAGTTAAATATGGTTTTTAAAGAAATGCAAGAGGCTCCAGAG	796
Qy	201	SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys	220
Db	797	TCAGTACAGTTATATTTCAGAGGAGATACAAATCTAAGGGATTCGAGAGGTTTACCAGATGT	856

RESULT 9

E23195 2499 bp DNA linear PAT 18-JUN-2001
LOCUS E23195
DEFINITION Topoisomerase binding protein.

ACCESSION E23195
VERSION E23195.1 GI:13024277
KEYWORDS JP 1999075856-A/1.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 2499)
AUTHORS Takashi,T. and Kazuhiko,Y.
TITLE Topoisomerase binding protein
JOURNAL Patent: JP 1999075856-A 1 23-MAR-1999;
TAKASHI TSURUO,CHUGAI PHARMACEUT CO LTD
OS Unidentified
PN JP 1999075856-A/1
PD 23-MAR-1999
PF 17-SEP-1997 JP 1997251544
PR
PI TAKASHI TSURUO, KAZUHIKO YAMANE
PC C12N15/09, C07K14/47, C12N9/90, C12N15/00
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..2499
/organism='Unidentified'.
FEATURES
source
Location/Qualifiers
1..2499
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ORIGIN

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Pred. No.: 5,94e-102 Length: 2499
Score: 1131.00 Matches: 220
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x E23195 (1-2499)

Qy	1	MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg	20
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Qy	21	ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr	40
Db	701	CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAACAAC	760
Qy	41	AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet	60
Db	761	GATTCACCACTTCTAAATCAGCCCATCTGAAGATACTCAGCAAGAAATGGCAGCATG	820
Qy	61	PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla	80
Db	821	TTCTCTCTCATTTACCTGGAATATTGATGGATTAGATCTTAACCAATCTGTACAGAGGGCT	880
Qy	81	ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal	100
Db	881	CGAGGGTGTTTCTCTTACGCTTTGTACAGCCCAAGATGATGATTTCTACAGAAAGTT	940
Qy	101	IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly	120
Db	941	ATTCCCCCATATTATAGTACTCTAAAGAAGAGATCAAGTAATTATGAGATTATTACAGGT	1000
Qy	121	HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer	140
Db	1001	CATGAAGAAGGATATTTTACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAGAAGC	1060
Qy	141	GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal	160
Db	1061	CAAGAGATTATTCCTTTTCCAAGTACCAAAATGATGAGAAACCTTTTATGTTGTCATGTG	1120
Qy	161	AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis	180

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 QY 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
 Db 1181 GCTGCGGAACGAATGAATCAGTTAAATGGTTTTAAAGAAATGCAAGAGGCTCCAGAG 1240
 QY 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
 Db 1241 TCAGCTACAGTTATATTTTCGAGAGATACAAATCTTAAGGATCGAGAGGTTACCAAGTGT 1300

RESULT 10

BD157138 1898 bp DNA linear PAT 17-JAN-2003
 LOCUS Primer for synthesizing full-length cDNA and use thereof.

DEFINITION BD157138

ACCESSION BD157138.1 GI:27862896

VERSION JP 2002191363-A/11981.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM

REFERENCE Ota.T., Isogai.T., Nishikawa.T., Hayashi.K., Saito.K., Yamamoto,J., Ishii.S., Sugiyama.T., Wakamatsu,A., Nagai,K. and Otsuki.T.

AUTHORS Primer for synthesizing full-length cDNA and use thereof

TITLE Patent: JP 2002191363-A 11981 09-JUL-2002;

JOURNAL HELIX RESEARCH INSTITUTE

COMMENT OS Homo sapiens (human)

PN JP 2002191363-A/11981

PD 09-JUL-2002

PF 28-JUL-2000 JP 2000280990

PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU

PI SAITO,

PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,

PI KEIICHI NAGAI,TETSUJI OTSUKI

PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10, PC

PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC

Primer for synthesizing full-length cDNA and use thereof FH Key

Location/Qualifiers

FT CDS (1)..(1086).

source

FEATURES

Location/Qualifiers

1..1898

/organism="Homo sapiens"

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ORIGIN

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Pred. No.: 3.38e-101 Length: 1898

Score: 1122.00 Matches: 219

Percent Similarity: 99.55% Conservative: 0

Best Local Similarity: 99.55% Mismatches: 1

Query Match: 99.20% Indels: 0

DB: 6 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x BD157138 (1-1898)

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QY 21 ArgProGluThrIleSerGluProLysThrValAspLeuThrAsnGluThrThr 40

Db 220 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCATGAAGAAACACT 279

QY 41 AspSerThrThrSerTyIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60

Db 280 GATTCCACCACTTCTAAATCAGCCCATCTGAGATACCTCAGCAAGAAATGCGAGCATG 339

QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80

Db 340 TTCTCTCTCAATTACCTGGAATATTGATGGAATTAGATCTAAACAATCTGTCAGAGAGGCT 399

QY 81 ArgGlyValCysSerTyPheAlaLeuTyPheProAspValIlePheLeuGlnGluVal 100

Db 400 CGAGGGGTGCTCTCTACTTACTTGTACAGCCAGATGTGATATTCTTACAGGAAGTT 459

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QY 121 HisGluGluGlyTyPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140

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QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180

Db 640 AACGTGTGAGGAATAGAGCTTTGCTTATGACATCCATTTTGAGAGCACCAGAGGCGAT 699

QY 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200

Db 700 GCTGCGGAACGAATGAATCAGTTAAATGGTTTTAAAGAAATGCAAGAGGCTCCAGAG 759

QY 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220

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RESULT 11

AX878304 1898 bp DNA linear PAT 17-DEC-2003

LOCUS Sequence 13209 from Patent EP1074617.

DEFINITION AX878304

ACCESSION AX878304

VERSION AX878304.1 GI:40033040

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM

REFERENCE Ota.T., Isogai.T., Nishikawa.T., Hayashi.K., Saito.K., Yamamoto,J., Ishii.S., Sugiyama.T., Wakamatsu,A., Nagai,K. and Otsuki.T.

AUTHORS Primers for synthesizing full-length cDNA and their use

TITLE Patent: EP 1074617-A 13209 07-FEB-2001;

JOURNAL Research Association for Biotechnology (JRP)

FEATURES Location/Qualifiers

1..1898

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LKRSNYSIIITGHEGYETAIMLKSRVKLKSQEIIPSTKMMNLLCVHNVSGN

EULMTSHLSTRGHAAERNQIKWLVKKNQAPESATVIFAGDTNLRDREVTCCGL

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ORIGIN

Alignment Scores:

Pred. No.: 3.38e-101 Length: 1898

Score: 1122.00 Matches: 219

Percent Similarity: 99.55% Conservative: 0

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Best Local Similarity: 99.55% Mismatches: 1
Query Match: 99.20% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_54_273 (1-220) x AX878304 (1-1898)

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QY 21 ArgProGluThrIleSerGluProLysThrTyrValAepLeuThrAsnGluGluThrThr 40
Db 220 CGACTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAACCT 279
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 280 GATTCACCACTTCTTAAATCAGGCCATCTCTGAAGATCTACGCAAGAAATATGGCAGCATG 339
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAepLeuAenAenSerGluArgAla 80
Db 340 TTCCTCTCATCTGGAATATTGATGATTGATCTTAAACAATCTGTACAGAGGGCT 399
QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 400 CGAGGGGTGCTCTCTACTTACTTGTACAGCCAGATGTGATATTCTACAGGAAGTT 459
QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleThrGly 120
Db 460 ATTCCCCCATATTATAGCTACCTAAGAAGAGATCAAGTAATTATGAGATTATTACAGGT 519
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 520 CATGAAGAAGGATATTTTACAGCTATATATGTTGAAGAAATCAAGAGTGAATTTAAAGGC 579
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysValHisVal 160
Db 580 CAAGAGATTATCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTGTCATGTG 639
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 640 AACGTGTCCAGAAATAGCTTTGCTTATGACATCCCATTTGGAGAGCACCAGAGGGCAT 699
QY 181 AlaAlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGlu 200
Db 700 GCTCGGAACCAATGAATCACTTAAATGTTTAAAGAAATGCAAGAGGCTCCAGAG 759
QY 201 SerAlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 760 TCAGCTACAGTTATTTTGCAGGAGATACAAATCTAAGGATCCGAGAGGTTACCAGATGT 819

RESULT 12
AK002168 LOCUS Homo sapiens cDNA FLJ11306 fis, clone PLACE1010031.
DEFINITION AK002168
ACCESSION AK002168
VERSION AK002168.1 GI:7023882
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1
Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,
Sekine, M., Ohtsashi, M., Nishi, T., Shibahara, T., Tanaka, T.,
Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,
Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M.,
Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T.,
Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K.,
Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H.,
Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M.,
Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S.,
Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A.,
Hara, H., Tanase, T., Nomura, Y., Togliya, S., Komai, F., Hara, R.,
Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A.,
Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T.,
Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S.,
Teraehima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H.,
Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T.,
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Kumaagi, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, K., Fujii, Y.,
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Sato, T., Shimura, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,
Nagase, T., Nishira, N., Kikuchi, H., Masuho, Y., Yamashita, R.,
Nakai, K., Yada, T., Nakamura, Y., Ohara O., Isogai, T. and Sugano, S.
Complete sequencing and characterization of 21,243 full-length
human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)

TITLE
JOURNAL PUBMED 14702039
REFERENCE
AUTHORS
Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H.,
Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K.,
Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K.,
Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A.,
Nakamura, Y., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T.
NEDO human cDNA sequencing project
Unpublished
3 (bases 1 to 1898)
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 232-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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Score: 99.55% Conservative: 0
Percent Similarity:
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ACCESSION      AJ420495
VERSION        AJ420495.1   GI:17066359
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1   Auffray, C., Ansoerge, W., Ballabio, A., Estivill, X., Gibson, K.,
    Lehrach, H., Poustka, A. and Lundeberg, J.
    The European IMAGE consortium for integrated Molecular analysis of
    human gene transcripts
    Unpublished
    2   (bases 1 to 2151)
    Persson, A.
    Direct Submission
    Submitted (02-OCT-2001) Persson A., Center for Molecular
    Biotechnology, KTH, SCFAB, Institute of Biotechnology, Roslagssvagen
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Qy      154  AsnLeuLeuCysValHisValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHis 173
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LOCUS
DEFINITION
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VERSION
HTG; HTGS_PHASE2; HTGS_DRAFT.
KEYWORDS
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SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Xenarthra; Dasypodidae; Dasypus.
1 (bases 1 to 150344)
Antonellis,A., Ayele,K., Benjamin,B., Blakesley,R.W., Boakye,A.,
Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,H.,
Engle,J., Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N.,
Ho,S.-L., Hu,P., Hurle,B., Idol,J.R., Jones,C., Kwong,P., Laric,P.,
Larson,S., Lee-Lin,S.-Q., Legaspi,R., Madden,M., Maduro,Q.L.,
Maduro,V.B., Margulies,E.H., Masello,C., Maskeri,B., McDowell,J.,
Mullikin,J.C., Oestreicher,J.S., Park,M., Portnoy,M.E., Prasad,A.,
Puri,O., Reddix-Dugue,N., Rosas,B., Schandler,K., Schueler,M.G.,
Shah,K., Sison,C., Stantripop,S., Stephen,E., Thomas,J.W.,
Thomas,P.J., Tsipouri,V., Vogt,J.L., Wetherby,K.D., Young,A. and
Green,E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 150344)
Green,E.D.
Direct Submission
Submitted (21-OCT-2004) NIH Intramural Sequencing Center, 8717
Grovermont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 150344)
Green,E.D.
Direct Submission
Submitted (11-NOV-2004) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
On Nov 11, 2004 this sequence version replaced gi:54312159.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_zoemhgr@nisc.nih.gov
----- Project Information
Center project name: ifi
Center clone name: 012D21

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The sequence data in this record represents an 'enhanced'

version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 149480 bases at least Q40
 Consensus quality: 149754 bases at least Q30
 Consensus quality: 149909 bases at least Q20
 Insert size: 155000; agarose-fp
 Insert size: 149944; sum-of-contigs
 Quality coverage: 9.52x in Q20 bases; agarose-fp
 Quality coverage: 9.84x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 5 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * been provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and
 * the accession number will be preserved.

* 1 36273: contig of 36273 bp in length
 * 36274 36373: gap of unknown length
 * 36374 55049: contig of 18676 bp in length
 * 55050 55149: gap of unknown length
 * 55150 101939: contig of 46790 bp in length
 * 101940 102039: gap of unknown length
 * 102040 114806: contig of 12767 bp in length
 * 114807 114906: gap of unknown length
 * 114907 150344: contig of 35438 bp in length.

FEATURES

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VERSION		BD150065.1 GI:27855823		Db		460	
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AUTHORS		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		Qy		160	
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		Ishii.S., Sugiyama.T., Wakamatsu.A., Nagai.K. and Otsuki.T.		Qy			
		Primer for synthesizing full-length cDNA and use thereof		Db			

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DEFINITION Sequence 4908 from Patent EP1074617.
ACCESSION AX870003
VERSION AX870003.1 GI:40024866
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
Primates for synthesising full-length cDNA and their use
TITLE Patent: EP 1074617-A 4908 07-FEB-2001;
JOURNAL Research Association for Biotechnology (JP)
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Best Local Similarity: 92.96% Mismatches: 10
Query Match: 79.93% Indels: 3
DB: 6 Gaps: 0
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QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
Db 220 CGACTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAAC 279
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnAsnGlySerMet 60
Db 280 GATTCACCACTTCTTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGCATG 339
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
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DEFINITION CD40-Interacting and TRAF-interacting protein.
ACCESSION BD205491
VERSION BD205491.1 GI:33015261
KEYWORDS JP 2002512796-A/2.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1312)
AUTHORS Pype, S.M.C., Ghislain, J.E.F.J., Remacle and Huylebroeck, D.F.E.
TITLE CD40-Interacting and TRAF-interacting protein
JOURNAL Patent: JP 2002512796-A 2 08-MAY-2002;
VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE VZW
COMMENT
OS Mus musculus (mouse)
PN JP 2002512796-A/2
PD 08-MAY-2002
PF 28-APR-1999 JP 2000546003
PR 29-APR-1998 EP 98201392-2
PI STEFAN MARIA CHRISTIAAN PYPE, DANNY
FRANCOIS EVELINE HUYLEBROECK
PC C12N15/09,A61K38/00,A61P9/10,A61P19/02,A61P25/00,A61P35/00, PC
A61P37/02,
PC A61P37/06,A61P43/00,C07K14/47,C07K16/18,G01N33/15,G01N33/50,
PC G01N33/566,
PC C12N15/00,A61K37/02
CC CD40-Interacting and TRAF-interacting protein. FH Key
Location/Qualifiers
FT CDS
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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Alignment Scores:
Pred. No.: 3.44e-66 Length: 1312
Score: 766.50 Matches: 150
Percent Similarity: 81.28% Conservative: 28
Best Local Similarity: 68.49% Mismatches: 40
Query Match: 67.77% Indels: 1
DB: 6 Gaps: 1
US-10-757-745-2_COPY_54_273 (1-220) x BD205491 (1-1312)
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Db 317 CAGAAAGCCCTGAGCGCTACTTCGAGCTCCAGAGAACACCAAGGTGCCCGCCGAG 376
QY 22 ProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThrAsp 41
Db 377 CCTCCCACGTCCTCAAGTCGAGCGCTATGTTGATCTAACCAACGAGGATGCAATGAT 436
QY 42 SerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPhe 61
Db 437 ACAACCACTTTTGAAGCCAGTCCTCATCTCT--GGAACCTCTCTAGAAGATAGCAGCACTATT 493
QY 62 SerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArg 81
Db 494 TCTTTCATTACCTCGAATATTGATGGATTAGATGGATGCAATCTGCCCGAGAGGGCTCGA 553
QY 82 GlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIle 101
Db 554 GGGGTGTGTTCCCTGCCTAGCTTTGTTATAGTCCAGATGCTGGTATTCTTACAGGAAGTTATC 613
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QY 102 ProProTyrTyrSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIle 121
DB 614 CCCCCTACTGTGCTTACCTAACGAAGAGAGAGCCAGTATTTCTACAGGAAGTTATC 673

QY 122 GluGluGlyTyrPheThrAlaIleMetLeuLysSerArgValLysLeuLysSerGln 141
DB 674 GAAGAAGGATATTTACAGCTATCTATTGAAGAAAGGAAGAGTGAATTTTAAAGTCAG 733

QY 142 GluIleIleProPheProSerThrLysMetMetArgAsnLeuLysValHisValAsn 161
DB 734 GAGATTATTCCTTTCCAAATACCAAAATGATGAGAAACCTGCTATGCGTAAATGTGAGT 793

QY 162 ValSerGlyAsnGluLeuLysLeuMetThrSerHisLeuGluSerThrArgGlyHisAla 181
DB 794 TTGGGTGGAATGAATTTTGGCTTTATGACATCCCATTTGGAGAGACCCAGAGAACTTCT 853

QY 182 AlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGluSer 201
DB 854 GCGGAACGAATAAGACAATTAATAACTGTTCTTGGAAAAATGCAAGAGGCTCCAGATTCA 913

QY 202 AlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
DB 914 ACCACGGTTATATTGACGAGATACAAATTTAAGAGATCAAGAAGTTATCAAAATGT 970

RESULT 18
LOCUS AR594295 1312 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 3 from patent US 6812203.
ACCESSION AR594295
VERSION AR594295.1 GI:56643901
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1312)
AUTHORS Pyne, S.M.C., Remacle, J.E.F. and Huylebroeck, D.P.E.
TITLE CD40-Interacting and TRAF-Interacting proteins
JOURNAL Patent: US 6812203-A 3 02-NOV-2004;
Vlaams Interuniversitair Instituut voor Biotechnologie VZW;
Zwijnnaarde;
WOX;

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/organism="unknown" Matches: 150
/mol_type="genomic DNA" Conservative: 28
Mismatch: 40
Indels: 1
Gaps: 1
DB: 6

ORIGIN
Alignment Scores: 3,44e-66 Length: 1312
Pred. No.: 766.50 Matches: 150
Score: 81.28% Conservative: 28
Percent Similarity: 68.49% Mismatches: 40
Best Local Similarity: 67.77% Indels: 1
Query Match: 67.77% Gaps: 1

US-10-757-745-2_COPY_54_273 (1-220) x AR594295 (1-1312)

QY 2 GluArgAlaLeuAsnSerTyrPheGluProProValGluSerAlaLeuGluArgArg 21
DB 317 CAGAAAGCCTGAGCGCTACTTCGAGCTCCAGAGACGACCAAGGTCGCGCCGAC 376

QY 22 ProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrAsp 41
DB 377 CTTCCACGCGCTTCAAGTCGAGGCTATGTTGATCAACCAACGAGGATGCAATGAT 436

QY 42 SerThrThrSerLysIleSerProSerGluAspThrGlnGlnAsnGlySerMetPhe 61
DB 437 ACAACCATTTTGAAGCCAGCTCCATCT---GGAACTCCTCTAGAAGATAGCAGCATATT 493

QY 62 SerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArg 81
DB 494 TCITTCATACCTGGATATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 553
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QY 82 GlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIle 101
DB 554 GGGTGTGTTCTCGCTAGCTTTGTATAGTCCAGATGTGTATTTCTACAGGAAGTTATC 613

QY 102 ProProTyrTyrSerTyrLeuLysLysSerSerAsnTyrGluIleIleThrGlyHis 121
DB 614 CCCCCTACTGTGCTTACCTAACGAAGAGAGAGCCAGTATTTCTACAGGAAGTTATC 673

QY 122 GluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGln 141
DB 674 GAAGAAGGATATTTACAGCTATCTATTGAAGAAAGGAAGAGTGAATTTTAAAGTCAG 733

QY 142 GluIleIleProPheProSerThrLysMetMetArgAsnLeuLysValHisValAsn 161
DB 734 GAGATTATTCCTTTCCAAATACCAAAATGATGAGAAACCTGCTATGCGTAAATGTGAGT 793

QY 162 ValSerGlyAsnGluLeuLysLeuMetThrSerHisLeuGluSerThrArgGlyHisAla 181
DB 794 TTGGGTGGAATGAATTTTGGCTTTATGACATCCCATTTGGAGAGACCCAGAGAACTTCT 853

QY 182 AlaGluArgMetAsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGluSer 201
DB 854 GCGGAACGAATAAGACAATTAATAACTGTTCTTGGAAAAATGCAAGAGGCTCCAGATTCA 913

QY 202 AlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
DB 914 ACCACGGTTATATTGACGAGATACAAATTTAAGAGATCAAGAAGTTATCAAAATGT 970

RESULT 19
LOCUS AX011601 1312 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 3 from Patent WO9955859.
ACCESSION AX011601
VERSION AX011601.1 GI:9998125
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Remacle, J.E., Huylebroeck, D.F. and Pyne, S.M.
TITLE Cd40-interacting and traf-interacting proteins
JOURNAL Patent: WO 9955859-A 3 04-NOV-1999;
REMACLE JACQUES EMILE FERNAND (BE); VLAAMS INTERUNIV INST BIOTECH
(BE); HUYLEBROECK DANNY FRANCOIS EVE (BE); PYNE STEFAN MARIA
CHRISTIAAN (BE)

FEATURES
source Location/Qualifiers
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/db_xref="taxon:10090" Mismatches: 40
122..1234 Indels: 1
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/codon_start=1
/protein_id="CAC07556.1"
/db_xref="GI:9998126"

ORIGIN
Alignment Scores: 3,44e-66 Length: 1312
Pred. No.: 766.50 Matches: 150
Score: 81.28% Conservative: 28
Percent Similarity: 68.49% Mismatches: 40
Best Local Similarity: 67.77% Indels: 1
Query Match: 67.77% Indels: 1

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QY 162 ValSerGlyAenGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAla 181
Db 720 TGGGTGAATGAATTTTGGCTTATGACATCCCAATTTGGAGAGCACCAGAGCAATCTCT 779
QY 182 AlaGluArgMetAenGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGluSer 201
Db 780 GCGGAACGAATAAGCAATTAATAAACTGTTCTTGGAAAAATGCAAGAGCTCCAGATTCA 839
QY 202 AlaThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 840 ACCACGGTTATATTTGCAGGAGATACAAATTTAAGAGATCAAGAAGTTTATCAAAATGT 896

RESULT 21
BD139846/c
LOCUS BD139846 1079 bp DNA linear PAT 18-SEP-2002
DEFINITION Compounds for immunotherapy and diagnosis of breast cancer and
methods for their use.
ACCESSION BD139846
VERSION BD139846.1 GI:23234791
KEYWORDS JP 2002507387-A/63.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1079)
AUTHORS Reed,S.G. and Xu,J.
TITLE Compounds for immunotherapy and diagnosis of breast cancer and
methods for their use
JOURNAL Patent: JP 2002507387-A 63 12-MAR-2002;
CORIXA CORP
OS Homo sapiens (human)
PN JP 2002507387-A/63
PF 12-MAR-2002
PR 22-DEC-1998 JP 2000526543
PR 24-DEC-1997 US 08/998253,24-DEC-1997 US 08/998255 PR
17-JUL-1998 US 09/118627,17-JUL-1998 US 09/118554 PI STEVEN
G REED,JIANGCHUN XU
PC C12N15/09,A61K38/00,A61K39/00,A61K39/39,A61K39/395,A61P35/00,
PC C07K14/47,
PC C07K16/18,C12N1/19,C12N1/21,C12N5/10,C12P21/08,C12Q1/68,G01N33/ PC
53,
PC G01N33/577,C12N15/00,A61K37/02,C12N5/00
CC Compounds for immunotherapy and diagnosis
of breast cancer and
CC their use
CC Key Location/Qualifiers
FT source 1..1079
FT Location/Qualifiers
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1..1079
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/mol_type="genomic DNA"
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Pred. No.: 711.00 Matches: 138
Score: 711.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 62.86% Gaps: 0
DB: 6

US-10-757-745-2_COPY_54_273 (1-220) x BD139846 (1-1079)

QY 83 ValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIlePro 102
Db 1077 GTGTGTTCTACTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTCCTCC 1018
QY 103 ProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGlyHisGlu 122
Db 1017 CCATATTATAGCTACCTTAAGAAGAGATCAAGTAATATTAGATATTATTACAGGTCATGAA 958
QY 123 GluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValIleLysLeuLysSerGlnGlu 142
Db 957 GAAGGATATTTCCAGCTATATAATGTTGAAGAAATCAAGAGTGAATTTAAAGCCCAAGAG 898
QY 143 IleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsnVal 162
Db 897 ATTATTCCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTGAATGTG 838
QY 163 SerGlyAenGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAla 182
Db 837 TCAGGAAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCACCAGAGGGCATGCTCGG 778

RESULT 22
AR202950/c
LOCUS AR202950 1079 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 63 from patent US 6365348.
ACCESSION AR202950
VERSION AR202950.1 GI:21499210
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1079)
AUTHORS Reed,S.G. and Xu,J.
TITLE Compounds for diagnosis of Breast cancer and methods for their use
JOURNAL Patent: US 6365348-A 63 02-APR-2002;
FEATURES
Location/Qualifiers
source 1..1079
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores: 8,58e-61 Length: 1079
Pred. No.: 711.00 Matches: 138
Score: 711.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 62.86% Gaps: 0
DB: 6

US-10-757-745-2_COPY_54_273 (1-220) x AR202950 (1-1079)

QY 83 ValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIlePro 102
Db 1077 GTGTGTTCTACTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTCCTCC 1018
QY 103 ProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGlyHisGlu 122
Db 1017 CCATATTATAGCTACCTTAAGAAGAGATCAAGTAATATTAGATATTATTACAGGTCATGAA 958
QY 123 GluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValIleLysLeuLysSerGlnGlu 142
Db 957 GAAGGATATTTCCAGCTATATAATGTTGAAGAAATCAAGAGTGAATTTAAAGCCCAAGAG 898
QY 143 IleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsnVal 162
Db 897 ATTATTCCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTGAATGTG 838
QY 163 SerGlyAenGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAla 182
Db 837 TCAGGAAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCACCAGAGGGCATGCTCGG 778

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Qy 183 GluArgMetAanGlnLeuLysMetValLeuLysLysMetGlnGlnAlaProGluSerAla 202
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Qy 203 ThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 717 ACAGTTATATTGTCAGGAGATACAAATCTAAGGGATCGAGAGGTTACCAGATGT 664
RESULT 23
LOCUS AR208051/c 1079 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 63 from patent US 6379951.
ACCESSION AR208051
VERSION AR208051.1 GI:21507966
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1079)
AUTHORS Reed,S.G. and Xu,J.
TITLE Compounds for immunotherapy of breast cancer and methods for their use
JOURNAL Patent: US 6379951-A 63 30-APR-2002;
FEATURES Location/Qualifiers
source 1..1079
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
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Pred. No.: 711.00 Matches: 138
Score: 711.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 62.86% Indels: 0
DB: 6 Gaps: 0
US-10-757-745-2_COPY_54_273 (1-220) x AR208051 (1-1079)
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Db 1077 GTGTGTTCTTACTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTCCC 1018
Qy 103 ProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGlyHisGlu 122
Db 1017 CCATATTATAGTACCTTAAAGAGAGATCAAGTAATTTATGAGATTATTACAGGTCATGAA 958
Qy 123 GluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysSerGlnGlu 142
Db 957 GAAGGATATTTCAGCTATAATGTTGAGAAATCAAGAGTGAAATTTAAAGCCAGAG 898
Qy 143 IleIleProPheProSerThrLysMetMetArgAsnLeuLysValHisValAsnVal 162
Db 897 ATTATTCCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTGAATGTG 838
Qy 163 SerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAla 182
Db 837 TCAGGAAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCACACAGAGGCATGCTGCG 778
Qy 183 GluArgMetAanGlnLeuLysMetValLeuLysLysMetGlnGlnAlaProGluSerAla 202
Db 777 GAACGAATGAATCAGTTTAAATAATGGTTTAAAGAAAATGCAAGAGGCTCCAGAGTCAGCT 718
Qy 203 ThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 717 ACAGTTATATTGTCAGGAGATACAAATCTAAGGGATCGAGAGGTTACCAGATGT 664
RESULT 24
LOCUS AX429924/c 1079 bp DNA linear PAT 21-JUN-2002
DEFINITION Sequence 63 from Patent WO0198339.
ACCESSION AX429924
VERSION AX429924.1 GI:21541088

KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1236)
AUTHORS Reed,S.G., Xu,J., Dillon,D.C., Retter,M.W. and Harlocker,S.L.
TITLE Compositions and methods for the therapy and diagnosis of breast cancer
JOURNAL Patent: WO 0198339-A 63 27-DEC-2001;
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores: 8.58e-61 Length: 1079
Pred. No.: 711.00 Matches: 138
Score: 711.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 62.86% Indels: 0
DB: 6 Gaps: 0
US-10-757-745-2_COPY_54_273 (1-220) x AX429924 (1-1079)
Qy 83 ValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIlePro 102
Db 1077 GTGTGTTCTTACTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTCCC 1018
Qy 103 ProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGlyHisGlu 122
Db 1017 CCATATTATAGTACCTTAAAGAGAGATCAAGTAATTTATGAGATTATTACAGGTCATGAA 958
Qy 123 GluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGlnGlu 142
Db 957 GAAGGATATTTCAGCTATAATGTTGAGAAATCAAGAGTGAAATTTAAAGCCAGAG 898
Qy 143 IleIleProPheProSerThrLysMetMetArgAsnLeuLysValHisValAsnVal 162
Db 897 ATTATTCCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTGAATGTG 838
Qy 163 SerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAla 182
Db 837 TCAGGAAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCACACAGAGGCATGCTGCG 778
Qy 183 GluArgMetAanGlnLeuLysMetValLeuLysLysMetGlnGlnAlaProGluSerAla 202
Db 777 GAACGAATGAATCAGTTTAAATAATGGTTTAAAGAAAATGCAAGAGGCTCCAGAGTCAGCT 718
Qy 203 ThrValIlePheAlaGlyAspThrAsnLeuArgAspArgGluValThrArgCys 220
Db 717 ACAGTTATATTGTCAGGAGATACAAATCTAAGGGATCGAGAGGTTACCAGATGT 664
RESULT 25
LOCUS CR761829 1236 bp mRNA linear VRT 15-SEP-2004
DEFINITION Xenopus tropicalis finished cDNA, clone TGas102g02.
ACCESSION CR761829
VERSION CR761829.1 GI:51967738
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1236)
AUTHORS Anaya,E., Ashurst,J.L., Bonfield,J.K., Croning,M.D.R., Davies,R.M., Francis,M.D., Garrett,N., Gilchrist,M.J., Graham,D.V., McLaren,S.R., Papalopulu,N., Rogers,J., Smith,J.C., Taylor,R.G.,

Voigt, J. and Zorn, A.M.
Direct Submission
Submitted (15-SEP-2004) Sanger Institute, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: tropesanger.ac.uk
Sanger Xenopus tropicalis EST/cDNA project.
This sequence is from a Xenopus Gene Collection (XGC) library, from
a library constructed by Aaron M. Zorn. cDNA was prepared from RNA
extracted from gastrula embryos. EcoRI-NotI cut cDNA was then
ligated into pCS107 with EcoRI at the 5' end and NotI at the 3'
end.
Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli XL1-blue.
Location/Qualifiers
1. 1236
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/clone_lib="XGC-gastrula"
/dev_stage="gastrula (stage 10.5-13 mixed)"

TITLE
JOURNAL
COMMENT

FEATURES
source
1. 1236
Location/Qualifiers

ORIGIN
Alignment Scores:
Pred. No.: 1236
Score: 708.00 Length: 1236
Percent Similarity: 75.64% Matches: 140
Best Local Similarity: 59.83% Conservative: 37
Query Match: 62.60% Mismatches: 39
Indels: 18
Gaps: 3

US-10-757-745-2_COPY_54_273 (1-220) x CR761829 (1-1236)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
DB 205 ATGGAAGGGCGGATTAATCTTCTTCTGAGCCTGGGTGGAGTCAGCCTTGC AAAACAAA 264
QY 21 ArgProGluThrIleSerGluPro-----Lys 29
DB 265 GCTGAGCTGATATAGCAGATCTTTAAAGCAAGAGACATATGCTTGGAACTGCTCCGAT 324
QY 30 ThrTyrValAspLeuThrAsnGlu-----ThrThrAspSerThrThrSer 45
DB 325 TCATGATATTGACCTCAGCGCGATGACTTAGTGGTTACCAATCAGAACTACCACTAC 384
QY 46 LysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThr 65
DB 385 AAT-----TCCTCCACTGTGAAGCAAGAGATGAGAGCCATTTTCTCTTCTGACT 435
QY 66 TrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArgGlyValCysSer 85
DB 436 TGAATATAGATGGCTTGATGAAATCAATGTCGAGAAAGGGCTCGTGGTGTGTGTTCC 495
QY 86 TyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIleProTyrTyr 105
DB 496 TATTGGCCCTTACAGTCCAGATGTAGTATTCTTACAGAGGTTATTCCACCATAT 555
QY 106 SerTyrLeuLysLysArgSerSerLeuIleIleThrGlyHisGluGluGlyTyr 125
DB 556 GAGTACCTCAAGAAGAGAGCTGTGACGTACACAAATTTATTACAGGTAATGAGGATGAATAC 615
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DB 616 TTCCTGCTATGATGCTGAAAGAGACAGGTAAGTTAATAGCCAGAAATTTGACCA 675
QY 146 PheProSerThrLysMetMetArgAsnLeuLeuLysValHisValAsnValSerGlyAsn 165
DB 676 TACCAATCCACGGTGATGAGAAATTTGCTTTGAGCAAAATGTAATCTCTGGCAAC 735
QY 166 GluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAlaGluArgMet 185
DB 736 AGTATATGCTTAATGACTTCTCATCTAGAGAGACAAAAGATCATTTCAAAGGAGCGATTA 795
QY 186 AsnGlnLeuLysMetValLeuLysLysMetGlnGluAlaProGluSerAlaThrValIle 205

Db 796 AAGCAGCTGGACATTTGCTATAAAAGATGATGCTCCCTTTAGCAACTGTATA 855
QY 206 PheAlaGlyAspThrAsnLeuArgAspArgGluValThrArg 219
DB 856 TTTGGAGGGGATACAAACCTGCGAGATCAGGAGGTTGCTAAA 897
RESULT 26
LOCUS CQ726600 858 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 12534 from Patent WO02068579.
ACCESSION CQ726600
VERSION CQ726600.1 GI:42290170
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
human exons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 12534 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source
1. 858
Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match: 60.26% Indels: 77
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US-10-757-745-2_COPY_54_273 (1-220) x CQ726600 (1-858)

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DB 405 ----- 405
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VERSION BD076937.1 GI:22622540
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 483)
Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
5' EST of secretory protein expressed in prostate
Patent: JP 2001512013-A 184 21-AUG-2001;
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PN JP 2001512013-A/184
PD 21-AUG-2001
PF 31-JUL-1998 JP 2000505291
PR 01-AUG-1997 US 08/905144
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO PI
LACROIX
PC C12N15/09,C07K14/47,C12P21/02,C12Q1/02,C12Q1/68,C12N15/00 CC
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Query Match: 49.43% Indels: 0
DB: 6 Gaps: 0
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Db 160 ATGGAAGGGCTCTGAACTCTTCTGAGCCTCCGGTGGAGGAGCGCTTGGAAACGC 219
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
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DEFINITION Human DNA sequence from clone RP11-948M1 on chromosome 6, complete
sequence.
ACCESSION CR942205
VERSION CR942205.4 GI:62989869
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 176819)
Almeida,J.
Direct Submission
Submitted (29-APR-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgehire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 30, 2005 this sequence version replaced gi:629551221.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk

Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/projects/C.elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at

http://www.sanger.ac.uk/HGP/Chr6
RP11-948M1 is from the library RP11-11.4 constructed by the group of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm

VECTOR: pBACE3.6.

FEATURES

source

Location/Qualifiers

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Query Match: 31.39% Indels: 224
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US-10-757-745-2_COPY_54_273 (1-220) x CR942205 (1-176819)

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Job time : 5953.11 secs

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GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 15:32:30 ; Search time 179.639 Seconds
(without alignments)
317.043 Million cell updates/sec

Title: US-10-757-745-2_COPY_54_236

Perfect score: 945

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Ygapop 10.0 , Ygapext 0.5
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Searched: 3289935 seqs, 155610033 residues

Total number of hits satisfying chosen parameters: 6579870

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	72.5	7.7	1503	6	US-10-821-234-606
6	72.5	7.7	2238	6	US-10-793-626-1499
7	72.5	7.7	3207	6	US-10-793-626-3413
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71	7.5	720	6	US-10-793-626-3009	Sequence 3009, Ap
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c 87	64	6.8	3175	6	US-10-750-185-48090	Sequence 48090, A	c 160	61.5	6.5	1062	6	US-10-793-626-1187	Sequence 1187, Ap
c 88	64	6.8	5527	7	US-11-192-987-3	Sequence 3, Appl	161	61.5	6.5	1062	6	US-10-750-185-44168	Sequence 44168, A
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c 91	63.5	6.7	1542	6	US-10-467-657-695	Sequence 695, App	c 164	61.5	6.5	1486	7	US-11-055-637-79	Sequence 79, Appl
c 92	63.5	6.7	1644	6	US-10-750-185-59804	Sequence 59804, A	c 165	61.5	6.5	1513	7	US-11-055-637-79	Sequence 79, Appl
c 93	63.5	6.7	1674	6	US-10-467-657-693	Sequence 693, App	c 166	61.5	6.5	1618	6	US-10-750-185-59804	Sequence 59804, A
c 94	63.5	6.7	1709	6	US-10-750-185-61369	Sequence 61369, A	c 167	61.5	6.5	1643	6	US-10-750-185-63649	Sequence 63649, A
c 95	63.5	6.7	2428	6	US-10-276-233A-23	Sequence 23, Appl	c 168	61.5	6.5	2062	6	US-10-750-185-62457	Sequence 62457, A
c 96	63.5	6.7	3094	6	US-10-750-185-62421	Sequence 62421, A	c 169	61.5	6.5	2215	7	US-11-147-047-22	Sequence 22, Appl
c 97	63.5	6.7	212805	7	US-11-112-908-19	Sequence 19, Appl	c 170	61.5	6.5	2381	6	US-10-750-185-43961	Sequence 43961, A
c 98	63	6.7	829	6	US-10-750-185-51266	Sequence 51266, A	c 171	61.5	6.5	2730	6	US-10-750-185-42545	Sequence 42545, A
c 99	63	6.7	941	6	US-10-750-185-61368	Sequence 61368, A	c 172	61.5	6.5	3119	6	US-10-750-185-34459	Sequence 34459, A
c 100	63	6.7	1095	6	US-10-750-185-58034	Sequence 58034, A	c 173	61.5	6.5	3213	7	US-11-147-047-23	Sequence 23, Appl
c 101	63	6.7	1233	6	US-10-467-657-4443	Sequence 4443, Ap	c 174	61.5	6.5	3481	6	US-10-750-185-43752	Sequence 43752, A
c 102	63	6.7	1422	6	US-10-750-185-47601	Sequence 47601, A	c 175	61.5	6.5	3501	6	US-10-793-626-3614	Sequence 3614, Ap
c 103	63	6.7	2547	6	US-10-750-185-30867	Sequence 30867, A	c 176	61.5	6.5	4248	6	US-10-793-626-3885	Sequence 3885, Ap
c 104	63	6.7	2941	6	US-10-750-185-33540	Sequence 33540, A	c 177	61.5	6.5	4417	6	US-10-750-185-49683	Sequence 49683, A
c 105	63	6.7	3062	6	US-10-750-185-30274	Sequence 30274, A	c 178	61.5	6.5	5134	7	US-11-060-005-1	Sequence 1, Appl
c 106	63	6.7	3232	6	US-10-750-185-62480	Sequence 62480, A	c 179	61.5	6.5	8948	6	US-10-623-155-119	Sequence 119, App
c 107	63	6.7	3413	6	US-10-909-125-941	Sequence 941, App	c 180	61	6.5	1042	6	US-10-750-185-29649	Sequence 29649, A
c 108	63	6.7	10373	6	US-10-821-234-64	Sequence 64, Appl	c 181	61	6.5	1178	6	US-10-750-185-29213	Sequence 29213, A
c 109	63	6.7	14911	7	US-11-112-908-63	Sequence 63, Appl	c 182	61	6.5	1190	6	US-10-750-185-28873	Sequence 28873, A
c 110	63	6.7	157230	7	US-11-112-908-64	Sequence 64, Appl	c 183	61	6.5	1435	6	US-10-750-185-29994	Sequence 29994, A
c 111	63	6.7	168656	7	US-11-112-908-59	Sequence 59, Appl	c 184	61	6.5	1530	6	US-10-750-185-53704	Sequence 53704, A
c 112	63	6.7	170285	7	US-11-112-908-58	Sequence 58, Appl	c 185	61	6.5	1616	6	US-10-750-185-45154	Sequence 45154, A
c 113	63	6.7	170508	7	US-11-112-908-62	Sequence 62, Appl	c 186	61	6.5	1750	6	US-10-750-185-58125	Sequence 58125, A
c 114	63	6.7	197781	7	US-11-112-908-34	Sequence 34, Appl	c 187	61	6.5	1801	6	US-10-750-185-51573	Sequence 51573, A
c 115	62.5	6.6	867	6	US-10-750-185-62841	Sequence 62841, A	c 188	61	6.5	1962	6	US-10-821-234-434	Sequence 434, App
c 116	62.5	6.6	1115	6	US-10-750-185-64842	Sequence 64842, A	c 189	61	6.5	2124	6	US-10-750-185-31641	Sequence 31641, A
c 117	62.5	6.6	1352	6	US-10-750-185-51740	Sequence 51740, A	c 190	61	6.5	2152	9	US-11-076-187-1	Sequence 1, Appl
c 118	62.5	6.6	1795	6	US-10-750-185-27375	Sequence 27375, A	c 191	61	6.5	2243	6	US-10-750-185-41972	Sequence 41972, A
c 119	62.5	6.6	2263	6	US-10-750-185-43360	Sequence 43360, A	c 192	61	6.5	2301	6	US-10-793-626-2577	Sequence 2577, Ap
c 120	62.5	6.6	2361	6	US-10-467-962B-102	Sequence 102, App	c 193	61	6.5	3214	6	US-10-750-185-44076	Sequence 44076, A
c 121	62.5	6.6	3055	6	US-10-793-626-4075	Sequence 4075, Ap	c 194	61	6.5	3370	6	US-10-793-626-3722	Sequence 3722, Ap
c 122	62.5	6.6	3058	6	US-10-750-185-48442	Sequence 48442, A	c 195	61	6.5	3973	6	US-10-750-185-34094	Sequence 34094, A
c 123	62.5	6.6	3289	6	US-10-750-185-31224	Sequence 31224, A	c 196	61	6.5	4243	6	US-10-821-234-59	Sequence 59, Appl
c 124	62.5	6.6	4053	6	US-10-131-826A-351	Sequence 351, App	c 197	61	6.5	197781	7	US-11-112-908-34	Sequence 34, Appl
c 125	62.5	6.6	6160	7	US-11-060-005-3	Sequence 3, Appl	c 198	61	6.5	217623	7	US-11-112-908-33	Sequence 33, Appl
c 126	62.5	6.6	161994	7	US-11-112-908-57	Sequence 57, Appl	c 199	60.5	6.4	597	6	US-10-793-626-2571	Sequence 2571, Ap
c 127	62.5	6.6	207908	7	US-11-112-908-21	Sequence 21, Appl	c 200	60.5	6.4	693	7	US-11-055-822-537	Sequence 537, App
c 128	62.5	6.6	319608	7	US-11-145-703-1	Sequence 1, Appl	c 201	60.5	6.4	714	7	US-11-055-822-907	Sequence 907, App
c 129	62	6.6	678	6	US-10-209-208-2	Sequence 2, Appl	c 202	60.5	6.4	990	6	US-10-793-626-1459	Sequence 1459, Ap
c 130	62	6.6	726	6	US-10-793-626-3147	Sequence 3147, Ap	c 203	60.5	6.4	1255	6	US-10-750-185-27289	Sequence 27289, A
c 131	62	6.6	744	6	US-10-131-826A-283	Sequence 283, App	c 204	60.5	6.4	1311	6	US-10-750-185-56697	Sequence 56697, A
c 132	62	6.6	855	6	US-10-750-185-50099	Sequence 50099, A	c 205	60.5	6.4	1343	6	US-10-750-185-51743	Sequence 51743, A
c 133	62	6.6	930	6	US-10-793-626-1607	Sequence 1607, Ap	c 206	60.5	6.4	1752	6	US-10-750-185-37399	Sequence 37399, A
c 134	62	6.6	956	7	US-11-055-822-799	Sequence 799, App	c 207	60.5	6.4	1776	6	US-10-750-185-27552	Sequence 27552, A
c 135	62	6.6	956	7	US-11-055-822-845	Sequence 845, App	c 208	60.5	6.4	1790	6	US-10-750-185-57305	Sequence 57305, A
c 136	62	6.6	963	7	US-11-055-822-843	Sequence 843, App	c 209	60.5	6.4	1935	6	US-10-750-185-50882	Sequence 50882, A
c 137	62	6.6	1203	6	US-10-793-626-1055	Sequence 1055, Ap	c 210	60.5	6.4	2052	6	US-10-821-234-462	Sequence 462, App
c 138	62	6.6	1481	6	US-10-750-185-32285	Sequence 32285, A	c 211	60.5	6.4	2407	6	US-10-485-517-42	Sequence 42, Appl
c 139	62	6.6	1539	6	US-10-750-185-61772	Sequence 61772, A	c 212	60.5	6.4	3098	6	US-10-750-185-46414	Sequence 46414, A
c 140	62	6.6	1887	6	US-10-793-626-2843	Sequence 2843, Ap	c 213	60.5	6.4	3119	6	US-10-689-742-45	Sequence 45, Appl
c 141	62	6.6	2031	7	US-11-135-855-5	Sequence 5, Appl	c 214	60.5	6.4	3159	6	US-10-793-626-4112	Sequence 4112, Ap
c 142	62	6.6	2048	6	US-10-750-185-54989	Sequence 54989, A	c 215	60.5	6.4	3775	6	US-10-793-626-3832	Sequence 3832, Ap
c 143	62	6.6	2154	7	US-11-135-855-6	Sequence 6, Appl	c 216	60.5	6.4	5735	6	US-10-821-234-155	Sequence 155, App
c 144	62	6.6	3155	6	US-10-793-626-3424	Sequence 3424, Ap	c 217	60.5	6.4	207908	7	US-11-102-978-3	Sequence 3, Appl
c 145	62	6.6	3155	6	US-10-793-626-3881	Sequence 3881, Ap	c 218	60.5	6.4	340000	7	US-11-102-978-3	Sequence 3, Appl
c 146	62	6.6	3194	6	US-10-793-626-4136	Sequence 4136, Ap	c 219	60	6.3	442	6	US-10-821-234-373	Sequence 373, App
c 147	62	6.6	3217	6	US-10-793-626-3915	Sequence 3915, Ap	c 220	60	6.3	471	6	US-10-793-626-1005	Sequence 1005, Ap
c 148	62	6.6	3310	6	US-10-793-626-4143	Sequence 4143, Ap	c 221	60	6.3	600	6	US-10-750-185-466	Sequence 466, App
c 149	62	6.6	3349	6	US-10-793-626-4175	Sequence 4175, Ap	c 222	60	6.3	600	6	US-10-750-185-21850	Sequence 21850, A
c 150	62	6.6	3462	6	US-10-793-626-4440	Sequence 4440, Ap	c 223	60	6.3	920	6	US-10-750-185-25054	Sequence 25054, A
c 151	62	6.6	3791	6	US-10-658-986-1	Sequence 1, Appl	c 224	60	6.3	948	6	US-10-750-185-29007	Sequence 29007, A
c 152	62	6.6	4055	6	US-10-793-626-3357	Sequence 3357, Ap	c 225	60	6.3	987	6	US-10-467-657-2239	Sequence 2239, Ap
c 153	62	6.6	4788	6	US-10-658-986-3	Sequence 3, Appl	c 226	60	6.3	1085	6	US-10-793-626-4463	Sequence 4463, Ap
c 154	62	6.6	4982	6	US-10-276-233A-17	Sequence 17, Appl	c 227	60	6.3	1146	6	US-10-821-234-490	Sequence 490, App

228	60	6.3	1266	6	US-10-750-185-58394	Sequence 58394, A	C 301	59	6.2	600	6	US-10-750-185-666	Sequence 666, App
229	60	6.3	1279	6	US-10-750-185-43208	Sequence 43208, A	C 302	59	6.2	600	6	US-10-750-185-1622	Sequence 1622, App
230	60	6.3	1287	6	US-10-750-185-25544	Sequence 25544, A	C 303	59	6.2	600	6	US-10-750-185-19642	Sequence 19642, A
231	60	6.3	1489	6	US-10-750-185-52718	Sequence 52718, A	C 304	59	6.2	696	6	US-10-750-185-46370	Sequence 46370, A
232	60	6.3	1601	6	US-10-750-185-31222	Sequence 31222, A	C 305	59	6.2	856	6	US-10-750-185-28518	Sequence 28518, A
233	60	6.3	1639	7	US-11-099-691-18	Sequence 18, Appl	C 306	59	6.2	867	6	US-10-750-185-37322	Sequence 37322, A
234	60	6.3	1664	6	US-10-750-185-60539	Sequence 60539, A	C 307	59	6.2	944	6	US-10-750-185-40727	Sequence 40727, A
235	60	6.3	1859	6	US-10-750-185-25504	Sequence 25504, A	C 308	59	6.2	1015	6	US-10-750-185-48563	Sequence 48563, A
236	60	6.3	1882	6	US-10-750-185-53598	Sequence 53598, A	C 309	59	6.2	1065	6	US-10-750-185-40891	Sequence 40891, A
237	60	6.3	1888	6	US-10-750-185-59957	Sequence 59957, A	C 310	59	6.2	1090	6	US-10-750-185-42756	Sequence 42756, A
238	60	6.3	1888	6	US-10-750-185-59957	Sequence 59957, A	C 311	59	6.2	1115	6	US-10-750-185-62220	Sequence 62220, A
239	60	6.3	2097	6	US-10-750-185-29804	Sequence 29804, A	C 312	59	6.2	1167	6	US-10-750-185-26393	Sequence 26393, A
240	60	6.3	2397	6	US-10-750-185-42569	Sequence 42569, A	C 313	59	6.2	1260	6	US-10-750-185-28376	Sequence 28376, A
241	60	6.3	2436	6	US-10-793-626-4427	Sequence 4427, App	C 314	59	6.2	1304	6	US-10-750-185-28067	Sequence 28067, A
242	60	6.3	2538	6	US-10-793-626-4424	Sequence 4424, App	C 315	59	6.2	1337	6	US-10-750-185-56955	Sequence 56955, A
243	60	6.3	2634	7	US-11-147-047-20	Sequence 20, Appl	C 316	59	6.2	1344	6	US-10-750-185-32460	Sequence 32460, A
244	60	6.3	2634	6	US-10-750-185-26835	Sequence 26835, A	C 317	59	6.2	1352	6	US-10-750-185-32096	Sequence 32096, A
245	60	6.3	2857	6	US-10-793-626-4004	Sequence 4004, App	C 318	59	6.2	1387	6	US-10-750-185-34240	Sequence 34240, A
246	60	6.3	3008	6	US-10-793-626-4460	Sequence 4460, App	C 319	59	6.2	1485	6	US-10-750-185-54962	Sequence 54962, A
247	60	6.3	3169	6	US-10-793-626-3356	Sequence 3356, App	C 320	59	6.2	1573	6	US-10-689-742-187	Sequence 187, App
248	60	6.3	3171	6	US-10-793-626-3537	Sequence 3537, App	C 321	59	6.2	1610	6	US-10-750-185-33166	Sequence 33166, A
249	60	6.3	3196	6	US-10-793-626-3454	Sequence 3454, App	C 322	59	6.2	1689	6	US-10-750-185-58247	Sequence 58247, A
250	60	6.3	3253	6	US-10-793-626-3887	Sequence 3887, App	C 323	59	6.2	1767	6	US-10-750-185-28237	Sequence 28237, A
251	60	6.3	3285	6	US-10-793-626-3955	Sequence 3955, App	C 324	59	6.2	1767	6	US-10-750-185-48428	Sequence 48428, A
252	60	6.3	3308	6	US-10-793-626-3905	Sequence 3905, App	C 325	59	6.2	1965	7	US-11-131-213-51	Sequence 51, Appl
253	60	6.3	3328	6	US-10-793-626-4195	Sequence 4195, App	C 326	59	6.2	1974	6	US-10-750-185-27854	Sequence 27854, A
254	60	6.3	3427	6	US-10-793-626-3884	Sequence 3884, App	C 327	59	6.2	2068	6	US-10-750-185-33695	Sequence 33695, A
255	60	6.3	3657	6	US-10-793-626-4187	Sequence 4187, App	C 328	59	6.2	2175	6	US-10-821-234-654	Sequence 654, App
256	60	6.3	3821	6	US-10-793-626-3967	Sequence 3967, App	C 329	59	6.2	2465	6	US-10-750-185-35775	Sequence 35775, A
257	60	6.3	4542	6	US-10-750-185-44606	Sequence 44606, App	C 330	59	6.2	2507	6	US-10-750-185-58317	Sequence 58317, A
258	60	6.3	4775	6	US-10-750-185-29408	Sequence 29408, A	C 331	59	6.2	2509	6	US-10-750-185-40536	Sequence 40536, A
259	60	6.3	149419	7	US-11-112-908-49	Sequence 49, Appl	C 332	59	6.2	2632	6	US-10-510-386-19	Sequence 19, Appl
260	60	6.3	166111	7	US-11-112-908-47	Sequence 47, Appl	C 333	59	6.2	2785	6	US-10-510-386-37	Sequence 37, Appl
261	59.5	6.3	588	6	US-10-750-185-38718	Sequence 38718, A	C 334	59	6.2	2908	6	US-10-793-626-4359	Sequence 4359, App
262	59.5	6.3	600	6	US-10-750-185-340	Sequence 340, App	C 335	59	6.2	3217	6	US-10-793-626-4051	Sequence 4051, App
263	59.5	6.3	603	6	US-10-467-657-5345	Sequence 5345, App	C 336	59	6.2	3415	6	US-10-750-185-31178	Sequence 31178, A
264	59.5	6.3	942	6	US-10-750-185-37702	Sequence 37702, A	C 337	59	6.2	3558	6	US-10-750-185-41015	Sequence 41015, A
265	59.5	6.3	943	6	US-10-750-185-59939	Sequence 59939, A	C 338	59	6.2	3623	6	US-10-750-185-60573	Sequence 60573, A
266	59.5	6.3	1075	6	US-10-750-185-26007	Sequence 26007, A	C 339	59	6.2	3848	6	US-10-821-234-258	Sequence 258, App
267	59.5	6.3	1100	6	US-10-742-634-1	Sequence 1, Appl	C 340	59	6.2	4243	6	US-10-821-234-59	Sequence 59, Appl
268	59.5	6.3	1121	6	US-10-131-826A-23	Sequence 23, Appl	C 341	59	6.2	4339	6	US-10-909-125-801	Sequence 801, App
269	59.5	6.3	1331	6	US-10-750-185-35764	Sequence 35764, A	C 342	59	6.2	4399	6	US-10-750-185-52104	Sequence 52104, A
270	59.5	6.3	1355	6	US-10-750-185-49597	Sequence 49597, A	C 343	59	6.2	5213	7	US-11-102-978-1	Sequence 1, Appl
271	59.5	6.3	1482	6	US-10-750-185-62857	Sequence 62857, A	C 344	59	6.2	5356	6	US-10-750-185-35251	Sequence 35251, A
272	59.5	6.3	1559	6	US-10-750-185-45828	Sequence 45828, A	C 345	59	6.2	5371	6	US-10-750-185-44798	Sequence 44798, A
273	59.5	6.3	1611	6	US-10-750-185-25369	Sequence 25369, A	C 346	59	6.2	11667	6	US-10-508-263-122	Sequence 122, App
274	59.5	6.3	1640	6	US-10-750-185-53147	Sequence 53147, A	C 347	59	6.2	11667	6	US-10-508-263-122	Sequence 122, App
275	59.5	6.3	1682	6	US-10-750-185-24947	Sequence 24947, A	C 348	59	6.2	55763	6	US-10-972-766-1	Sequence 1, Appl
276	59.5	6.3	1890	6	US-10-750-185-63942	Sequence 63942, A	C 349	58.5	6.2	675	6	US-10-750-185-59484	Sequence 59484, A
277	59.5	6.3	1801	6	US-10-750-185-31119	Sequence 31119, A	C 350	58.5	6.2	1032	6	US-10-750-185-37102	Sequence 37102, A
278	59.5	6.3	1812	6	US-10-750-185-32941	Sequence 32941, A	C 351	58.5	6.2	1066	6	US-10-750-185-52943	Sequence 52943, A
279	59.5	6.3	1856	9	US-11-082-389-435	Sequence 435, App	C 352	58.5	6.2	1173	6	US-10-750-185-62524	Sequence 62524, A
280	59.5	6.3	1907	6	US-10-750-185-59627	Sequence 59627, A	C 353	58.5	6.2	1173	7	US-11-058-727-118	Sequence 118, App
281	59.5	6.3	1915	6	US-10-750-185-34691	Sequence 34691, A	C 354	58.5	6.2	1173	7	US-11-058-727-120	Sequence 120, App
282	59.5	6.3	2187	6	US-10-750-185-31689	Sequence 31689, A	C 355	58.5	6.2	1173	7	US-11-058-727-122	Sequence 122, App
283	59.5	6.3	2552	6	US-10-750-185-26492	Sequence 26492, A	C 356	58.5	6.2	1173	7	US-11-08-389-118	Sequence 118, App
284	59.5	6.3	2868	6	US-10-431-826A-119	Sequence 119, App	C 357	58.5	6.2	1173	7	US-11-108-389-120	Sequence 120, App
285	59.5	6.3	3059	7	US-11-108-172-1097	Sequence 1097, App	C 358	58.5	6.2	1173	7	US-11-108-389-122	Sequence 122, App
286	59.5	6.3	3459	6	US-10-750-185-25437	Sequence 25437, A	C 359	58.5	6.2	1191	6	US-10-467-657-3431	Sequence 3431, App
287	59.5	6.3	3504	6	US-10-793-626-3859	Sequence 3859, App	C 360	58.5	6.2	1248	6	US-10-750-185-62726	Sequence 62726, A
288	59.5	6.3	3506	6	US-10-793-626-3423	Sequence 3423, App	C 361	58.5	6.2	1252	6	US-10-750-185-60663	Sequence 60663, A
289	59.5	6.3	3511	6	US-10-793-626-3930	Sequence 3930, App	C 362	58.5	6.2	1272	6	US-10-750-185-53234	Sequence 53234, A
290	59.5	6.3	3845	6	US-10-750-185-61154	Sequence 61154, A	C 363	58.5	6.2	1306	6	US-10-750-185-53379	Sequence 53379, A
291	59.5	6.3	4765	6	US-10-821-234-110	Sequence 110, App	C 364	58.5	6.2	1314	6	US-10-750-185-61321	Sequence 61321, A
292	59.5	6.3	4884	6	US-10-821-234-431	Sequence 431, App	C 365	58.5	6.2	1399	6	US-10-750-185-36195	Sequence 36195, A
293	59.5	6.3	5700	6	US-10-513-786-7	Sequence 7, Appl	C 366	58.5	6.2	1500	6	US-10-467-657-47	Sequence 47, Appl
294	59.5	6.3	5700	6	US-10-513-786-9	Sequence 9, Appl	C 367	58.5	6.2	1511	6	US-10-750-185-43983	Sequence 43983, A
295	59.5	6.3	5777	6	US-10-821-234-51	Sequence 51, Appl	C 368	58.5	6.2	1617	6	US-10-467-657-7735	Sequence 7735, App
296	59.5	6.3	11115	6	US-10-513-786-6	Sequence 6, Appl	C 369	58.5	6.2	1624	6	US-10-750-185-50876	Sequence 50876, A
297	59.5	6.3	11115	6	US-10-513-786-8	Sequence 8, Appl	C 370	58.5	6.2	1658	6	US-10-750-185-62507	Sequence 62507, A
298	59.5	6.3	150450	7	US-11-112-908-54	Sequence 54, Appl	C 371	58.5	6.2	1660	6	US-10-750-185-61680	Sequence 61680, A
299	59.5	6.3	207600	7	US-11-112-908-31	Sequence 31, Appl	C 372	58.5	6.2	1665	6	US-10-750-185-36578	Sequence 36578, A
300	59.5	6.3	340000	7	US-11-102-978-3	Sequence 3, Appl	C 373	58.5	6.2	1697	6	US-10-750-185-45405	Sequence 45405, A

C 374	58.5	6.2	1767	6	US-10-750-185-62400	Sequence 62400, A	C 447	57.5	6.1	1659	6	US-10-750-185-50453	Sequence 50453, A
C 375	58.5	6.2	1787	6	US-10-750-185-38021	Sequence 38021, A	C 448	57.5	6.1	1722	6	US-10-750-185-47241	Sequence 47241, A
C 376	58.5	6.2	1913	6	US-10-750-185-57835	Sequence 57835, A	C 449	57.5	6.1	1826	6	US-10-750-185-34783	Sequence 34783, A
C 377	58.5	6.2	2398	6	US-10-750-185-27774	Sequence 27774, A	C 450	57.5	6.1	1908	6	US-10-750-185-31257	Sequence 31257, A
C 378	58.5	6.2	2691	7	US-11-108-172-121	Sequence 121, Appl	C 451	57.5	6.1	1941	6	US-10-750-185-44600	Sequence 44600, A
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C 381	58.5	6.2	3003	6	US-10-793-626-4167	Sequence 4167, Ap	C 454	57.5	6.1	2126	6	US-10-750-185-30680	Sequence 30680, A
C 382	58.5	6.2	3493	6	US-10-750-185-56579	Sequence 56579, A	C 455	57.5	6.1	2212	6	US-10-750-185-27595	Sequence 27595, A
C 383	58.5	6.2	4113	6	US-10-624-932-21	Sequence 21, Appl1	C 456	57.5	6.1	2601	7	US-11-147-047-6	Sequence 6, Appl1
C 384	58.5	6.2	4136	6	US-10-793-626-3686	Sequence 3686, Ap	C 457	57.5	6.1	2993	6	US-10-645-441-10	Sequence 10, Appl1
C 385	58.5	6.2	4420	6	US-10-131-826A-411	Sequence 411, Appl	C 458	57.5	6.1	3073	6	US-10-750-185-25750	Sequence 25750, A
C 386	58.5	6.2	5048	6	US-10-750-185-40762	Sequence 40762, A	C 459	57.5	6.1	3073	6	US-10-793-626-3606	Sequence 3606, Ap
C 387	58.5	6.2	5306	6	US-10-750-185-34792	Sequence 34792, A	C 460	57.5	6.1	3132	6	US-10-793-626-3455	Sequence 3455, Ap
C 388	58.5	6.2	8096	6	US-10-909-125-792	Sequence 792, App	C 461	57.5	6.1	3138	6	US-10-750-185-45175	Sequence 45175, A
C 389	58	6.1	574	6	US-10-750-185-4140	Sequence 4140, Ap	C 462	57.5	6.1	3247	6	US-10-793-626-3771	Sequence 3771, Ap
C 390	58	6.1	660	6	US-10-793-626-2525	Sequence 2525, Ap	C 463	57.5	6.1	3339	6	US-10-750-185-52226	Sequence 52226, A
C 391	58	6.1	814	6	US-10-750-185-40537	Sequence 40537, A	C 464	57.5	6.1	3465	6	US-10-793-626-1779	Sequence 1779, Ap
C 392	58	6.1	920	6	US-10-750-185-57097	Sequence 57097, A	C 465	57.5	6.1	3515	6	US-10-750-185-60777	Sequence 60777, A
C 393	58	6.1	921	6	US-10-467-657-7005	Sequence 7005, Ap	C 466	57.5	6.1	3915	6	US-10-750-185-50975	Sequence 50975, A
C 394	58	6.1	1102	6	US-10-750-185-63037	Sequence 63037, A	C 467	57.5	6.1	4018	6	US-10-750-185-51049	Sequence 51049, A
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C 396	58	6.1	1179	6	US-10-793-626-193	Sequence 193, Appl	C 469	57.5	6.1	5253	6	US-10-821-234-293	Sequence 293, App
C 397	58	6.1	1279	6	US-10-750-185-60775	Sequence 60775, A	C 470	57.5	6.1	13672	7	US-11-055-035-2	Sequence 2, Appl1
C 398	58	6.1	1299	6	US-10-750-185-57299	Sequence 57299, A	C 471	57.5	6.1	135594	6	US-10-658-986-5	Sequence 5, Appl1
C 399	58	6.1	1486	6	US-10-750-185-58238	Sequence 58238, A	C 472	57.5	6.1	191343	7	US-11-112-508-53	Sequence 53, Appl1
C 400	58	6.1	1617	6	US-10-750-185-44020	Sequence 44020, A	C 473	57	6.0	413	7	US-11-108-172-606	Sequence 606, App
C 401	58	6.1	1618	6	US-10-750-185-61770	Sequence 61770, A	C 474	57	6.0	600	6	US-10-750-185-1926	Sequence 1926, Ap
C 402	58	6.1	1637	6	US-10-750-185-41849	Sequence 41849, A	C 475	57	6.0	600	6	US-10-750-185-30813	Sequence 30813, Ap
C 403	58	6.1	1871	6	US-10-750-185-49599	Sequence 49599, A	C 476	57	6.0	782	6	US-10-750-185-40813	Sequence 40813, Ap
C 404	58	6.1	1896	6	US-10-750-185-31784	Sequence 31784, A	C 477	57	6.0	796	6	US-10-750-185-27629	Sequence 27629, A
C 405	58	6.1	1934	6	US-10-507-106-3	Sequence 3, Appl1	C 478	57	6.0	889	6	US-10-750-185-53175	Sequence 53175, A
C 406	58	6.1	1940	6	US-10-750-185-61854	Sequence 61854, A	C 479	57	6.0	918	7	US-11-074-176-289	Sequence 289, App
C 407	58	6.1	1960	6	US-10-750-185-36777	Sequence 36777, A	C 480	57	6.0	947	6	US-10-750-185-55038	Sequence 55038, A
C 408	58	6.1	2200	6	US-10-510-386-149	Sequence 149, App	C 481	57	6.0	986	6	US-10-750-185-50350	Sequence 50350, A
C 409	58	6.1	2443	6	US-10-131-826A-57	Sequence 57, Appl	C 482	57	6.0	1021	6	US-10-750-185-61280	Sequence 61280, A
C 410	58	6.1	2614	6	US-10-750-185-41690	Sequence 41690, A	C 483	57	6.0	1027	6	US-10-750-185-59538	Sequence 59538, A
C 411	58	6.1	3029	6	US-10-750-185-60959	Sequence 60959, A	C 484	57	6.0	1040	6	US-10-750-185-53322	Sequence 53322, A
C 412	58	6.1	3045	6	US-10-750-185-24745	Sequence 24745, A	C 485	57	6.0	1133	6	US-10-750-185-36325	Sequence 36325, A
C 413	58	6.1	3231	6	US-10-821-234-21	Sequence 21, Appl	C 486	57	6.0	1165	6	US-10-750-185-35142	Sequence 35142, A
C 414	58	6.1	3435	6	US-10-467-962B-88	Sequence 88, Appl	C 487	57	6.0	1197	6	US-10-750-185-49857	Sequence 49857, A
C 415	58	6.1	3496	6	US-10-750-185-27401	Sequence 27401, A	C 488	57	6.0	1283	6	US-10-750-185-42267	Sequence 42267, A
C 416	58	6.1	3509	9	US-11-077-550-19	Sequence 19, Appl	C 489	57	6.0	1289	6	US-10-750-185-49833	Sequence 49833, A
C 417	58	6.1	3874	6	US-10-793-626-4339	Sequence 4339, Ap	C 490	57	6.0	1301	6	US-10-750-185-64792	Sequence 64792, A
C 418	58	6.1	3958	6	US-10-793-626-4279	Sequence 4279, Ap	C 491	57	6.0	1331	6	US-10-750-185-46539	Sequence 46539, A
C 419	58	6.1	4057	6	US-10-821-234-189	Sequence 189, App	C 492	57	6.0	1338	6	US-10-821-234-754	Sequence 754, App
C 420	58	6.1	4158	6	US-10-793-626-3879	Sequence 3879, Ap	C 493	57	6.0	1422	7	US-11-055-637-65	Sequence 65, Appl
C 421	58	6.1	4247	6	US-10-793-626-4255	Sequence 4255, Ap	C 494	57	6.0	1458	6	US-10-750-185-35127	Sequence 35127, A
C 422	58	6.1	4637	6	US-10-750-185-38859	Sequence 38859, A	C 495	57	6.0	1536	6	US-10-750-185-58570	Sequence 58570, A
C 423	58	6.1	5366	7	US-11-091-928-4	Sequence 4, Appl1	C 496	57	6.0	1545	7	US-11-085-637-66	Sequence 66, Appl
C 424	58	6.1	5984	7	US-11-091-928-3	Sequence 3, Appl1	C 497	57	6.0	1562	6	US-10-750-185-37349	Sequence 37349, A
C 425	58	6.1	179892	7	US-11-112-908-39	Sequence 39, Appl	C 498	57	6.0	1608	6	US-10-750-185-37878	Sequence 37878, A
C 426	57.5	6.1	600	6	US-10-750-185-20916	Sequence 20916, A	C 499	57	6.0	1665	6	US-10-750-185-36578	Sequence 36578, A
C 427	57.5	6.1	696	9	US-11-082-389-25	Sequence 25, Appl	C 500	57	6.0	1741	6	US-10-750-185-63772	Sequence 63772, A
C 428	57.5	6.1	742	6	US-10-750-185-62008	Sequence 62008, A							
C 429	57.5	6.1	792	6	US-10-750-185-51068	Sequence 51068, A							
C 430	57.5	6.1	857	6	US-10-750-185-57061	Sequence 57061, A							
C 431	57.5	6.1	939	6	US-10-750-185-61139	Sequence 61139, A							
C 432	57.5	6.1	1051	6	US-10-750-185-26305	Sequence 26305, A							
C 433	57.5	6.1	1103	6	US-10-750-185-3232	Sequence 3232, A							
C 434	57.5	6.1	1115	6	US-10-750-185-30430	Sequence 30430, A							
C 435	57.5	6.1	1118	6	US-10-750-185-42969	Sequence 42969, A							
C 436	57.5	6.1	1182	6	US-10-750-185-54968	Sequence 54968, A							
C 437	57.5	6.1	1411	6	US-10-750-185-51988	Sequence 51988, A							
C 438	57.5	6.1	1431	6	US-10-750-185-33765	Sequence 33765, A							
C 439	57.5	6.1	1451	6	US-10-750-185-39708	Sequence 39708, A							
C 440	57.5	6.1	1492	6	US-10-750-185-53583	Sequence 53583, A							
C 441	57.5	6.1	1522	6	US-10-750-185-42479	Sequence 42479, A							
C 442	57.5	6.1	1545	6	US-10-793-626-2681	Sequence 2681, Ap							
C 443	57.5	6.1	1591	6	US-10-750-185-45433	Sequence 45433, A							
C 444	57.5	6.1	1634	6	US-10-750-185-49774	Sequence 49774, A							
C 445	57.5	6.1	1636	7	US-11-102-240-77	Sequence 77, Appl							
C 446	57.5	6.1	1640	6	US-10-750-185-45095	Sequence 45095, A							

RESULT 1

US-10-750-185-25698/c
; Sequence 25698, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNise, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750.185

ALIGNMENTS

```
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25698
; LENGTH: 952
; TYPE: DNA
; ORGANISM: Bovine 19866881510436
US-10-750-185-25698

Alignment Scores:
Pred. No.: 2,88e-15 Length: 952
Score: 136.00 Matches: 38
Percent Similarity: 91.30% Conservative: 4
Best Local Similarity: 82.61% Mismatches: 4
Query Match: 20.74% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x US-10-750-185-25698 (1-952)
QY 116 GluIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysSerArg 135
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QY 136 ValLysLeuLysSerGlnGluIlePheProSerThrLysMetMetArgAsnLeu 155
Db 740 GTGAAGTTTAAAGCCAGAAATATTCCTTTTCCAAATACGCAATGATGAGAAACCTT 681
QY 156 LeuCyValHisValAsn 161
Db 680 TTGTGTGTTCAATGAAGT 663

RESULT 2
US-10-821-234-301
; Sequence 301, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 301
; LENGTH: 3672
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-301

Alignment Scores:
Pred. No.: 54.6 Length: 3672
Score: 78.00 Matches: 26
Percent Similarity: 48.53% Conservative: 7
Best Local Similarity: 38.24% Mismatches: 32
Query Match: 8.25% Indels: 3
DB: 6 Gaps: 1

US-10-757-745-2_COPY_54_236 (1-183) x US-10-821-234-301 (1-3672)
QY 7 SerTyrPheGluProProValGluGluSerAlaIleGluArg-ArgProGluThrIleSe 26
Db 1760 TCACGTGTTCTTTCCACCCTATTCCTTTTCATCTTTGAGCAGTATATCCAACTAGGATCTG 1819
QY 26 rGluProLysThrTyrValAspLeuThrAsnGluGluThrAspSerThrSerLys 46
Db 1820 CCAAGTGGATACTGGGGTGCCATCCCTCCTGAGAAAGAACTAGCCAGGAACCTCAAGCTC 1879

; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25698
; LENGTH: 952
; TYPE: DNA
; ORGANISM: Bovine 19866881510436
US-10-750-185-25698

Alignment Scores:
Pred. No.: 2,88e-15 Length: 952
Score: 136.00 Matches: 38
Percent Similarity: 91.30% Conservative: 4
Best Local Similarity: 82.61% Mismatches: 4
Query Match: 20.74% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x US-10-510-386-71 (1-1621)
QY 46 s-----IleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeu1 64
Db 1880 CCCCACATCTCTCCAGCCTGGACCTAATCTTGAGAGGGGCTCTCTTCACGGACTG 1939
QY 64 eThrTrpAsnIleAspGlyLeu 71
Db 1940 TGTCTGGACTTTGACGAGGCTT 1961

RESULT 3
US-10-510-386-71
; Sequence 71, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 71
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
; NAME/KEY: CDS
; LOCATION: (271)..(1122)
US-10-510-386-71

Alignment Scores:
Pred. No.: 21.3 Length: 1621
Score: 77.00 Matches: 43
Percent Similarity: 41.72% Conservative: 25
Best Local Similarity: 26.38% Mismatches: 55
Query Match: 8.15% Indels: 41
DB: 6 Gaps: 7

US-10-757-745-2_COPY_54_236 (1-183) x US-10-510-386-71 (1-1621)
QY 9 PheGluProProValGluGlu-----SerAlaLeuGluArgArg--- 21
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QY 22 ProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr--- 40
Db 751 CCGGAATGGATC-----TTTAAAGAAATGCTATCCTCTTACTACTACTT 795
QY 41 -----AspSerThrThrSerLysIleSerProSerGlu----- 51
Db 796 CCGTGTGATCAGCGCATGCTGAAAGTCACGGAGGAGATATTGAAGAAATGAGAAAAATG 855
QY 52 AspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeu 71
Db 856 AACACACAGACAGCGTTCAAGTCGAGGGTCTTGTCTTGATTTAAAAAATATAGACGATT 915
QY 72 AspLeuAsnAsnLeuSerGluArgAlaArgGlyVal-----CysSerTyr-Le 87
Db 916 TCTTCCATCATTTGAGGAGATTTCTTGTCCGGTATTAATATGATGATGCCCATGATGAT 975
QY 87 uAlaLeuTyrSerProAspValIlePheLeuGlnGlnValIleProProTyrTyrSerTy 107
Db 976 CGTGTGTTCCAGCCGAGCATGCTTTTCATGCAAAAAA-CTGATTCCTTTTTCAGAAAGT 1034
QY 107 rLeuLysLysArgSerSerAsnTyrGluIleIleThrGlyHisGluGluGlyTyrPheTh 127
Db 1035 CTATCAGGCAGACAGCTGGGGTTCATCTCATTTTGGCTGGGAACAGAGGGT----- 1083
QY 127 rAlaIleMetLeuLysSerArgValLysLeuLysSerGlnGluIleIleProPhePr 147
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Db 535 ACCAGGTCCTGCTGGGCTGGGAGAACACAAACAAACCTGGAGACATCCTCTCT 594
Qy 146 PheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsnValSerGly 164
Db 595 TACCCC-----AAGGACTTCACCTGTGTCCACCAAGCCCTGAAGGC 636

RESULT 6

US-10-793-626-1499
; Sequence 1499, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1499
; LENGTH: 2238
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-1499

Alignment Scores:
Pred. No.: 134 Length: 2238
Score: 72.50 Matches: 37
Percent Similarity: 39.47% Conservative: 23
Best Local Similarity: 24.34% Mismatches: 35
Query Match: 7.67% Indels: 57
DB: 6 Gaps: 9

US-10-757-745-2_COPY_54_236 (1-183) x US-10-793-626-1499 (1-2238)

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Qy 23 GluThrIleSerGluPro---LysThrTyrValAspLeuThrAsnGluGluThrAsp 41
Db 1846 CAAGTGATTAATGAAGCTGTATCTATTTTAAATAATTTAACAAAT-----1890

Qy 42 SerThrThrSerLysIleSerProSerGluAsp-----ThrGlnGlnGluAsn 57
Db 1891 GGTACTTACATATGATTCATTATCTAGTAATAATCAATAATATCATGTAAGCATTTCTAAC 1950

Qy 58 GlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSer 77
Db 1951 GGACAGATATTTGAGCCAGTT-----GAGTTGAGT 1980

Qy 78 GluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeu 97
Db 1981 CAATCTACAAAAGAAATTAATTA---TATGTGGCTTTACGT-----ATTAGTCTT 2025

Qy 98 GlnGluValIleProProTyrTyr-----105
Db 2026 ATTAAGATATTAAACCGTATATTCATCCAGTGATTTAGATGATGATGATTTGTCAT 2085

Qy 106 -----SerTyrLeuLysLysArgSerSerAsnTyr 115
Db 2086 TTTGATAAAATATCGTAAAGAACGATGTTGAAATATTTGAGAGAACTATCAGAACATAT 2145

Qy 116 GluIleIleThrGlyHisGluGluGlyTyrPheThr 127
Db 2146 CAATAACTT-----TATTTTACT 2163

RESULT 7
US-10-793-626-3413/c

; Sequence 3413, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3413
; LENGTH: 3207
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3413

Alignment Scores:
Pred. No.: 232 Length: 3207
Score: 72.50 Matches: 37
Percent Similarity: 39.47% Conservative: 23
Best Local Similarity: 24.34% Mismatches: 35
Query Match: 7.67% Indels: 57
DB: 6 Gaps: 9

US-10-757-745-2_COPY_54_236 (1-183) x US-10-793-626-3413 (1-3207)

Qy 7 SerTyrPheGluProValGluGluSerAlaLeuGlu-----ArgArgPro 22
Db 1916 AGTTATATGCAAGCTTTAGTGGAGAACATATCAAGCAATAAAGATAGCGCTACCA 1857

Qy 23 GluThrIleSerGluPro---LysThrTyrValAspLeuThrAsnGluGluThrAsp 41
Db 1856 CAAGTGATTAATGAAGCTGTATCTATTTTAAATAATTTAACAAAT-----1812

Qy 42 SerThrThrSerLysIleSerProSerGluAsp-----ThrGlnGlnGluAsn 57
Db 1811 GGTACTTACATATGATTCATTATCTAGTAATAATCAATAATATCATGTAAGCATTTCTAAC 1752

Qy 58 GlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSer 77
Db 1751 GGACAGATATTTGAGCCAGTT-----GAGTTGAGT 1722

Qy 78 GluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeu 97
Db 1721 CAATCTACAAAAGAAATTAATTA---TATGTGGCTTTACGT-----ATTAGTCTT 1677

Qy 98 GlnGluValIleProProTyrTyr-----105
Db 1676 ATTAAGATATTAAACCGTATATTCATCCAGTGATTTAGATGATGATGATTTGTCAT 1617

Qy 106 -----SerTyrLeuLysLysArgSerSerAsnTyr 115
Db 1616 TTTGATAAAATATCGTAAAGAACGATGTTGAAATATTTGAGAGAACTATCAGAACATAT 1557

Qy 116 GluIleIleThrGlyHisGluGluGlyTyrPheThr 127
Db 1556 CAATAACTT-----TATTTTACT 1539

RESULT 8
US-10-793-626-3737
; Sequence 3737, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04


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; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3009
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3009

Alignment Scores:
Pred. No.: 37.6 Length: 720
Score: 71.00 Matches: 27
Percent Similarity: 41.94% Conservative: 12
Best Local Similarity: 29.03% Mismatches: 42
Query Match: 7.51% Indels: 12
DB: 6 Gaps: 2

US-10-757-745-2_COPY_54_236 (1-183) x US-10-793-626-3009 (1-720)

QY 12 ProValGluSerAlaLeuGluArgProGluThrIleSerGluProLysThrTyr 31
DB 368 CCAGTTTCTCTATCTAAGTACAGTATTTTACCACCACTACCGTCTGAACCCATTTTCATAG 309
QY 32 ValAspLeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSerProSerGlu 51
DB 308 CTAATGATACCAAGCAGCTTCAGCAACTTCTCCATGACACAGCTCCAGCAGCTTCCA 249
QY 52 AspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeu 71
DB 248 AATAATACAGCAGTACGAGTCCAGTATCGGTAATC----- 210
QY 72 AspLeuAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSer 91
DB 209 ---TTAGATAAATTTATCAGCACCACCACTAAATAATGT-----TTGTAATCA 165
QY 92 ProAspValIlePheLeuGlnGluValIleProProTyr 104
DB 164 CCAGATTGTATATATTGTTTAGCAGTAATCATTTGAATAC 126

RESULT 11
US-10-793-626-3527
; Sequence 3527, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3572
; LENGTH: 3572
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3527

Alignment Scores:
Pred. No.: 428 Length: 3572
Score: 71.00 Matches: 27
Percent Similarity: 41.94% Conservative: 12

; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3009
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-757-745-2_COPY_54_236 (1-183) x US-10-793-626-3009 (1-720)

QY 12 ProValGluSerAlaLeuGluArgProGluThrIleSerGluProLysThrTyr 31
DB 368 CCAGTTTCTCTATCTAAGTACAGTATTTTACCACCACTACCGTCTGAACCCATTTTCATAG 309
QY 32 ValAspLeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSerProSerGlu 51
DB 308 CTAATGATACCAAGCAGCTTCAGCAACTTCTCCATGACACAGCTCCAGCAGCTTCCA 249
QY 52 AspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeu 71
DB 248 AATAATACAGCAGTACGAGTCCAGTATCGGTAATC----- 210
QY 72 AspLeuAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSer 91
DB 209 ---TTAGATAAATTTATCAGCACCACCACTAAATAATGT-----TTGTAATCA 165
QY 92 ProAspValIlePheLeuGlnGluValIleProProTyr 104
DB 164 CCAGATTGTATATATTGTTTAGCAGTAATCATTTGAATAC 126

RESULT 12
US-10-793-626-4046/c
; Sequence 4046, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4046
; LENGTH: 3668
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4046

Alignment Scores:
Pred. No.: 446 Length: 3668
Score: 71.00 Matches: 27
Percent Similarity: 41.94% Conservative: 12
Best Local Similarity: 29.03% Mismatches: 42
Query Match: 7.51% Indels: 12
DB: 6 Gaps: 2

US-10-757-745-2_COPY_54_236 (1-183) x US-10-793-626-4046 (1-3668)

QY 12 ProValGluSerAlaLeuGluArgProGluThrIleSerGluProLysThrTyr 31
DB 2171 CCAGTTTCTCTATCTAAGTACAGTATTTTACCACCACTACCGTCTGAACCCATTTTCATAG 2112
QY 32 ValAspLeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSerProSerGlu 51
DB 2111 CTAATGATACCAAGCAGCTTCAGCAACTTCTCCATGACACAGCTCCAGCAGCTTCCA 2052
QY 52 AspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeu 71
DB 2051 AATAATACAGCAGTACGAGTCCAGTATCGGTAATC----- 2013
QY 72 AspLeuAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSer 91
DB 72 AspLeuAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSer 91
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Qy 12 ProValGluGluSerAlaLeuGluArgProGluThrIleSerGluProLysThrTyr 31
Db 430 CCGGTGAAGCAGCATGCTCATGAAGCAGA---AGTACTGTGGCAAAAGGATGCTACAAA 486
Qy 32 ValAspLeuThrAsnGluGluThrAspSerThrThrSerLysIleSerProSerGlu 51
Db 487 GGGGACTTGCTCAAGATATGACGACTATTAACAANTTTGAGAGGGGAAAGCCAAATAC 546
Qy 52 AspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeu 71
Db 547 GTGGCTCAGTGGCCGGGAACCTCTCTCTACTCTA-----CATGGACATCTG 594
Qy 72 Aspleu-----AsnAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeu 87
Db 595 GAGCTCTGGTTCACCACTGCTCTACAGAGAAATAAAAGAGAGATCTTTTCCTGCCAT 654
Qy 88 AlaLeuTyrSerProAspValIlePheLeuGlnGluValIleProProTyrTyrSerTyr 107
Db 655 GCAGGGTCTCACCA-----GTAGCCCTCTCCCTGGTACTCAAGT 693
Qy 108 LeuLysArgSerSerAsnTyrGluIleIleThrGlyHisGluGlyTyrPheThr 127
Db 694 CAGGAAGCCGCTCATCTACCAACACACTGTGAGGAGATCTCTGAACAGGGCTTACACC 753
Qy 128 Ala-----IleMetLeuLysSerArgValLysLeu----- 138
Db 754 AGTTCTGACAGAACCTTTCTCAAAATTCAAAATAGCAGACATAAATCTCTCTTTGTAAT 813
Qy 138 ----- 138
Db 814 ATGAAGACAAAAACAATCACTAGATATATAAGATACCTAGTACTCCACAAAAGGATAC 873
Qy 139 -----LysSerGlnGluIleIleProPheProSerThrLys---MetMetArgAsn 154
Db 874 CATCTGAGAAATCACAGCAAAATATCTCTCTTCTATAAGAGAAATACCTTTAAAAACT 933
Qy 155 LeuLeuCysValHisValAsnValSerGlyAsnGluLeu 169
Db 934 CTTATTTGTATTTTAAATAAAATCTCAGCAAAACATTTATTTATTA 978

RESULT 17
US-10-750-185-50173/c
; Sequence 50173, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50173
; LENGTH: 1425
; TYPE: DNA
; ORGANISM: Bovine 19866880871938
US-10-750-185-50173

Alignment Scores:
Pred. No.: 166 Length: 1425
Score: 69.50 Matches: 33
Percent Similarity: 41.80% Conservative: 18
Best Local Similarity: 27.05% Mismatches: 56
Query Match: 7.35% Indels: 15
```

```
DB: 6 Gaps: 3
US-10-757-745-2_COPY_54_236 (1-183) x US-10-750-185-50173 (1-1425)
Qy 59 SerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGlu 78
Db 562 TCTGTTTTCTCCACAGTCTCTCTGACTTCCCTGGTCTTGACTTACATCTCAAAAGTAGA 503
Qy 79 ArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGln 98
Db 502 CCTTCAAAATTAACATTTTACAAACTTCTTGTCTCTTGGCAATGCTGTTTCCATGTC 443
Qy 99 GluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIle 118
Db 442 ACTGTCAATTCATTTGGTGAAGCTCTTGAAGATGAGAGGCGGTATATCTGTACAGT 383
Qy 119 ThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeu 138
Db 382 TTTTCAAAAAAATTGATATATTGACCTTTATTCATCAACAGCTCTCGCAGGTACACTG 323
Qy 139 LysSerGlnGluIleIleProPheProSerThrLysMetMetArgAsn----- 154
Db 322 GCTTCAGAGCAT-----CCTTTGTACAAAGTACTCTGACAAAATAAACATGTGTTC 275
Qy 155 -----LeuLeuCysValHis-----ValAsnValSerGlyAsnGluLeu 167
Db 274 AGTAGCCTTTTGATTATTTCATAAAATGTGTGAGATAACATGATTAGTGTAACTCAGTT 215
Qy 168 CysLeu 169
Db 214 TGCATA 209

RESULT 18
US-10-750-185-24828
; Sequence 24828, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24828
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Bovine 19866881178608
US-10-750-185-24828

Alignment Scores:
Pred. No.: 208 Length: 1650
Score: 69.50 Matches: 14
Percent Similarity: 62.79% Conservative: 13
Best Local Similarity: 32.56% Mismatches: 11
Query Match: 7.35% Indels: 5
DB: 6 Gaps: 1

US-10-757-745-2_COPY_54_236 (1-183) x US-10-750-185-24828 (1-1650)
Qy 103 ProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGlyHisGlu 122
Db 348 CCATTTTTTTCTTTTGGACTTCAGAAACTTTAA-----GGACACCAG 392
Qy 123 GluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGlnGlu 142
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Db 393 GAGGCTACTGAGAGCTGGGCTGACCGCCAATCCCGCATCAGGGTGAGTGTGAGACC 452
QY 143 lleilePro 145
Db 453 GTCTGTCTCT 461

RESULT 19

US-10-750-185-36519
; Sequence 36519, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: Denise, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR IMPROVING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36519
; LENGTH: 2233
; TYPE: DNA
; ORGANISM: Bovine 19866880416267
US-10-750-185-36519

Alignment Scores:
Pred. No.: 329 Length: 2233
Score: 69.50 Matches: 41
Percent Similarity: 37.66% Conservative: 17
Best Local Similarity: 26.62% Mismatches: 43
Query Match: 7.35% Indels: 54
DB: 6 Gaps: 8

US-10-757-745-2_COPY_54_236 (1-183) x US-10-750-185-36519 (1-2233)

QY 33 AspLeuThrAsnGluThrThrAspSerThrThrSerLyIleSerPro----- 49
Db 1244 GACTTCCTCTAAGAGAAACATTTAAAGAAACGACACACATTTATGTCTCTGAATCAGTG 1303
QY 50 -----SerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThr 65
Db 1304 CTGAATGCCATCTCTAGTGATCAGAACCCACACCATGGAGTCATGTTCTCCCTCGTG--- 1360
QY 66 TrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArgGlyValCysSer 85
Db 1361 -----ATGTGCTCA 1369
QY 86 TyrLeuAlaLeuTyrSerProAspVal---IlePheLeuGlnGluValIleProTyr 104
Db 1370 CACTTCCTCTTTGGCTGCTGAGAAATATGTGCTTTTGAGAGATAGTATTTGAAGCTCGCAT 1429
QY 105 TyrSerTyrLeuIleValArgSerSerAsnTyrGluIleThrGlyHisGluGluGly 124
Db 1430 TACATGTATGTCGCAAAAGG-----AGCAAAAGACTTTGACTTCCCAAGNA----- 1477
QY 125 TyrPheThrAlaIleMetLeuTyrLysSerArgValLeuLysSerGlnGluIleIle 144
Db 1478 -----ATCACTGGATCCGTAAGAAA----- 1498
QY 145 ProPheProSerThrLysMetMetArgAsn-----LeuLeuCysValHisVal 160
Db 1499 -----CACATAGCCCAATAGAGAAATAGATAAGTAATCTTGTGTCACGAC--- 1546
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeu 174

Db 1547 -----CCTGGTAGGGAATTAAA-CTCACAACTTCCACGTTTA 1581

RESULT 20

US-10-401-386B-63
; Sequence 63, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; TITLE OF INVENTION: For Use
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(471)
US-10-401-386B-63

Alignment Scores:
Pred. No.: 36.4 Length: 474
Score: 69.00 Matches: 30
Percent Similarity: 44.09% Conservative: 26
Best Local Similarity: 23.62% Mismatches: 45
Query Match: 7.30% Indels: 26
DB: 6 Gaps: 6

US-10-757-745-2_COPY_54_236 (1-183) x US-10-401-386B-63 (1-474)

QY 31 TyrValAspLeuThrAsnGluThrThrAspSer-----ThrThrSerLyIle 47
Db 88 TTTGAAGATATGACTGATCTGACTGTAGAGATATGACCCCGGACCATATTATTATA 147
QY 48 SerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsn 67
Db 148 AGTATGTATAAGATAGCAGCCTAGAGGT-----ATGCTGTAACCTATCTCT 195
QY 68 IleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeu 87
Db 196 GTGAAGTGTGAGAAAATTTCACTCTCTCTCTGTGAGAACAAA---ATTATTCCTTTAAG 252
QY 88 AlaLeuTyrSerPro-----AspValIlePheLeuGlnGlu 99
Db 253 GAATATGAATCCTCTCTGATAACATCAAGGATACAAAAGTGACATCATATCTTTCAGAGA 312
QY 100 ValIleProProTyrTyrSerTyrLeuIleValArgSerSerAsnTyrGluIleIleThr 119
Db 313 ACTGTCCCGGAGCATGATAAAGATGCAATTTGAATCTTCATCATAC----- 360
QY 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysSerArgValLeu--- 138
Db 361 -----GAAGGATACCTTCTAGCTTGTGAAAAAGAGAGAGACCTTTTAACTCAT 411
QY 139 -----LysSerGlnGluIle 143
Db 412 TTGAAAAAAGAGGATGAATTG 432

RESULT 21

US-10-750-185-35895/c

```
; Sequence 35895, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35895
; LENGTH: 970
; TYPE: DNA
; ORGANISM: Bovine 19866881020546
US-10-750-185-35895

Alignment Scores:
Pred. No.: 108 Length: 970
Score: 69.00 Matches: 22
Percent Similarity: 41.25% Conservative: 11
Best Local Similarity: 27.50% Mismatches: 30
Query Match: 7.30% Indels: 17
DB: 6 Gaps: 1

US-10-757-745-2_COPY_54_236 (1-183) x US-10-750-185-35895 (1-970)
Qy 53 ThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAsp 72
Db 317 ACGAGGAAATCGAACCCACATCTCTGTGCTCTCGCATGGCAGGTAGATCTTTACCA 258
Qy 73 LeuAsnAsnLeuSerGluArgAlaAargGlyValCysSer----- 85
Db 257 CTGAGCCACTCGGAAGCCAGCCGCTAATGAGTATTGCTGTAATCTGACACTGAAATGC 198
Qy 86 -----TyrLeuAlaLeuTyrSerProAspValIlePhe 96
Db 197 ATAATCATCATCTGCTTAACAAATGTTTATATGCGATTGTAGAAAAGTCTTTATTTT 138
Qy 97 LeuGlnGluValIleProProTyrTyrSer-TyrLeuLysLysArgSerSerAsnTyr 115
Db 137 CTAAATGTAACCTTTTATTCTGTGTATAGCATACATACAGAAACATGCACAAAAGTAT 80

RESULT 22
US-10-632-150-51
; Sequence 51, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chiau, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
```

```
; LENGTH: 1777
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: all n positions
; OTHER INFORMATION: n-a, c, g or t
US-10-632-150-51

Alignment Scores:
Pred. No.: 271 Length: 1777
Score: 69.00 Matches: 50
Percent Similarity: 37.73% Conservative: 33
Best Local Similarity: 22.73% Mismatches: 70
Query Match: 7.30% Indels: 67
DB: 6 Gaps: 11

US-10-757-745-2_COPY_54_236 (1-183) x US-10-632-150-51 (1-1777)
Qy 13 ValGluSerAlaLeuGluArgProGluThrIleSerGluProLysThrTyrVal 32
Db 809 ATTACTTCAACTGCGTGGNAAAAATAAGACATTACCATGCGATCCACCAAGCAGTATGCC 868
Qy 33 -----AspLeuThrAsnGluThrThrAspSerThrThrSerLysIleSerPro 49
Db 869 TGTTTGCACGATTTAACTAACAGGGCATTGGAGAGAAATAGATAATAGACACCCCTGG 928
Qy 50 SerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAsp 69
Db 929 ACTAAGCGCTGTTCTTCTGAGAAT-----TTCACCTTCTCCTATGTGTGATGTAGAT 982
Qy 70 GlyLeuAspLeuAsnAsnLeuSerGlu-----ArgAlaAargGlyVal----- 83
Db 983 GCTGAAGATTGGCTGATATATGAAGATACACTGTGGAATGGAGACATAGAAATGTTGAAAGT 1042
Qy 84 -----CysSerTyrLeuAlaLeuTyrSerPro 92
Db 1043 CTTTGTGTAATGGNAAACAGCATCCAACTTTAGTTGTTCCACCTCTGGTGTGTTTAGTAAG 1102
Qy 93 AspValIlePheLeu-----GlnGluValIleProProTyrTyr 105
Db 1103 GACATCTGTGGACTAAGCACTAGTGTCTGTGGCAGCAGCATTTGTGCTTCTCCAGCCTTT 1162
Qy 106 SerTyr-----LeuLysLysArgSerSerAsn 114
Db 1163 GCGTATTGTGTCATCATTTTGTGTACAGGAACAGCTTTAAGAACTATGTCATCACTC 1222
Qy 115 TyrGluIleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSer 134
Db 1223 CCAGAA-----TCTTTCGAATGTGTAGAAAGACGCA 1255
Qy 135 ArgValLysLeu-----LysSerGlnGluIleIleProPheProSerThrLys-MetMetAr 153
Db 1256 AGGACTAGATTGCTAGGGGAAAAGACTAATTTACTTTGGGAGTGAATAATCTGATCAA 1315
Qy 153 gAsnLeu-----LeuCysValHisVal-----As 161
Db 1316 GAGACTGAGCGTACTTCTGTTTCTCAGTTTATCTGGATGTTATCAGATCAGACCAT 1375
Qy 161 nValSerGly-----AsnGluLeuCysLeuMetThrSerHisLeuGluSer 176
Db 1376 GGTTCTAGGGTTTGTACTCTGGGAGGAGGGCTGCTATTATTGGAGCACCTTAATCTCT 1433

RESULT 23
US-11-073-457-51
; Sequence 51, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
```

```
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 51
; LENGTH: 1777
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: all n positions
; OTHER INFORMATION: n=a, c, g or t
US-11-073-457-51

Alignment Scores:
Pred. No.: 271          Length: 1777
Score: 69.00           Matches: 50
Percent Similarity: 37.73% Conservative: 33
Best Local Similarity: 22.73% Mismatches: 70
Query Match: 7.30%     Indels: 67
DB: 7                  Gaps: 11

US-10-757-745-2_COPY_54_236 (1-183) x US-11-073-457-51 (1-1777)
QY 13 ValGluGluSerAlaLeuGluArgProGluThrIleSerGluProIysThrTyrVal 32
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 809 ATTACTTCAACTGCGTGGAAATAAAGACATTACCAGTCAGTCCACCAAGCAGTATGCC 868
QY 33 -----AspLeuThrAsnGluGluThrAspSerThrThrSerLysIleSerPro 49
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 869 TGTGTGCACGATTTACTAACAGGCGCATTTGGAGAGAAATAGATAATGAACACCCCTGG 928
QY 50 SerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAsp 69
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 929 ACTAAGCCGTGTTCTTCTCAGAAAT-----TTCACTTCTCCTTATGTGTGGATGTATAG 982
QY 70 GlyLeuAspLeuAsnAsnLeuSerGlu-----ArgAlaArgGlyVal----- 83
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 983 GCTGAAGATTTGCTGATATTGAAGATACGTGTGGAATGGAGACATAGAAATGTTGAAGT 1042
QY 84 -----CysSerTyrLeuAlaLeuTyrSerPro 92
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 1043 CTTTGTGTAATGAAACAGCATCCAACTTTAGTTGTTCCACCTCTGTTGTTTGTAGTAAG 1102
QY 93 AspValIlePheLeu-----GlnGluValIleProProTyrTyr 105
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 1103 GACATTGTTGGACTAAGGACTAGTGTCTGTTGGCAGCAGCATGTGCTTCCGCCCTTT 1162
QY 106 SerTyr-----LeuLysLysArgSerSerAsn 114
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 1163 GCGTATGTGGTCACCTCACTTTTGTGTACAGGAACAGCTTTAAGAACTATGTCATCCTC 1222
QY 115 TyrGluIleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysSer 134
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 1223 CCAGAA-----TCTTCTGCAATGTGTAGAAAGCAGCA 1255
QY 135 ArgValLysLeu---LysSerGlnGluIleIleProPheProSerThrLys-MetMetAr 153
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 1256 AGGACTAGATTGCTAGGGGAAAGACTTAATTTACTTTTGGGAGTGAAATAATCTGATCAA 1315
QY 153 gAsnLeu-----LeuCysValHisVal-----As 161
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 1316 GAGACTGGACGTGACTTCTGTTTCTCAGTTTATCTGGATGTTATCAGATCAGACCAT 1375
QY 161 nValSerGly-----AsnGluLeuCysLeuMetThrSerHisLeuGluSer 176
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 1376 GGTCTCAGGGTTTTGACTCTGGGAGGAGGCGCTGCTTATTATTGGAGCACCTTAATCTCT 1433

RESULT 24
US-10-750-185-51119/c

; Sequence 51119, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 51119
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Bovine
; ORGANISM: Bovine 19866880513405
US-10-750-185-51119

Alignment Scores:
Pred. No.: 273          Length: 1788
Score: 69.00           Matches: 40
Percent Similarity: 42.95% Conservative: 27
Best Local Similarity: 25.64% Mismatches: 44
Query Match: 7.30%     Indels: 45
DB: 6                  Gaps: 10

US-10-757-745-2_COPY_54_236 (1-183) x US-10-750-185-51119 (1-1788)
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 491 TTTTCTGTGCTTTCTGGAATGGGTGAGGG---AGGATTCAAGGAGTCAATTGAAGGATC 435
QY 81 ArgGlyVal-----CysSer-TyrLeuAlaLeuTyrSerProAspValIlePheLe 97
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 434 AGACAAGTTAGGATTTGCTGTGTTCTGTGGATCATATAATTATCAGAGTTGGAAGAGACATCT 375
QY 97 uGlnGlu-----ValIleProProTyr---TyrSerTyrLeuLysLysArgSerSerAs 114
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 374 ACAGATAAAATAAATAATATCCAACTTACTTACTATACATGAGAAACTGACTTCCAG 315
QY 114 nTyrGluIleIleThrGlyHisGlu-----GluGlyTyrPheTh 127
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 314 AGAA-----GTTGAAGGACATAAGTCACCCCAACAATGGATGATGACCAAGATCAGACTTTTC 261
QY 127 rAlaIle-----MetLeuLysLysSerArgVal-----LysLeuLys 139
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 260 TCCAGTCTCTTCTTCTGTTGTTTAAATGTTAGTTCCTTTCTTCTGTCCTTAAGAAACTAGC 201
QY 139 sSerGlnGluIleIleProPhePro-----LysLeuLys 147
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 200 TTTTCTTACACTGTGACCAACTCTTTTAATAGCCAGCAGCCGCTTTTCTTACACTTGTAC 141
QY 148 -----SerThrLysMetMetArgAsnLeuLeuCysValHisVal----- 160
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 140 CAACCTCTTTAATAGCCAGCAGCCTCAATCATGCATCTGCTCAGTGTGTAGTCTTCAT 81
QY 161 ----AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeu 174
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
Db 80 CCTTGATGTGGCACTGAATCAGCTCTGTTTGGTGGTGGGCATCTT 35

RESULT 25
US-10-750-185-34532
; Sequence 34532, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
```

```
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34532
; LENGTH: 2523
; TYPE: DNA
; ORGANISM: Bovine 19866881171401
US-10-750-185-34532

Alignment Scores:
Pred. No.: 461 Length: 2523
Score: 69.00 Matches: 34
Percent Similarity: 38.41% Conservative: 24
Best Local Similarity: 22.52% Mismatches: 55
Query Match: 7.30% Indels: 38
DB: 6 Gaps: 8

US-10-757-745-2_COPY_54_236 (1-183) x US-10-750-185-34532 (1-2523)

Qy 6 AsnSerTyrPheGluProValGluGluSerAla-----Leu 18
Db 64 AATTCCTGG-----CCACAGACAACTCTCAGACTCAGCTACTCACTCC 114

Qy 19 GluArgArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGlu 38
Db 115 AAAAGTGATGATGAAATAGCAATAGCAATAGCCAGTTGTTTCTGACTATGACGGAAGAAAC 174

Qy 39 ThrThrAspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGly 58
Db 175 ACCTCTGATGATGAGTCAATGCTTCT---GGAGAAAGCAACCATGAGGAAATTC 231

Qy 59 SerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGlu 78
Db 232 AATTTCTATCTAAATC-----AAGAGTCTATGTGAT 264

Qy 79 ArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGln 98
Db 265 AAACAAAAAAGT---TGCCTATGG-----CAGACACCTCAG----- 297

Qy 99 GluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIle 118
Db 298 -----AAACAGCTGAAAAAGAAAGCTCTGGCAACAAGTTCAA 336

Qy 119 ThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLys-----SerArgVal 136
Db 337 TATGCCCAATGATCAGTTTATATGTTCTCTAATTTCTTAAGTTGTTCTTCCAAAGTG 396

Qy 137 LysLeuLysSerGlnGluIleIleProPhePro 147
Db 397 AAAATTCCTAAATATACACGATTGACAAACCA 429

RESULT 26
US-10-750-185-31052/c
; Sequence 31052, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31052
; LENGTH: 6616
; TYPE: DNA
; ORGANISM: Bovine 19866880586304
US-10-750-185-31052

Alignment Scores:
Pred. No.: 1.99e+03 Length: 6616
Score: 69.00 Matches: 43
Percent Similarity: 42.55% Conservative: 37
Best Local Similarity: 22.87% Mismatches: 63
Query Match: 7.30% Indels: 46
DB: 6 Gaps: 11

US-10-757-745-2_COPY_54_236 (1-183) x US-10-750-185-31052 (1-6616)

Qy 11 ProProValGluGluSerAlaLeuGluArgArgPro-----GluThrIleSerGluPro 28
Db 5746 CCTCTCTCTC-----TCAGCAGGTAGGCCACCCGGTCCATCCGGAGTATCAGAGCCC 5693

Qy 29 LysThrTyrValAspLeuThrAsnGluGluThrThrAspSerThrThrSerLys----- 46
Db 5692 CTCCTTTTCTCGACTTTTGCAAGAGCAAGAAATCTGTCCTGCTTCTCCACCCGACCTTTGTGT 5633

Qy 47 IleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrp 66
Db 5632 CTACCTCTAGTCAGACCAAG----- 5612

Qy 67 AsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArgGlyValCysSerTyr 86
Db 5611 AATTTGACAGTAGTAACATCAGTCTGCTCAGAAAGGCTCTCTTAATTTGTGCC--- 5555

Qy 87 LeuAlaLeuTyrSerProAspVal---IlePheLeuGlnGluValIleProPro----- 103
Db 5554 ---TCCTTACTCACTCCAGATTTTAGAGTCTTTTCCCTTTAGATCTGTGCTCCAGGTGG 5498

Qy 104 ---TyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGlyHisGlu 122
Db 5497 GTCACTGGCCATCCCTTTGATCTTGTCTCTGAGCTGGCCAGGCTGTGGAGGAGG 5438

Qy 123 GluGlyTyrPheThrAlaIleMetLeuLysLysSerArgVal---LysLeuLysSerGln 141
Db 5437 CGGAGCTGCTCACGAGCGGCTCTGCTCTCCAGGCTCACCTGGCTGGCGGTGGCGCG 5378

Qy 142 GluIle-----IleProPhePro 147
Db 5377 GAGATCTGCACCTGCCTGCATACCTGTAATCAATCTTCTGCCACCTGTGTGCCATGGCC 5318

Qy 148 Ser-----ThrLysMetMetArgAsnLeuLeuCysValHisValAsnValSerGly 164
Db 5317 CC-TGGCTAGGAACGCTAGCCTCTTAGTCTACCTCTACCCACCTGAGGCTGTGGGG 5259

Qy 165 Asn-----GluLeuCysLeuMet 170
Db 5258 TCCTAATGCCAGCTGCTCCTAATG 5235

RESULT 27
US-10-508-263-101
; Sequence 101, Application US/10508263
; Publication No. US20050260754A1
; GENERAL INFORMATION:
; APPLICANT: BASF Plant Science GmbH
; TITLE OF INVENTION: Constructs and methods for regulating gene expression
; FILE REFERENCE: 53262-20085.00
; CURRENT APPLICATION NUMBER: US/10/508,263
```

```
; CURRENT FILING DATE: 2004-09-20
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(801)
; OTHER INFORMATION: 19 kd zein B2
US-10-508-263-101

Alignment Scores:
Pred. No.: 94.3 Length: 804
Score: 68.50 Matches: 36
Percent Similarity: 35.40% Conservatve: 21
Best Local Similarity: 22.36% Mismatches: 56
Query Match: 7.25% Indels: 48
DB: 6 Gaps: 6

US-10-757-745-2_COPY_54_236 (1-183) x US-10-508-263-101 (1-804)
Qy 22 ProGluThrIleSerGluProLysThr-----TyrValAspLeuThr 35
Db 219 CTTCCAAACATCATCAGCCCTATTACAGCAGTTACCTTTGGTGCGATTATTGGCACAAAA 278
Qy 36 AsnGluGluThrThrAspSerThrThrSerLysIleSerPro-SerGluAspThrGlnGl 55
Db 279 CATCAGGGCACAACTACAACTACAACTCGTGCTAGCAAACTTTGCTGCTACTCTCAGCA 338
Qy 55 nGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAs 75
Db 339 ACAGCAGTTACCTTTGGTGCAATTGTGGCACAAACATCAGGGCACAACTACAACTACAA 398
Qy 75 nLeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValI1 95
Db 399 ATCT-----GTGCTAGCAAACTTTGCTGCTACTCTCAGCAA----- 435
Qy 95 ePheLeuGlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTy 115
Db 436 -----CAACAGTTTCTGCCA-----TTCAACCAACTAGCTGCGATTGAATCTGCG 479
Qy 115 rGluIleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerAr 135
Db 451 -----TTCAACCAACTAGCTGCGATTGAATCTGCG 479
Qy 135 vGallysLeuLysSerGlnGluIleIleProPhePro-----SerThrLysMetMetAr 153
Db 480 TGCTTATTTGCAGCACAACTACTACTACATTCAGCCAGCTAGCTGCTGCTACCCCG 539
Qy 153 gAsnLeuLeuCysValHisValAsnValSerGlyAsnGluLeuLeuCysLeuMetThrSerHi 173
Db 540 GCAATTTCTT-----CCATTCACCACTGGCAGCATTTGAATCTCTCA 581
Qy 173 s 173
Db 582 t 582

RESULT 28
US-10-401-386B-75
; Sequence 75, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19

; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 804
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(471)
US-10-401-386B-75

Alignment Scores:
Pred. No.: 48.6 Length: 471
Score: 68.00 Matches: 31
Percent Similarity: 42.19% Conservatve: 23
Best Local Similarity: 24.22% Mismatches: 46
Query Match: 7.20% Indels: 28
DB: 6 Gaps: 6

US-10-757-745-2_COPY_54_236 (1-183) x US-10-401-386B-75 (1-471)
Qy 31 TyrValAspLeuThrAsnGluGluThrThrAspSer-----ThrThrSerLysIle 47
Db 88 TTTGAAGATATGACTGATTCGACTGTAGAGATAATGCAACCCGGACCATATTTATTATA 147
Qy 48 SerProSerGluAspThrGlnGlnGluAsnGlySerMet---PheSerLeuIleThrTrp 66
Db 148 AGTATGTATTAAGATAGCCAGCTAGAGGTATGGCTGTAGCTATCTCTGTGAAGTGTGAG 207
Qy 67 AsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArgGlyValCysSerTyr 86
Db 208 AAAATTTCAACTCTCTCTCTGTGAGAAC-----AAAATTTCTCTTT 249
Qy 87 LeuAlaLeuTyrSerPro-----AspValIlePheLeuGln 98
Db 250 AAGAAATGAATCTCTCTGATACATCAAGGATACAAAAGTGACATCATATTTCTTCAG 309
Qy 99 GluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIle 118
Db 310 AGAAGTGCCAGGACATGATTAAGATGCAATTTGAATCTTCATCATAC----- 360
Qy 119 ThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeu 138
Db 361 -----GAAGGATACCTTTCTAGCTTGTGAAAAGAGAGAGACCTTTTAAACTC 408
Qy 139 -----LysSerGlnGluIle 143
Db 409 ATTTTGAATAAAGAGAGATGAATTG 432

RESULT 29
US-10-401-386B-77
; Sequence 77, Application US/10401386B
; Publication No. US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallion
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
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```
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(471)
US-10-401-386B-77

Alignment Scores:
Pred. No.: 48.6 Length: 471
Score: 68.00 Matches: 31
Percent Similarity: 42.19% Conservative: 23
Best Local Similarity: 24.22% Mismatches: 46
Query Match: 7.20% Indels: 28
DB: 6 Gaps: 6

US-10-757-745-2_COPY_54_236 (1-183) x US-10-401-386B-77 (1-471)

Qy 31 TyrValAspLeuThrAsnGluThrThrAspSer-----ThrThrSerLysIle 47
Db 88 TTTGAAGATATGACTGATCTGACTGTAGAGATAATGCACCCCGGACCATATTTATTATA 147
Qy 48 SerProSerGluAspThrGlnGlnGluAsnGlySerMet---PheSerLeuIleThrTrp 66
Db 148 AGTATGTATAAAGATAGCCAGCCTAGAGGTATGGCTGTGGCCATCTCTGTGAAGTGTGAG 207
Qy 67 AsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArgGlyValCysSerTyr 86
Db 208 AAAATTTCAACTCTCTCTGTGAGAAC-----AAAAATTATTTCCTTT 249
Qy 87 LeuAlaLeuTyrSerPro-----AspValIlePheLeuGln 98
Db 250 AAGAAATGAATCTCTCTGATAACATCAAGGATACAAAAAGTGACATCATATTTCTTCAG 309
Qy 99 GluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIle 118
Db 310 AGAAGTGTCCAGGACATGATAAAGATGCAATTTGAATCTTCATCATAC----- 360
Qy 119 ThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeu 138
Db 361 -----GAAGGATACTTTCTAGCTTTGTGAAAAAGAGAGAGACCTTTTTTAAACTC 408
Qy 139 -----LysSerGlnGluIle 143
Db 409 ATTTTGAAAAAAGAGGATGAATTG 432

Search completed: December 4, 2005, 21:00:55
Job time : 206.639 secs
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```
RESULT 30
US-10-401-386B-79
; Sequence 79, Application US/10401386B
; Publication No: US20050261213A1
; GENERAL INFORMATION:
; APPLICANT: Patrick Branigan
; APPLICANT: Theresa J Goletz
; APPLICANT: David M Knight
; APPLICANT: Stephen G McCarthy
; APPLICANT: Bernard J Scallan
; APPLICANT: Linda A Snyder
; TITLE OF INVENTION: Nucleic Acid Compositions and Methods
; FILE REFERENCE: CEN 310CIP
; CURRENT APPLICATION NUMBER: US/10/401,386B
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/247,203
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/328,371
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 00:49:56 ; Search time 170.302 Seconds
(without alignment)
1910.099 Million cell updates/sec

Title: US-10-757-745-2_COPY_54_236

Perfect score: 945

Sequence: 1 MERALNSYFPPVESALER.....GNELCLMTSHLESTRGHAAS 183

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-O=/cgn2_1/USPTO.spool/US10757745/runat_01122005_091749_10105/app_query.fasta_1.981
-DB=Issued Patents NA -OPMT=fastap -SURFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=500 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30
-MODE=LOCAL -OUTFMT=ptc -HEAPSIZ=500 -MINLEN=0 -NCPU=6 -ICPU=3
-USER=US10757745 @CNG 1 1 282 @runat_01122005_091749_10105 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:.*
1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/8B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfileseq1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	945	100.0	1920	3	US-09-697-863A-1
2	945	100.0	1948	3	US-09-620-312D-889
3	623.5	66.0	1312	3	US-09-697-863A-3
C 4	525	55.6	1079	3	US-09-118-554-63
C 5	525	55.6	1079	3	US-09-118-554-63
C 6	525	55.6	1079	3	US-09-602-877A-63
7	145	15.3	379	3	US-09-621-976-8403
8	91.5	9.7	3640	3	US-09-976-594-888
9	91.5	9.7	4061	3	US-09-620-312D-363
					Sequence 1, Appli
					Sequence 889, App
					Sequence 3, Appli
					Sequence 63, Appl
					Sequence 63, Appl
					Sequence 8403, Ap
					Sequence 888, App
					Sequence 363, App

10	87.5	9.3	727	3	US-09-328-475C-279	Sequence 279, App
11	87.5	9.3	748	3	US-09-328-475C-278	Sequence 278, App
12	87.5	9.3	2637	3	US-10-101-464A-881	Sequence 881, App
13	84.5	8.9	256287	3	US-09-949-016-14608	Sequence 14608, A
14	84	8.9	1458	3	US-09-270-767-14698	Sequence 14698, A
15	84	8.9	1782	3	US-09-489-039A-1438	Sequence 1438, Ap
16	82	8.7	15213	3	US-08-961-527-26	Sequence 26, Appl
C 17	82	8.7	269223	3	US-09-596-002-41	Sequence 41, Appl
18	81.5	8.6	683	3	US-09-533-559-7228	Sequence 7228, Ap
19	81.5	8.6	960	2	US-08-245-511-3	Sequence 3, Appli
20	81.5	8.6	960	2	US-08-600-933A-3	Sequence 3, Appli
21	81.5	8.6	2049	3	US-08-481-435-5	Sequence 5, Appli
22	81.5	8.6	2604	3	US-10-101-464A-834	Sequence 834, App
23	81	8.6	1899	3	US-09-567-458A-3	Sequence 3, Appli
24	81	8.6	2601	3	US-09-134-001C-2093	Sequence 2093, Ap
25	80	8.5	2032	3	US-09-241-581B-5	Sequence 5, Appli
26	80	8.5	2032	3	US-08-265-428-5	Sequence 5, Appli
27	80	8.5	2032	6	PCT-US95-07721-5	Sequence 5, Appli
C 28	80	8.5	232547	3	US-09-949-016-16603	Sequence 16603, A
29	79.5	8.4	1365	2	US-08-114-072-1	Sequence 1, Appli
30	79.5	8.4	1365	6	PCT-US94-09361-1	Sequence 1, Appli
31	79.5	8.4	1493	3	US-09-376-781-24	Sequence 24, Appl
C 32	79.5	8.4	10322	3	US-09-902-540-989	Sequence 989, App
C 33	79.5	8.4	71387	3	US-09-949-016-16754	Sequence 16754, A
34	79	8.4	2652	3	US-09-248-796A-4828	Sequence 4828, Ap
35	78.5	8.3	1053	3	US-09-248-796A-4335	Sequence 4335, Ap
36	78.5	8.3	1350	3	US-09-248-796A-4759	Sequence 4759, Ap
37	78.5	8.3	2166	3	US-09-583-110-1312	Sequence 1312, Ap
38	78.5	8.3	2166	3	US-08-107-433-1102	Sequence 1102, Ap
C 39	78.5	8.3	4540	2	US-08-770-761A-6	Sequence 6, Appli
C 40	78	8.3	797	3	US-09-328-475C-167	Sequence 167, App
41	78	8.3	6696	3	US-10-272-459-29	Sequence 29, Appl
42	78	8.3	6757	3	US-10-272-459-30	Sequence 30, Appl
43	78	8.3	7478	3	US-10-104-966-15	Sequence 15, Appl
44	78	8.3	7478	3	US-09-929-955-15	Sequence 15, Appl
45	77.5	8.2	1569	2	US-08-680-726A-57	Sequence 57, Appl
46	77.5	8.2	1569	3	US-09-092-409-57	Sequence 57, Appl
C 47	77.5	8.2	1575	3	US-09-774-528-260	Sequence 260, App
C 48	77.5	8.2	1575	3	US-10-120-988-260	Sequence 260, App
C 49	77.5	8.2	3291	6	PCT-US96-03940-10	Sequence 10, Appl
C 50	77.5	8.2	3705	6	PCT-US96-03940-7	Sequence 7, Appli
C 51	77.5	8.2	5648	6	PCT-US96-03940-1	Sequence 1, Appli
C 52	77.5	8.2	5984	3	US-09-949-016-2745	Sequence 2745, Ap
C 53	77.5	8.2	6635	3	US-09-949-016-773	Sequence 773, App
54	77.5	8.2	7881	2	US-08-751-189-1	Sequence 1, Appli
55	77.5	8.2	7881	2	US-09-060-836-1	Sequence 1, Appli
56	77.5	8.2	7881	3	US-09-184-445-1	Sequence 1, Appli
57	77.5	8.2	10592	2	US-08-680-726A-51	Sequence 51, Appl
C 58	77.5	8.2	10592	2	US-08-680-726A-52	Sequence 52, Appl
59	77.5	8.2	10592	3	US-09-092-409-51	Sequence 51, Appl
C 60	77.5	8.2	10592	3	US-09-092-409-52	Sequence 52, Appl
C 61	77.5	8.2	30843	3	US-09-949-016-14487	Sequence 14487, A
62	77	8.1	471	3	US-08-982-285-19	Sequence 19, Appl
63	77	8.1	471	3	US-08-982-285-20	Sequence 20, Appl
64	77	8.1	471	3	US-10-100-057-14	Sequence 14, Appl
C 65	77	8.1	601	3	US-09-949-016-161322	Sequence 161322, A
C 66	77	8.1	3127	3	US-09-620-312D-613	Sequence 613, App
C 67	77	8.1	13188	3	US-08-961-527-70	Sequence 70, Appl
C 68	77	8.1	29291	3	US-09-949-016-16263	Sequence 16263, A
C 69	76.5	8.1	2397	3	US-09-221-017B-272	Sequence 272, App
70	76.5	8.1	39299	3	US-09-949-016-16625	Sequence 16625, A
C 71	76.5	8.1	106380	3	US-09-949-016-17553	Sequence 17553, A
72	76	8.0	471	3	US-08-982-285-21	Sequence 21, Appl
73	76	8.0	471	3	US-10-100-057-16	Sequence 16, Appl
74	76	8.0	2328	3	US-09-328-352-2969	Sequence 2969, Ap
C 75	75.5	8.0	1836	3	US-09-601-198-69	Sequence 69, Appl
76	75.5	8.0	8224	9	5180808-1	Patent No. 5180808
77	75.5	8.0	8257	3	US-09-595-684B-30	Sequence 30, Appl
78	75.5	8.0	8503	3	US-09-620-312D-130	Sequence 130, App
C 79	75.5	8.0	32042	3	US-09-245-281-44	Sequence 44, Appl
C 80	75.5	8.0	32042	3	US-09-340-620A-63	Sequence 63, Appl
C 81	75.5	8.0	32042	3	US-09-728-721-63	Sequence 63, Appl
C 82	75.5	8.0	39553	3	US-09-949-002-810	Sequence 810, App

C 83	75.5	8.0	58111	3	US-09-949-002-673	Sequence 673, App	156	73	7.7	2624	3	US-09-919-039-113	Sequence 113, App
C 84	75.5	8.0	86439	3	US-09-949-016-11945	Sequence 11945, App	157	73	7.7	2823	3	US-09-704-611-4	Sequence 4, Appli
C 85	75.5	8.0	86440	3	US-09-949-016-16990	Sequence 16990, A	158	73	7.7	2892	3	US-09-702-611-3	Sequence 3, Appli
C 86	75.5	8.0	102520	3	US-09-949-016-17367	Sequence 17367, A	159	73	7.7	3603	3	US-09-902-540-3266	Sequence 3266, Ap
C 87	75.5	8.0	102526	3	US-09-949-016-12448	Sequence 12448, A	C 160	73	7.7	15371	3	US-09-949-016-15981	Sequence 15981, A
C 88	75.5	8.0	105050	3	US-09-949-016-15953	Sequence 15953, A	C 161	73	7.7	19954	3	US-09-902-540-1150	Sequence 1150, Ap
C 89	75.5	8.0	175236	3	US-09-949-016-14353	Sequence 14353, A	C 162	73	7.7	462589	3	US-09-949-016-12900	Sequence 12900, A
C 90	75.5	8.0	294836	3	US-09-949-016-15974	Sequence 15974, A	C 163	73	7.7	476044	3	US-09-949-016-12412	Sequence 12412, A
C 91	75.5	8.0	331814	3	US-09-949-016-12008	Sequence 12008, A	C 164	73	7.7	580073	3	US-08-545-5280-1	Sequence 1, Appli
C 92	75.5	8.0	331814	3	US-09-949-016-17056	Sequence 17056, A	165	72.5	7.7	522	3	US-09-543-681A-3701	Sequence 3701, Ap
C 93	75.5	8.0	818128	3	US-09-949-016-14556	Sequence 14556, A	166	72.5	7.7	573	3	US-09-248-796A-1008	Sequence 1008, Ap
C 94	75.5	8.0	818128	3	US-09-949-016-14547	Sequence 14547, A	167	72.5	7.7	601	3	US-09-949-016-103534	Sequence 103534, A
C 95	75.5	8.0	818128	3	US-09-949-016-14548	Sequence 14548, A	C 168	72.5	7.7	601	3	US-09-949-016-127370	Sequence 127370, A
C 96	75.5	8.0	818128	3	US-09-949-016-14549	Sequence 14549, A	C 169	72.5	7.7	601	3	US-09-949-016-127371	Sequence 127371, A
C 97	75.5	8.0	818128	3	US-09-949-016-14550	Sequence 14550, A	C 170	72.5	7.7	953	3	US-09-270-767-6678	Sequence 6678, Ap
C 98	75.5	8.0	818128	3	US-09-949-016-14551	Sequence 14551, A	C 171	72.5	7.7	953	3	US-09-270-767-21960	Sequence 21960, A
C 99	75.5	8.0	818128	3	US-09-949-016-14552	Sequence 14552, A	172	72.5	7.7	957	3	US-09-270-767-11142	Sequence 11142, A
C 100	75.5	8.0	818128	3	US-09-949-016-14553	Sequence 14553, A	173	72.5	7.7	1683	3	US-09-614-221A-487	Sequence 487, App
C 101	75.5	8.0	818128	3	US-09-949-016-14554	Sequence 14554, A	174	72.5	7.7	1828	3	US-09-949-016-4715	Sequence 4715, Ap
C 102	75.5	8.0	818128	3	US-09-949-016-14555	Sequence 14555, A	175	72.5	7.7	1875	3	US-09-877-730-23	Sequence 23, Appli
C 103	75.5	8.0	818128	3	US-09-949-016-14556	Sequence 14556, A	176	72.5	7.7	2000	3	US-09-376-781-25	Sequence 25, Appli
C 104	75.5	8.0	818128	3	US-09-949-016-14557	Sequence 14557, A	177	72.5	7.7	2000	3	US-09-376-781-30	Sequence 30, Appli
C 105	75.5	8.0	818128	3	US-09-949-016-14558	Sequence 14558, A	178	72.5	7.7	2139	3	US-09-877-730-21	Sequence 21, Appli
C 106	75.5	8.0	818128	3	US-09-949-016-14559	Sequence 14559, A	179	72.5	7.7	2238	3	US-09-710-279-1499	Sequence 1499, Ap
C 107	75.5	8.0	818128	3	US-09-949-016-14560	Sequence 14560, A	180	72.5	7.7	2382	3	US-09-877-730-27	Sequence 27, Appli
C 108	75.5	8.0	818128	3	US-09-949-016-14561	Sequence 14561, A	181	72.5	7.7	2952	3	US-09-134-001C-977	Sequence 977, App
C 109	75.5	8.0	818128	3	US-09-949-016-14562	Sequence 14562, A	182	72.5	7.7	2976	3	US-09-877-730-11	Sequence 11, Appli
C 110	75.5	8.0	818128	3	US-09-949-016-14564	Sequence 14564, A	C 183	72.5	7.7	3207	3	US-09-710-279-3413	Sequence 3413, Ap
C 111	75.5	8.0	818128	3	US-09-949-016-14565	Sequence 14565, A	184	72.5	7.7	3210	3	US-09-877-730-1	Sequence 1, Appli
C 112	75.5	8.0	818128	3	US-09-949-016-14566	Sequence 14566, A	185	72.5	7.7	3219	3	US-09-877-730-17	Sequence 17, Appli
C 113	75.5	8.0	818128	3	US-09-949-016-14567	Sequence 14567, A	186	72.5	7.7	3453	3	US-09-877-730-7	Sequence 7, Appli
C 114	75	7.9	486	3	US-09-248-796A-13914	Sequence 13914, A	187	72.5	7.7	3874	3	US-09-877-730-31	Sequence 31, Appli
C 115	75	7.9	999	3	US-09-248-796A-12164	Sequence 12164, A	188	72.5	7.7	5534	3	US-09-949-016-15256	Sequence 15256, A
C 116	75	7.9	1730	3	US-09-672-785-3	Sequence 3, Appli	189	72.5	7.7	20923	3	US-09-949-016-14335	Sequence 14335, A
C 117	75	7.9	1758	3	US-09-107-532A-472	Sequence 472, App	190	72.5	7.7	24912	3	US-09-949-016-11889	Sequence 11889, A
C 118	75	7.9	7963	3	US-08-956-171E-168	Sequence 168, App	C 191	72.5	7.7	75799	3	US-09-949-016-15231	Sequence 15231, A
C 119	75	7.9	7963	3	US-08-781-986A-168	Sequence 168, App	C 192	72.5	7.7	116966	3	US-09-949-016-17557	Sequence 17557, A
C 120	75	7.9	150597	3	US-09-949-016-15379	Sequence 15379, A	C 193	72.5	7.7	131631	3	US-09-949-016-11757	Sequence 11757, A
C 121	74.5	7.9	1194	3	US-09-270-767-13527	Sequence 13527, A	194	72.5	7.7	227750	3	US-09-949-016-17175	Sequence 17175, A
C 122	74.5	7.9	206433	3	US-09-949-016-13527	Sequence 13527, A	195	72	7.6	471	3	US-08-982-285-15	Sequence 15, Appli
C 123	74.5	7.9	228896	3	US-09-949-016-17127	Sequence 17127, A	196	72	7.6	480	3	US-09-621-976-8543	Sequence 8543, Ap
C 124	74.5	7.9	239815	3	US-09-949-016-16274	Sequence 16274, A	197	72	7.6	673	3	US-09-533-559-5730	Sequence 5730, Ap
C 125	74.5	7.9	254778	3	US-09-949-016-12417	Sequence 12417, A	198	72	7.6	1029	3	US-09-543-681A-959	Sequence 959, App
C 126	74	7.8	471	3	US-08-982-285-16	Sequence 16, Appli	199	72	7.6	1560	3	US-09-248-796A-4631	Sequence 4631, Ap
C 127	74	7.8	1812	3	US-09-248-796A-637	Sequence 637, App	200	72	7.6	2304	3	US-09-543-681A-2296	Sequence 2296, Ap
C 128	74	7.8	2757	3	US-09-248-796A-4868	Sequence 4868, Ap	201	72	7.6	2817	6	PCT-US93-05944-1	Sequence 1, Appli
C 129	74	7.8	3697	2	US-08-571-758-1	Sequence 1, Appli	202	72	7.6	4358	3	US-09-308-953-1	Sequence 1, Appli
C 130	74	7.8	3697	2	US-08-909-984A-1	Sequence 1, Appli	203	72	7.6	4434	3	US-09-710-279-3737	Sequence 3737, Ap
C 131	74	7.8	3697	2	US-08-909-983-1	Sequence 1, Appli	204	72	7.6	11559	3	US-10-025-225-3	Sequence 3, Appli
C 132	73.5	7.8	893	3	US-09-863-677B-1	Sequence 1, Appli	205	72	7.6	13758	3	US-10-025-225-5	Sequence 5, Appli
C 133	73.5	7.8	1065	3	US-09-328-352-3136	Sequence 3136, Ap	206	72	7.6	13767	3	US-10-025-225-1	Sequence 1, Appli
C 134	73.5	7.8	1101	3	US-09-248-796A-1389	Sequence 1389, Ap	207	72	7.6	13770	3	US-10-025-225-1	Sequence 1, Appli
C 135	73.5	7.8	1102	3	US-09-016-434-1131	Sequence 1131, App	C 208	72	7.6	24459	3	US-09-902-540-5004	Sequence 5004, Ap
C 136	73.5	7.8	1102	3	US-09-023-655-943	Sequence 943, App	209	72	7.6	32241	3	US-09-902-540-1247	Sequence 1247, Ap
C 137	73.5	7.8	1102	3	US-09-949-016-224	Sequence 224, App	C 210	72	7.6	44248	3	US-09-949-016-11829	Sequence 11829, A
C 138	73.5	7.8	1104	3	US-09-949-016-4635	Sequence 4635, Ap	C 211	72	7.6	44249	3	US-09-949-016-14491	Sequence 14491, A
C 139	73.5	7.8	1120	3	US-08-884-324-2	Sequence 2, Appli	C 212	72	7.6	126200	3	US-09-949-016-11824	Sequence 11824, A
C 140	73.5	7.8	1120	3	US-08-832-180-6	Sequence 2, Appli	C 213	72	7.6	126200	3	US-09-949-016-13193	Sequence 13193, A
C 141	73.5	7.8	1120	3	US-09-479-862-2	Sequence 2, Appli	C 214	72	7.6	126200	3	US-09-533-559-7121	Sequence 7121, Ap
C 142	73.5	7.8	1796	3	US-09-270-767-30632	Sequence 30632, A	215	71.5	7.6	705	3	US-09-543-681A-103	Sequence 103, App
C 143	73.5	7.8	1800	3	US-09-513-878-1	Sequence 1, Appli	216	71.5	7.6	741	3	US-09-248-796A-103	Sequence 103, App
C 144	73.5	7.8	1810	2	US-07-755-573C-7	Sequence 7, Appli	C 217	71.5	7.6	910	3	US-09-221-017B-712	Sequence 712, App
C 145	73.5	7.8	2307	3	US-09-792-024-43	Sequence 43, Appli	218	71.5	7.6	969	3	US-09-248-796A-1829	Sequence 1829, Ap
C 146	73.5	7.8	2351	3	US-09-270-767-14459	Sequence 14459, A	219	71.5	7.6	2436	3	US-09-248-796A-5862	Sequence 5862, Ap
C 147	73.5	7.8	2422	3	US-09-949-016-3805	Sequence 3805, Ap	220	71.5	7.6	2471	3	US-09-915-060A-3	Sequence 3, Appli
C 148	73.5	7.8	2490	3	US-09-487-558B-323	Sequence 323, App	221	71.5	7.6	2785	3	US-10-104-047-354	Sequence 354, App
C 149	73.5	7.8	2998	3	US-10-104-047-448	Sequence 448, App	222	71.5	7.6	35837	3	US-09-949-016-15232	Sequence 15232, A
C 150	73.5	7.8	4836	3	US-09-799-451-519	Sequence 519, App	C 223	71.5	7.6	81681	3	US-09-949-016-13274	Sequence 13274, A
C 151	73.5	7.8	1830121	3	US-09-557-884-1	Sequence 1, Appli	C 224	71.5	7.6	86936	3	US-09-949-016-17314	Sequence 17314, A
C 152	73.5	7.8	1830121	3	US-09-643-990A-1	Sequence 1, Appli	225	71.5	7.6	152655	3	US-09-949-016-16246	Sequence 16246, A
C 153	73.5	7.8	1830121	3	US-10-158-865-1	Sequence 1, Appli	C 226	71.5	7.6	421491	3	US-09-949-016-12805	Sequence 12805, A
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375	69	7.3	570	3	US-08-982-285-26	Sequence 26, Appl	448	68.5	7.2	8310	3	US-09-445-247-11	Sequence 11, Appl
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ALIGNMENTS

RESULT 1

US-09-697-863A-1
; Sequence 1, Application US/09697863A
; Patent No. 6812203
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut Voor Biotechnologie VZW
; TITLE OF INVENTION: CD-40 INTERACTING AND TRAP-INTERACTING PROTEINS
; FILE REFERENCE: 2676-4555US
; CURRENT APPLICATION NUMBER: US/09/697,863A
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: PCT/EP99/03025
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EPO 98201392.2
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1

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; LOCATION: (1627)..(1627)
; OTHER INFORMATION: N stands for any nucleotide.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1108)
; OTHER INFORMATION:
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; NAME/KEY: misc feature
; LOCATION: (1849)..(1849)
; OTHER INFORMATION: N stands for any nucleotide.
; US-09-697-863A-1

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; Sequence 889, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
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; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Felyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_fl_genes version 1.0
; SEQ ID NO 889
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(1127)
; US-09-620-312D-889

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Score: 945.00 Matches: 183
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; Sequence 3, Application US/09697863A
; Patent No. 6812203
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut Voor Biotechnologie VZW
; TITLE OF INVENTION: CD-40 INTERACTING AND TRAP-INTERACTING PROTEINS
; FILE REFERENCE: 2676-4555US
; CURRENT APPLICATION NUMBER: US/09/697, 863A
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: PCT/EP99/03025
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EPO 98201392.2
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
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; ORGANISM: Mus musculus
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; NAME/KEY: CDS
; LOCATION: (122)..(1234)
; OTHER INFORMATION:
US-09-697-863A-3

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Query Match: 65.98% Indels: 1
DB: 3 Gaps: 1

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; Patent No. 6365348
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
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; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.450C1
; CURRENT APPLICATION NUMBER: US/09/118,554A
; CURRENT FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 08/988,255
; EARLIER FILING DATE: 1997-12-24
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Query Match: 55.56% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x US-09-118-554-63 (1-1079)
```

```
Qy 83 ValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIlePro 102
Db 1077 GTGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATATTTCACAGGAAGTTATTCCTC 1018
Qy 103 ProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGlyHisGlu 122
Db 1017 CCATATTATAGCTACTTAAGAGAGATCAAGTAATTATGAGATTATTACAGTCAATGAA 958
Qy 123 GluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGlnGlu 142
Db 957 GAAGGATATTTCCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAGAGCCAGAG 898
Qy 143 IleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAenVal 162
Db 897 ATTAATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTAATG 838
Qy 163 SerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAla 182
Db 837 TCAGGAATGAGCTTTTGCCTTATGACATCCCATTTTGGAGAGCACCAGAGGGCATGCTCG 778
Qy 183 Glu 183
Db 777 GAA 775
```

RESULT 5

US-09-118-627-63/c
; Sequence 63, Application US/09118627A
; Patent No. 6379951
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF BREAST CANCER
; FILE REFERENCE: 210121.446C1
; CURRENT APPLICATION NUMBER: US/09/118,627A
; CURRENT FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 1079
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-118-627-63

Alignment Scores: 2,21e-60 Length: 1079
Pred. No.: 525.00 Matches: 101
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 55.56% Gaps: 0
DB:

US-10-757-745-2_COPY_54_236 (1-183) x US-09-118-627-63 (1-1079)

QY 83 ValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIlePro 102
DB 1077 GTGTGTTCTTACAGTATATGTTGACAGCCAGATGATATTTCTACAGGAAGTTATTC 1018
QY 103 ProTyrTyrSerTyrLeuLysArgSerSerAsnTyrGluIleIleThrGlyHisGlu 122
DB 1017 CCATATTATAGCTACCTTAAGAGAGATCAAGTAATATGAGATTATTCAGGTCAATGAA 958
QY 123 GluGlyTyrPheThrAlaIleMetLeuLysSerArgValIlePheLeuGlnGlu 142
DB 957 GAAGGATATTTTACAGCTATAATGTTGAAGAAATCAAGAGTGAATATAAAGCCCAAGAG 898
QY 143 IleIleProPheProSerThrLysMetMetArgAsnLeuLysValHisValAsnVal 162
DB 897 ATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGCAATGGAATGTG 838
QY 163 SerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAla 182
DB 837 TCAGGAATGAGCTTTGCCTTATGACATCCCATTTGGAGAGACCAGAGGGCATGCTGCG 778
QY 183 Glu 183
DB 777 GAA 775

RESULT 6

US-09-602-877A-63/c
; Sequence 63, Application US/09602877A
; Patent No. 6432707
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.446C5
; CURRENT APPLICATION NUMBER: US/09/602,877A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 1079
; TYPE: DNA
; ORGANISM: Homo sapien

US-09-602-877A-63

Alignment Scores: 2,21e-60 Length: 1079
Pred. No.: 525.00 Matches: 101
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 55.56% Gaps: 0
DB:

US-10-757-745-2_COPY_54_236 (1-183) x US-09-602-877A-63 (1-1079)

QY 83 ValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIlePro 102
DB 1077 GTGTGTTCTTACAGTATATGTTGACAGCCAGATGATATTTCTACAGGAAGTTATTC 1018
QY 103 ProTyrTyrSerTyrLeuLysArgSerSerAsnTyrGluIleIleThrGlyHisGlu 122
DB 1017 CCATATTATAGCTACCTTAAGAGAGATCAAGTAATATGAGATTATTCAGGTCAATGAA 958
QY 123 GluGlyTyrPheThrAlaIleMetLeuLysValSerArgValIleLeuLysSerGlnGlu 142
DB 957 GAAGGATATTTTACAGCTATAATGTTGAAGAAATCAAGAGTGAATATAAAGCCCAAGAG 898
QY 143 IleIleProPheProSerThrLysMetMetArgAsnLeuLysValHisValAsnVal 162
DB 897 ATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGCAATGGAATGTG 838
QY 163 SerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAla 182
DB 837 TCAGGAATGAGCTTTGCCTTATGACATCCCATTTGGAGAGACCAGAGGGCATGCTGCG 778
QY 183 Glu 183
DB 777 GAA 775

RESULT 7

US-09-621-976-8403
; Sequence 8403, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8403
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8403

Alignment Scores: 4,55e-10 Length: 379
Pred. No.: 145.00 Matches: 28
Score: 100.00% Conservative: 1
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 96.55% Indels: 0
Query Match: 15.34% Gaps: 0
DB:

US-10-757-745-2_COPY_54_236 (1-183) x US-09-621-976-8403 (1-379)

QY 2 GluArgAlaLeuAsnSerTyrPheGluProValGluSerAlaLeuGluArgArg 21
DB 19 CAGAGGGCTCTGAACCTCTACTCTCGAGCCCTCCGCTGGAGAGAGCCCTTGGAAACCCGA 78
QY 22 ProGluThrIleSerGluProLysThr 30
DB 79 CCTGAAACCATCTCTGAGCCCAAGACC 105


```
Db 269 GAGGCCCGCCGCTGTATGAGACCCCGCCAGATCAGAAACC----- 310
Qy 46 LysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThr 65
Db 311 -----TCACCCAGT-----GSCAAACCTGCCACACTCAAGATCTGCTCT 349
Qy 66 TrpAsnIleAspGlyLeu-----AspLeuAsnLeuSerGlu 78
Db 350 TGGAAATGGATGGGCTTCGAGCCTGGATTAGAGAAAGAGATTAGATTGGGTAAGGAA 409
Qy 79 ArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGln 98
Db 410 GAGGCC-----CAGATATACCTGTGCCTTCA 436
Qy 99 GluVal-----IleProProTyrTyrSerTyrLeuLysLysArgSer 112
Db 437 GAGACCAAAATGTTACAGAACAACTACCAGCTGAACCTCAGGAGCTGCCTGGACTCTCT 496
Qy 113 SerAsnTyrGluIleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLys 132
Db 497 CATCAATACTGCTCAGCTCCTTCGGACAAGGAGGGTACTAGCAACTAACCATCGTTAAA 556
Qy 133 LysSerArgValLysLeuLysSerGlnGluIle 143
Db 557 AGGCTTTAGTCAGAAATTCAAAACAAACATT 589

RESULT 12
US-10-101-464A-881
; Sequence 881, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 881
; LENGTH: 2637
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-101-464A-881

Alignment Scores:
Pred. No.: 1.26 Length: 2637
Score: 84.50 Matches: 35
Percent Similarity: 42.62% Conservative: 17
Best Local Similarity: 28.63% Mismatches: 45
Query Match: 8.94% Indels: 25
DB: 3 Gaps: 6

US-10-757-745-2_COPY_54_236 (1-183) x US-10-101-464A-881 (1-2637)
Qy 32 ValAspLeuThrAsnGluThrThrAspSerThrThrSerLysIleSerProSerGlu 51
Db 1381 CTTGATTATTCAAAATAACAAATTTGACTGGATCTCTCCCGCTTAGTATAAGTCACATAG 1440
Qy 52 AspThrGlnGln-----GluAsnGlySerMetPhe----- 61
Db 1441 GATTTACAAGAACTAGATCTATATAATAATATTTTGGCACTATACCAATACAAATT 1500
```

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Qy 62 SerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSer-----Glu 78
Db 1501 AGTTTGATCTTCCCTTCAGATTTTATAGATTATCAAGAACAAATTTAGATGGATCAATCCCT 1560
Qy 79 ArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGln 98
Db 1561 GAACCTTAATGGTAGTCTCCAGTTAAAGTTTTTCTCTGTTCACTATAAATTAACCTTTT 1620
Qy 99 GluValIleProProTyrTyrSer-----TyrLeuLysLysArgSer 112
Db 1621 GGGACTTTGGCAATGTTTTTGGCTAAATGTATTGAAATTCAGTATTATAGATTTAAGAAAA 1680
Qy 113 SerAsnTyrGluIleIleThrGlyHisGluGluGlyTyr-----PheThrAlaIle 129
Db 1681 AACAAAT-----TTGACAGGGCACCTTCCTCCTCATTATTGAAATCTTTTTCAGAATTG 1731
Qy 130 MetLeu 131
Db 1732 TTAATT 1737

RESULT 13
US-09-949-016-14608
; Sequence 14608, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14608
; LENGTH: 256287
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc_feature
; LOCATION: (1)...(256287)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14608

Alignment Scores:
Pred. No.: 1.6e+03 Length: 256287
Score: 84.50 Matches: 49
Percent Similarity: 40.18% Conservative: 39
Best Local Similarity: 22.37% Mismatches: 74
Query Match: 8.94% Indels: 57
DB: 3 Gaps: 12

US-10-757-745-2_COPY_54_236 (1-183) x US-09-949-016-14608 (1-256287)
Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProPro-----ValGluGluSerAla 17
Db 45817 TTAAGGGAGCTCTAAATCTTGAATAAACCCTCAAAAATACACCAAAATAGAACCTCC 45876
Qy 18 LeuGluArgArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGlu 37
Db 45877 ATAAAGCATAAACCTCAC-----AGGACCTATATAACAATAACAATA 45921
Qy 38 Glu-----ThrThrAspSerThrThrSerLysIleSerProSerGluAspThr 53
Db 45922 AAAAAAAGTATTTAGTCAACAAATAGTAAGATGAATAGGATAGTACCTCAC----- 45972
Qy 54 GlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeu 73
```



```
Db 376 ATGTTCTCA-----GGTGAGAGATCAACCGCAGCGACCGC 414
Qy 80 AlaArgGlyValCysSerTyrLeuAlaLeu-----TyrSerProAspValle 95
Db 415 GCG-----GTACTGACGTCGCGCTGGTAAACCGCAGCAATACCGCGATGTGGTT 465
Qy 96 PheLeuGlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyr 115
Db 466 GATGCCAAAGATGTGATGCCGGAAGTGAACGCTGTGCTGGAGAAGATGAACACCTTCTCC 525
Qy 116 Glu-----IleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSer 134
Db 526 GAAGCGATATCTCCGCTAGCTGGAAAGCTACACCGCGCAACCGATCACCGCGTGGTT 585
Qy 135 ArgValLysLeuLysSerGlnGluIleIleProPheProSerThrLysMetMetArg--- 153
Db 586 AACATCGGCATCGCGGCGTCCGACCTCTTTCATGGTGACCGAGCGCTGCGTCCG 645
Qy 154 -----AsnLeuLeuCysValHisVal-----AsnValSerGlyAsnGluLeu 167
Db 646 TATAAAACACCACTCAACATGCATTTGTCTCTAACTGATGGCACCCATATC 699
```

RESULT 16

```
; Sequence 26, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
```

```
; COMPUTER: HP Vectra 486/33
```

```
; OPERATING SYSTEM: MSDOS version 6.2
```

```
; SOFTWARE: ASCII Text
```

```
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/08/961,527
```

```
; FILING DATE:
```

```
; CLASSIFICATION: 424
```

```
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER:
```

```
; FILING DATE:
```

```
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Brookes, A. Anders
```

```
; REGISTRATION NUMBER: 36,373
```

```
; REFERENCE/DOCKET NUMBER: PB340P1
```

```
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: (301) 309-8504
```

```
; TELEFAX: (301) 309-8512
```

```
; INFORMATION FOR SEQ ID NO: 26:
```

```
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 15213 base pairs
```

```
; TYPE: nucleic acid
```

```
; STRANDEDNESS: double
```

```
; TOPOLOGY: linear
```

```
US-08-961-527-26
```

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Alignment Scores:
Pred. No.: 42.1 Length: 15213
Score: 82.00 Matches: 42
Percent Similarity: 42.20% Conservative: 31
Best Local Similarity: 24.28% Mismatches: 44
Query Match: 8.68% Indels: 56
DB: 3 Gaps: 8
```

```
US-10-757-745-2_COPY_54_236 (1-183) x US-08-961-527-26 (1-15213)
Qy 10 GluProProValGluGluSerAlaLeuGluArgArgProGluThrIleSerGluProLys 29
Db 3550 AAACCCACGAGTTGAAGATCAATCAACCGAAACGAAACGGAACGCAACAAACCGAA 3491
Qy 30 ThrTyrValAspLeuThrAsnGluGlu----- 38
Db 3490 AATTCAGTAATCAACATCAGAGATGGCAACAGACAGACCAACCATCAACCGAAAT 3431
Qy 39 -----ThrThrAspSerThrThrSerLysIleSerProSerGluAspThr 53
Db 3430 TCAACTCAGGATGTTTCAACCGAATCAACACATCCCAATTCAAAATGGAACGAAAGAAATT 3371
Qy 54 GlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAsp----- 69
Db 3370 AAACAAGANAAT-----GAACTAGACCCCTGATATAAAAG 3338
Qy 70 -----GlyLeuAspLeuAsnLeuSerGluArgAlaArgGlyVal 83
Db 3337 GTAGAAGACACGAGAGAAACACTTGAATTAAAGAAATGTTCCGAC----- 3293
Qy 84 CysSerTyrLeuAlaLeuTyrSer-----ProAspValIlePheLeu 97
Db 3292 -----CTAGAGTTTATACAGTTTGTCAAAATGGTACTTATAAACAACACATTCGTGA 3242
Qy 98 GlnGluVal-----IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGlu 116
Db 3241 GAGCAAGTTCACGAATCCAAATAGCTACTTTGTTAAAGTGAATCTTCTTCATTCAAA 3182
Qy 117 -----IleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeu 131
Db 3181 GATGTATACCTACCAGTAGCATCAATATCAGAGGAGAGAAAATGATAAAATCCTTTAT 3122
Qy 132 Lys---LysSerArgValLysLeuLysSerGlnGluIle 143
Db 3121 AAAATCAGCAAAAGTAGAGAGCTTCAGCAGGAGATA 3083
```

RESULT 17

```
US-09-596-002-41
```

```
; Sequence 41, Application US/09596002
```

```
; Patent No. 6632636
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Lagace, Robert, E.
```

```
; APPLICANT: Patterson, Chandra
```

```
; APPLICANT: Berg, Kim, L.
```

```
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
```

```
; FILE REFERENCE: PM-0008-4 US
```

```
; CURRENT APPLICATION NUMBER: US/09/596,002
```

```
; CURRENT FILING DATE: 2000-06-16
```

```
; PRIOR APPLICATION NUMBER: 60/140,121
```

```
; PRIOR FILING DATE: 1999-06-18
```

```
; NUMBER OF SEQ ID NOS: 41
```

```
; SOFTWARE: PERL Program
```

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; SEQ ID NO 41
```

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; LENGTH: 269223
```

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; TYPE: DNA
```

```
; ORGANISM: Moraxella catarrhalis
```

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; FEATURE:
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```
; NAME/KEY: misc feature
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; OTHER INFORMATION: Incyte template ID No. 6632636 41
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; PUBLICATION INFORMATION:
```

```
US-09-596-002-41
```

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Alignment Scores:
Pred. No.: 3.75e+03 Length: 269223
Score: 82.00 Matches: 29
Percent Similarity: 47.58% Conservative: 30
Best Local Similarity: 23.39% Mismatches: 31
Query Match: 6.68% Indels: 34
DB: 3 Gaps: 7
```

```
US-10-757-745-2_COPY_54_236 (1-183) x US-09-596-002-41 (1-269223)
```

Qy 61 PheSerLeuIleThrTrpAsnIleAepGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 234910 TTTTCGGTACTGACC-----GATGGCTT-----TTGCGGAGCGTGAG 234948
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 234949 CAAGGCATC-----ACCATGATGTGGCGTAT----- 234975
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArg-----SerSerAsnTyr 115
Db 234976 -----CGCTACTTCTCGACAGCCAGCGTAATTCATTCATTCGCCACACGCCAGCGCAT 235029
Qy 116 Glu-----IleIleThrGlyHisGluGluGluGlyTyrPheThrAlaIleMet 130
Db 235030 GAGCAGTATACAGCGCAATATGGTTACTGGTGCCCTCAACCGCTCATGCGCGGTGGTACTC 235089
Qy 131 LeuLysLysSerArgValLysLeuLysSerGlnGluIleIleProPheProSerThrLys 150
Db 235090 ATTGATGCATCAGCATGATTGTTTGGACCAAGCTGGAAGTTTGGCTTTTACCACAACTAAG 235149
Qy 151 -----MetMetArgAsnLeuLeuCysValHisValAsnValSerGlyAsnGlu 166
Db 235150 CGGCATTACGCCCATCTTAAAGCATTTACGCTCTCTCATATTATCGTGGCGATTATAAG 235209
Qy 167 LeuCysLeuMet 170
Db 235210 ATGGATTATTG 235221
RESULT 18
US-09-533-559-7228
; Sequence 7228, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rev
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849 200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7228
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(683)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-7228
Alignment Scores:
Pred. No.: 0.384 Length: 683
Score: 81.50 Matches: 33
Percent Similarity: 45.45% Conservative: 17
Best Local Similarity: 30.00% Mismatches: 35
Query Match: 8.62% Indels: 25
DB: 3 Gaps: 6
US-10-757-745-2_COPY_54_236 (1-183) x US-09-533-559-7228 (1-683)
Qy 13 ValGluGluSerAlaLeuGluArg-----ProGluThrIleSerGluProLys 29
Db 129 ATCAAGGACACCGGACCTTTCGGAAGACGTCGGTGCCATGGAGCTTTGGAGAGCCCTTAT 188

Qy 30 ThrTyrValAspLeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSerPro 49
Db 189 ACCCAGACTTACTATGTTGTTTGGACCCGCAACATCTACTCGGTCTCCAAG---TCGCCA 245
Qy 50 Ser-----GluAspThrGlnGlnGluAsnGlySerMet-----PheSer 62
Db 246 TCCGCCCTCGGAAGCTCAGTAAGAATGATAATGATAGTCTAGCACCACACAGCTATTGCA 305
Qy 63 LeuIleThrTrpAsnIleAspGlyLeu-----Asp 72
Db 306 CTCATATACATGGAATATCGACTTCATGTTCCCTTCGTCGAGCCGCGCATGGACGCG 365
Qy 73 LeuAsnAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaIleTyrSerPro 92
Db 366 CTTGCACATCTGTACCACTCACGCGC-----CTTCTCCCTCTACATGTGCGCC 413
Qy 93 AspValIlePheLeuGlnGluValIlePro 102
Db 414 COTGTTATCTTTCTCCAAAGATGCACCCCT 443
RESULT 19
US-08-245-511-3
; Sequence 3, Application US/08245511
; Patent No. 5928900
; GENERAL INFORMATION:
; APPLICANT: Measure, H Robert
; APPLICANT: Pearce, Barbara J
; APPLICANT: Tuomanen, Elaine
; TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESS: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/245,511
; FILING DATE: 18-MAY-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/116,541
; FILING DATE: 01-SRP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-069 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 960 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; STRAIN: R6
; IMMEDIATE SOURCE:
; CLONE: SPUR42
; FEATURE:

```
; NAME/KEY: CDS
; LOCATION: 1..960
US-08-245-511-3

Alignment Scores:
Pred. No.: 0.654 Length: 960
Score: 81.50 Matches: 55
Percent Similarity: 38.05% Conservative: 31
Best Local Similarity: 24.34% Mismatches: 69
Query Match: 8.62% Indels: 71
DB: 2 Gaps: 10

US-10-757-745-2_COPY_54_236 (1-183) x US-08-245-511-3 (1-960)

Qy 15 GluSerAlaLeuGluArgProGluThrIleSerGluProLysThrTyr-----Val 32
Db 189 CAATCTGCAAGCAATTCCTCCAGAGTGGATCAGCTCTCACTCAACAGTTGATTAGTT 248
Qy 33 AspLeuThr-AenGluGluThrThrAspSerThrThrSerLysIleSer----- 48
Db 249 GACTTACTTTTCAACTTCGACTTCGACCAAGACTATTTCTCGTAGGCTCAGGAAGCTTG 308
Qy 49 -----ProSerGluAspThrGlnGlnGlu----- 56
Db 309 GTTAGCGATTTCAGTTAGAACAAAGCAACCAAGCAAGAAATCTTGCCTACTATATAA 368
Qy 57 -----AenGlySerMet---PheSerLeuIleThrTrpAsnIleAspG1 70
Db 369 TAAGGCTTACATGCTCTAATGGGAAGTATGGAATGCAGACAGCAGCTCAAACTACTATGG 428
Qy 70 yLeuAspLeuAenAenLeuSerGluArgAlaArgGlyValCysSerThrLeuAlaLeu-- 89
Db 429 TAAAGACCTCAATAATTTAAGT-----TTACCTCAGTTAGCTTGCT 470
Qy 90 -----Tyr-SerProAspValIlePheLeuGlnGluV 100
Db 471 GCCTGGAATGCTCAGGCACCAACCAATATGACCCCTATTACATCCAGAGCAGCCCA 530
Qy 100 alileProProTyrTyrSerThrLeuLys----- 109
Db 531 AGACCGCGAAACTTGGTCTTATCTGAAATGAAAAATCAAGGCTACATCTCTGCTGAACA 590
Qy 110 -----LysArgSerAenThrGluIleThrGlyHisGluGlyThrPheThrA 128
Db 591 GTATGAGAAAGCAGTCAATACCAACTTACTGGCTGATGAGTACAACTCTCAATCAGCAAG 650
Qy 128 laIleMetLeu-----LysLysSerArgValLysLeuLysSerg 141
Db 651 TAAATTACCTGCTTATACATGGATAATTACCTCAAGGAAGTCATCAATCAAGTTGAAGA 710
Qy 141 InGluIleIleProPheProSer-----ThrLysMetM 152
Db 711 AACAGGCTATACCTTACTCACAACCTGGGATGGATGCTTACACAAATGTAGACCAAGAGC 770
Qy 152 eArAsnLeuLeuCysValHisValAenValSerGlyAenGluLeuCysLeuMetThrs 172
Db 771 TCAAAAAC---ATCTGTGGGATATTACATATTTACATACAGCAAGTACGTTGCTTCCAGAC 827
Qy 172 erHisLeuGluSer 176
Db 828 TCAATTGCAAGTCTG 841

RESULT 20
US-08-600-993A-3
; Sequence 3, Application US/08600993A
; Patent No. 5981229
; GENERAL INFORMATION:
; APPLICANT: Measure, H Robert
; APPLICANT: Pearce, Barbara J
; APPLICANT: Tuomanen, Elaine
; TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
; TITLE OF INVENTION: CELLULAR VACCINES BASED THEREON
; NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,993A
FILING DATE: 1-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/245,511
FILING DATE: 18-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
STRAIN: R6
IMMEDIATE SOURCE:
CLONE: SPRU42
FEATURE:
NAME/KEY: CDS
LOCATION: 1..960
US-08-600-993A-3

Alignment Scores:
Pred. No.: 0.654 Length: 960
Score: 81.50 Matches: 55
Percent Similarity: 38.05% Conservative: 31
Best Local Similarity: 24.34% Mismatches: 69
Query Match: 8.62% Indels: 71
DB: 2 Gaps: 10

US-10-757-745-2_COPY_54_236 (1-183) x US-08-600-993A-3 (1-960)

Qy 15 GluSerAlaLeuGluArgProGluThrIleSerGluProLysThrTyr-----Val 32
Db 189 CAATCTGCAAGCAATTCCTCCAGAGTGGATCAGCTCTCACTCAACAGTTGATTAGTT 248
Qy 33 AspLeuThr-AenGluGluThrThrAspSerThrThrSerLysIleSer----- 48
Db 249 GACTTACTTTTCAACTTCGACTTCGACCAAGACTATTTCTCGTAGGCTCAGGAAGCTTG 308
Qy 49 -----ProSerGluAspThrGlnGlnGlu----- 56
Db 309 GTTAGCGATTTCAGTTAGAACAAAGCAACCAAGCAAGAAATCTTGCCTACTATATAA 368
Qy 57 -----AenGlySerMet---PheSerLeuIleThrTrpAsnIleAspG1 70
Db 369 TAAGGCTTACATGCTCTAATGGGAAGTATGGAATGCAGACAGCAGCTCAAACTACTATGG 428
Qy 70 yLeuAspLeuAenAenLeuSerGluArgAlaArgGlyValCysSerThrLeuAlaLeu-- 89
Db 429 TAAAGACCTCAATAATTTAAGT-----TTACCTCAGTTAGCTTGCT 470
Qy 90 -----Tyr-SerProAspValIlePheLeuGlnGluV 100
Db 471 GCCTGGAATGCTCAGGCACCAACCAATATGACCCCTATTACATCCAGAGCAGCCCA 530
Qy 100 alileProProTyrTyrSerThrLeuLys----- 109
Db 531 AGACCGCGAAACTTGGTCTTATCTGAAATGAAAAATCAAGGCTACATCTCTGCTGAACA 590
Qy 110 -----LysArgSerAenThrGluIleThrGlyHisGluGlyThrPheThrA 128
Db 591 GTATGAGAAAGCAGTCAATACCAACTTACTGGCTGATGAGTACAACTCTCAATCAGCAAG 650
Qy 128 laIleMetLeu-----LysLysSerArgValLysLeuLysSerg 141
Db 651 TAAATTACCTGCTTATACATGGATAATTACCTCAAGGAAGTCATCAATCAAGTTGAAGA 710
Qy 141 InGluIleIleProPheProSer-----ThrLysMetM 152
Db 711 AACAGGCTATACCTTACTCACAACCTGGGATGGATGCTTACACAAATGTAGACCAAGAGC 770
Qy 152 eArAsnLeuLeuCysValHisValAenValSerGlyAenGluLeuCysLeuMetThrs 172
Db 771 TCAAAAAC---ATCTGTGGGATATTACATATTTACATACAGCAAGTACGTTGCTTCCAGAC 827
Qy 172 erHisLeuGluSer 176
Db 828 TCAATTGCAAGTCTG 841
```

```
Db 369 TAAGGTTACATGCTTAATGGGAAGTATGAATGCAGACAGCAGCTCAAACTACTATGG 428
Qy 70 yLeuAepLeuAenAenSerGluAlaArgGlyValCysSerTyrLeuAlaLeu-- 89
Db 429 TAAAGACCTCAATAATTTAAGT-----TTACCTCAGTTAGCCTTGCT 470
Qy 90 -----Tyr-SerProAepValIlePheLeuGluGluV 100
Db 471 GGCTGGAATGCCTCAGGCACCAACCAATATGACCCCTATTACATCCAGAGACGCCA 530
Qy 100 alileProProTyrTyrSerTyrLeuLys----- 109
Db 531 AGACCCCGCAAACTTGCTTATCTGAATGAATGAATCAAGGCTACATCTCTGCTGAACA 590
Qy 110 -----LysArgSerSerAenTyrGluIleThrGlyHisGluGluGlyTyrPheThra 128
Db 591 GTATGAGAAAGCAGTCAATACACCAATTACTGATGGCTACAAAGTCTCAAAATCAGCAAG 650
Qy 128 laileMetLeu-----LysLysSerArgValLysLeuLysSerG 141
Db 651 TAATTACCTGCTTACATGGATTAATTACCTCAAGGAAGTCATCAATCAAGTTGAAGAAGA 710
Qy 141 lnGluIleIleProPheProSer-----ThrLysMetM 152
Db 711 AACAGGCTATACCTACTCACAACTGGGATGGATGCTACACAAATGTAGACCAAGAGC 770
Qy 152 etArgAenLeuLeuCysValHisValAenValSerGlyAenGluLeuCysLeuMetThrs 172
Db 771 TCAAAAAC---ATCTGTGGGATATTTACAATAACAGACGAATACGTTGCTTATCCAGACGA 827
Qy 172 erHisLeuGluSer 176
Db 828 TGAATTGCAAGTCG 841
```

RESULT 21

```
US-10-757-745-2_COPY_54_236 (1-183) x US-08-481-435-5 (1-2049)
Qy 15 GluSerAlaLeuGluArgArgProGluThrIleSerGluProLysThrTyr-----Val 32
Db 225 CAATCTGCAAGCAATTCCTCCAGGTGGATCAGCTCTCACTCAACAGTTGATTAAAGTT 284
Qy 33 AspLeuThr-AenGluGluThrThrAaspSerThrThrSerLysIleSer----- 48
Db 285 GACTTACTTTTCAACTTCGACTTCGACCCAGCAGACTATTTCTCGTAGGCTCAGGAAGCTTG 344
Qy 49 -----ProSerGluAaspThrGlnGlnGlu----- 56
Db 345 GTTAGCGATTGAGTGTAGAACAAACCAACCAAGCAAGAAATCTTGACCTACTATATAA 404
Qy 57 -----AsnGlySerMet---PheSerLeuIleThrTrpAsnIleAaspG 70
Db 405 TAAGGTCTACATGCTTAATGGGAAGTATGGAATGCAGACAGCAGCTCAAACTACTATGG 464
Qy 70 yLeuAepLeuAenAenSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeu-- 89
Db 465 TAAAGACCTCAATAATTTAAGT-----TTACCTCAGTTAGCCTTGCT 506
Qy 90 -----Tyr-SerProAepValIlePheLeuGluGluV 100
Db 507 GGCTGGAATGCCTCAGGCACCAACCAATATGACCCCTATTACATCCAGAGACGCCA 566
Qy 100 alileProProTyrTyrSerTyrLeuLys----- 109
Db 567 AGACCCCGCAAACTTGCTTATCTGAATGAATGAATCAAGGCTACATCTCTGCTGAACA 626
Qy 110 -----LysArgSerSerAenTyrGluIleThrGlyHisGluGluGlyTyrPheThra 128
Db 627 GTATGAGAAAGCAGTCAATACACCAATTACTGATGGCTACAAAGTCTCAAAATCAGCAAG 686
Qy 128 laileMetLeu-----LysLysSerArgValLysLeuLysSerG 141
Db 687 TAATTACCTGCTTACATGGATTAATTACCTCAAGGAAGTCATCAATCAAGTTGAAGAAGA 746
Qy 141 lnGluIleIleProPheProSer-----ThrLysMetM 152
Db 747 AACAGGCTATACCTACTCACAACTGGGATGGATGCTACACAAATGTAGACCAAGAGC 806
Qy 152 etArgAenLeuLeuCysValHisValAenValSerGlyAenGluLeuCysLeuMetThrs 172
```

```

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2049 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; STRAIN: PM 1
; IMMEDIATE SOURCE:
; LIBRARY: PCR cloning
; CLONE: PARC 0512 Soluble PBP 1A del 38
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2049
; NAME/KEY: mat_peptide
; LOCATION: 1..2046
US-08-481-435-5
```

```

Alignment Scores:
Pred. No.: 2,114 Length: 2049
Score: 81.50 Matches: 55
Percent Similarity: 38.05% Conservative: 31
Best Local Similarity: 24.34% Mismatches: 69
Query Match: 8.62% Indels: 71
DB: 3 Gaps: 10
```

US-08-481-435-5

```
Sequence 5, Application US/08481435
Patent No. 6027906
GENERAL INFORMATION:
APPLICANT: Balganes, Tanjore S
APPLICANT: Town, Christine
TITLE OF INVENTION: No. 6027906el Polypeptides
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-JUL-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IN 580/MAS/94
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9404072-2
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
```

```
Db      807 TCARAAAC---ATCTGTGGGATATTACAAATACAGCAAGTAACGTTGCTTATCCAGACGA 863
Qy      172 erHisLeuGluSer 176
      :: ::|||
Db      864 TGAATTGCAAGTCG 877

RESULT 22
US-10-101-464A-834
; Sequence 834, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1998-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 834
; LENGTH: 2604
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-101-464A-834

Alignment Scores:
Pred. No.:      3,11      Length:      2604
Score:          81.50     Matches:      34
Percent Similarity: 41.80% Conservative: 17
Best Local Similarity: 27.87% Mismatches: 46
Query Match:      8.62%  Indels:      25
DB:              3       Gaps:       6

US-10-757-745-2_COPY_54_236 (1-183) x US-10-101-464A-834 (1-2604)
Qy      32 ValAspLeuThrAsnGluGluThrThrAspSerThrSerLysIleSerProSerGlu 51
      ::|||::|||::|||::|||::|||::|||
Db      1299 CTTGATTTATCAATAACAAATTTGACTGGATCTCTCCCGCTTAGTATAAGTCACATAGAG 1358
Qy      52 AspThrGlnGln-----GluAsnGlySerMetPhe----- 61
      |||::|||::|||::|||::|||::|||
Db      1359 GATTTACAGAACTAGACTATATATAATAATAATATTTTGGCAGCTATACCCCAATACAATT 1418
Qy      62 SerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSer-----Glu 78
      |||||::|||::|||::|||::|||::|||
Db      1419 AGTTTGACTCTCCCTCAGATTTTAGATTTATCAAGAACAAATTTAGATGGATCAATCCCT 1478
Qy      79 ArgAlaAspGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGln 98
      |||||::|||::|||::|||::|||::|||
Db      1479 GAACITTAATGGTAGTGTGCCCGAGTAGTTTCTCTCTGTTCACACTAATAAACTTTCT 1538
Qy      99 GluValIleProProTyrTyrSer-----TyrIleuLysLysArgSer 112
      |||||::|||::|||::|||::|||::|||
Db      1539 GGGACTTTGGCCAATGTTTGGCTAATTTGTTAATTCAGTATTTAGATTTAAGAAAA 1598
Qy      113 SerAsnTyrGluIleThrGlyHisGluGluGlyTyr-----PheThrAlaIle 129
      ::|||::|||::|||::|||::|||::|||
Db      1599 AACAAT-----TTGACGGGCACCTTCCTCACTATTGAAATCTTTTTCAGAAATTG 1649
Qy      130 MetLeu 131
      ::|||::|||::|||::|||::|||::|||
Db      1650 TTAATT 1655
      ::|||::|||::|||::|||::|||::|||
```

```
RESULT 23
US-09-567-458A-3
; Sequence 3, Application US/09567458A
; Patent No. 6730305
; GENERAL INFORMATION:
; APPLICANT: Wertz, Gail
; APPLICANT: Lerch, Robert
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES ENCODING BOVINE RESPIRATORY SYNCYTIAL VIRUS
; TITLE OF INVENTION: IMMUNOGENIC PROTEINS
; FILE REFERENCE: UAB-11904/22
; CURRENT APPLICATION NUMBER: US/09/567,458A
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1899
; TYPE: DNA
; ORGANISM: Bovine respiratory syncytial virus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(257)
; OTHER INFORMATION: n is a, c, t, or g
US-09-567-458A-3

Alignment Scores:
Pred. No.:      2,22      Length:      1899
Score:          81.00     Matches:      38
Percent Similarity: 39.49% Conservative: 24
Best Local Similarity: 24.20% Mismatches: 61
Query Match:      8.57%  Indels:      34
DB:              3       Gaps:       6

US-10-757-745-2_COPY_54_236 (1-183) x US-09-567-458A-3 (1-1899)
Qy      29 LysThrTyrValAsp-----LeuThrAsnGluGluThrThrAspSerThrSer 45
      |||::|||::|||::|||::|||::|||
Db      599 AAGAACTATATAGACAAAGAGCTTCTACCTAAAGTTTAAACATCATGATTTGAGGATATCC 658
Qy      46 LysIleSerProSerGluAspThrGlnGlnGlnAsnGlySerMetPheSerLeuIleThr 65
      |||::|||::|||::|||::|||::|||
Db      659 AACATAGAAACTGTGTAGATATTCACACAAAAAAC----- 694
Qy      66 TrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArg----- 81
      |||::|||::|||::|||::|||::|||
Db      695 -----AATAGATTGTTAGAAATTGCTAGGGAATTTAGTGTA 730
Qy      82 -----GlyValCysSerTyrLeuAlaLeuTyr-----SerProAspValIlePhe 96
      |||::|||::|||::|||::|||::|||
Db      731 AATGCTGGTATTACCACACCCCTCAGTACATACATGTTGACCAATAGTGAATTACTATCA 790
Qy      97 LeuGlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGlu 116
      |||::|||::|||::|||::|||::|||
Db      791 CTAATTAATGATATGCTCTATACGAATGACCAAAAAAGCTAATGTCAGTAATGTTCAA 850
Qy      117 IleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSer----- 134
      |||::|||::|||::|||::|||::|||
Db      851 ATAGTC-----AGACACACAGATTATTCATTATGTCAGTGGTCAAGAGAGGTGATA 904
Qy      135 -----ArgValLysLeuLysSerGlnGluIleIleProPheProSerThrLysMetMet 152
      |||::|||::|||::|||::|||::|||
Db      905 GCTTATGTTGTACAAATTCCTATTATGAGAGTTATAGACACCCCTGTTGGAAACTACAC 964
Qy      153 ArgAsnLeuLeuCysValHisValAsnValSerGlyAsnGluLeuCysLeu 169
      ::|||::|||::|||::|||::|||::|||
Db      965 ACCTCTCCATTATGCACCACCTGATAATAAAGAGGGTCAAAACATCTGCTTA 1015

RESULT 24
US-09-134-001C-2093
; Sequence 2093, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
```


; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

```
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2093
; LENGTH: 2601
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2093
```

```
Alignment Scores:
Pred. No.: 3.62 Length: 2601
Score: 81.00 Matches: 37
Percent Similarity: 40.00% Conservative: 23
Best Local Similarity: 24.67% Mismatches: 56
Query Match: 8.57% Indels: 34
DB: 3 Gaps: 9
```

US-10-757-745-2_COPY_54_236 (1-183) x US-09-134-001C-2093 (1-2601)

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QY 29 LysThrTyrValAspLeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSer 48
DB 1372 AAGCGATACAT-----AATCAAGTTTCTATAACTCGGCTATACAAAGATCGTTA 1422
QY 49 ProSerGluAspThrGlnGlnAsnGlySerMetPheSerLeuIleThrTyrAsnIle 68
DB 1423 GTAAGAAGATGACCAACTAGATGACGAT-----CAACGATTAATTCGCGTGC 1476
QY 69 AspGlyLeuAspLeuAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeuAla 88
DB 1477 GATGAACAAGATAATACCCCTATGTATCAAAATTTTAAAGGA-----CTTAGT 1524
QY 89 LeuTyrSerProAspValIlePheLeuGlnGluValIleProTyrTyrSerTyrLeu 108
DB 1525 ATTACTCTAGT-----ATATTTCATCAACACATTTCTCGATTCTTATTATGAGCTTA 1578
QY 109 Lys-----LysArgSerSerAsnTyrGluIleIleThrGlyHisGlu--- 122
DB 1579 AAATTAATTAGCTGAAGATCTGTCAGTCGATACAGTCTACTAATGCTCGGAAAT 1638
QY 123 ---GluGlyTyrPheThrAla-----IleMetLeuLysLys----- 133
DB 1639 ATCGAGAGTCTGTTTCAGTAAATATTTAATGATGAAGATTATCAAAATTTTATTCCA 1698
QY 134 -----SerArgValLysLeuLysSerGlnGluIleIle-----Pro 145
DB 1699 TCTTATTTTAAAGAAAGTTAAGTCAGCGTGACATATATATTTATATAAAATCAACTCCA 1758
QY 146 PheProSerThrLysMetMetArgAsnLeu 155
DB 1759 CTACCAAGTGAAGAAAGTAACACAAACATTT 1788
```

RESULT 25

```
US-09-241-581B-5
; Sequence 5, Application US/09241581B
; Patent No. 6350859
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patricia L. Pabst
; STREET: 2800 One Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/241,581B
FILING DATE: 02-Feb-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT6620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
```

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 2032 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: misc. feature

LOCATION: 40..1926

OTHER INFORMATION: /Function = "Nucleotides 40 through 1926 encode the amino acid sequence for the Drosophila Melanogaster Scavenger Receptor Class CI."

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-241-581B-5

```
Alignment Scores:
Pred. No.: 3.36 Length: 2032
Score: 80.00 Matches: 40
Percent Similarity: 35.80% Conservative: 18
Best Local Similarity: 24.69% Mismatches: 48
Query Match: 8.47% Indels: 56
DB: 3 Gaps: 7
```

US-10-757-745-2_COPY_54_236 (1-183) x US-09-241-581B-5 (1-2032)

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QY 20 ArgArgProGluThrIleSer-----GluProLysThrTyrValAspLeuThrAsn 36
DB 1384 AAAAAACCGACAACAACTTCAACACGCGCAAGCCCAACCAACGACTTCAACACCA 1443
QY 37 GluGluThrThrAspSerThrThrSerLysIleSer----- 48
DB 1444 AAGTCTACAACCT---TCTACAACGCTCTACAACCTTCAACCAACCAACCAACTACA 1500
QY 49 -----ProSerGluAspThrGlnGln 55
DB 1501 ATAAATGTGTTTACAAACAAAGAAACAAATAATGATCCCTACTTCCAGTACCGAAAG 1560
QY 56 GluAsnGlySerMetPheSerLeu-----IleThrTrpAsnIleAspGly 70
DB 1561 ACTACAGGCATCATCACCACCATGAAGACACGCAAGCGCATCATCTTGGAACTGTGATCCT 1620
QY 71 LeuAspLeuAsnAsnLeuSerGluArgAlaArgGly-----ValCys 84
DB 1621 CAGGACATCAGGGTGCATGATGACACGAGCGGAAGTACCCCAATCAGCTTTAGTAGTA 1680
QY 85 SerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal----- 100
DB 1681 CTTTACTCTACTCGGCATTGTTCTGGTGGTAGTTCTGGCCCAACGCTGTAATCGCTGG 1740
QY 101 ---IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThr 119
DB 1741 ATAATACCA-----ATCACT 1755
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```
Qy 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysSerArgValLysLeuLys 139
Db 1756 GGATCAAGACGAGCAGGAAAGCGTGTGAGATTCAAGAGGCGATTTCGATAGTCTGAAG 1815
Qy 140 SerGln 141
Db 1816 AAGCAA 1821

RESULT 26
US-08-265-428-5
; Sequence 5, Application US/08265428
; Patent No. 6429289
; GENERAL INFORMATION:
; APPLICANT: Krieger, Monty
; TITLE OF INVENTION: Class BI Scavenger Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,428
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELEPHONE: (404) 815-6508
; TELEFAX: (404) 815-6555
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2032 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 40..1926
; OTHER INFORMATION: /Function = "Nucleotides 40 through 1926 encode the amino acid"
US-08-265-428-5

Alignment Scores:
Pred. No.: 3.36 Length: 2032
Score: 80.00 Matches: 40
Percent Similarity: 35.80% Conservative: 18
Best Local Similarity: 24.69% Mismatches: 48
Query Match: 8.47% Indels: 56
DB: Gaps: 7

US-10-757-745-2_COPY_54_236 (1-183) x US-08-265-428-5 (1-2032)

Qy 20 ArgArgProGluThrIleSer-----GluProLysThrTyrValAspLeuThrAsn 36
Db 1384 AAAAACCACCAACAACTTCAACACGCGGAGCCCAACACAGCACTTCAACACACCA 1443
Qy 37 GluGluThrThrAspSerThrThrSerLysIleSer----- 48
Db 1444 AAGTCTACAAC---TCTACAACGCTTCAACAAACACCAACCAACCAACTACA 1500
Qy 49 -----ProSerGluAspThrGln 55

Db 1501 ATAAATGTTTACAAACAAGAAAAACAATAATATGATCCCTACTTCCAGTACCGAAAAG 1560
Qy 56 GluAsnGlySerMetPheSerLeu-----IleThrTrpAsnIleAspGly 70
Db 1561 ACTACAGGCGATCATCACCACCATCAAGACACACGCAAGCGCATCACTTGGAACTGTGATCCT 1620
Qy 71 LeuAspLeuAsnLeuSerGluArgAlaArgGly-----ValCys 84
Db 1621 CAGGACATCGAGGTCACATGGACACGCGGAAAGTACCCCAATCCAGCTTTAGTAGTA 1680
Qy 85 SerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal----- 100
Db 1681 CTTTACCTGTACTCTCGCATTTGTTCTGTGTAGTCTTGGCCAACGTCGTTTAATCGCTGG 1740
Qy 101 ---IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThr 119
Db 1741 ATAATACCA-----ATCACT 1755
Qy 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLys 139
Db 1756 GGATCAAGACGAGCAGGAAAGCGTGTGAGATTCAAGAGGCGATTTCGATAGTCTGAAG 1815
Qy 140 SerGln 141
Db 1816 AAGCAA 1821

RESULT 27
PCT-US95-07721-5
; Sequence 5, Application PC/TUS9507721
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute of Technology
; TITLE OF INVENTION: Class BI and CI Scavenger Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07721
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: MIT6620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2032 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: 40..1926
; OTHER INFORMATION: /Function = "Nucleotides 40 through 1926 encode the amino acid sequence"
OTHER INFORMATION: 1926 encode the amino acid sequence
OTHER INFORMATION: for the Drosophila Melanogaster
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OTHER INFORMATION: Scavenger Receptor Class CI."

PCT-US95-07721-5

Alignment Scores: 3.36 Length: 2032
Pred. No.: 80.00 Matches: 40
Score: 80.00
Percent Similarity: 35.80% Conservative: 18
Best Local Similarity: 24.69% Mismatches: 48
Query Match: 8.47% Indels: 56
DB: Gaps: 7

US-10-757-745-2_COPY_54_236 (1-183) x PCT-US95-07721-5 (1-2032)

QY 20 ArgArgProGluThrIleSer-----GluProLysThrTyrValAspLeuThrAsn 36
Db 1384 AAAAAACCGACAACTTCAACACGCGGACCAACACACGACTTCAACACCA 1443
QY 37 GluGluThrThrAspSerThrSerLysIleSer----- 48
Db 1444 AGCTCTACACT---TCTACACGCTCTACACTTCAACACCAACGACCAACTACA 1500
QY 49 -----ProSerGluAspThrGlnGln 55
Db 1501 ATAAATGTGTTTACAAACAAAGAAACAAACAATAATGATCGCTACTTCCAGTACCGAAAG 1560
QY 56 GluAsnGlySerMetPheSerLeu-----IleThrTrpAsnIleAspGly 70
Db 1561 ACTACAGGCATCATCACCAACCATGAGACACGCAACGCGCATCATCTTGGAAACGTTGATCCT 1620
QY 71 LeuAspLeuAsnAsnLeuSerGluArgAlaArgGly-----ValCys 84
Db 1621 CAGGATCATCAGGGTCATGACGACAGCGGGAAGTACCCCAATCCAGCTTTAGTAGTA 1680
QY 85 SerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal----- 100
Db 1681 CTTTACCTGCTACTCGGCATGTTCTGGTGGTAGTTCTGGCCCAACGTTGTAATCGCTGG 1740
QY 101 ---IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleThr 119
Db 1741 ATAATACCA-----ATCACT 1755
QY 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLys 139
Db 1756 GGATCAAGACAGCAGCGAAAGGCTGTGAGATTCAAGAGGCATCGATAGTCTGAG 1815
QY 140 SerGln 141
Db 1816 AAGCAA 1821

RESULT 28

US-09-949-016-16603/c
; Sequence 16603, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16603
; LENGTH: 232547
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16603

Alignment Scores:

Pred. No.: 5.54e+03 Length: 232547
Score: 80.00 Matches: 39
Percent Similarity: 47.95% Conservative: 31
Best Local Similarity: 26.71% Mismatches: 60
Query Match: 8.47% Indels: 16
DB: Gaps: 5

US-10-757-745-2_COPY_54_236 (1-183) x US-09-949-016-16603 (1-232547)

QY 38 GluThrThrAspSerThr-ThrSerLysIleSerProSerGluAspThrGlnGln-GluA 57
Db 72006 GAAGAACTCCATCACTAACGAGCAAAATAACACGCCAACATCATATAATGACAGGATCAA 71947
QY 57 enGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuS 77
Db 71946 AT---TCACACATAACAATATTAACTTAAATGTAATGGA-----CTAAATTCCTCAA 71896
QY 77 erGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheL 97
Db 71895 TTAAAGAAACAGA---CTGGCAATTTGGATAAAGAGTCAAGACCCATCAGTGTGCTGTA 71839
QY 97 euGlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluI 117
Db 71838 TTCAGGA-----ACCATCTCAGTCGTCAGAGACACACATAGGCTCA 71797
QY 117 leileThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgVal 137
Db 71796 AATAAAAGGATGGAGGAGATCTACCAAGCAAAATGGAACAAACAAAAAGGCGGGTTG 71737
QY 137 ysLeuLysSerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeu 157
Db 71736 CAATCTCTCTCTGATAAAACAGACTTTAAACCAACAAAGATCAAAAGACAGCAAGAAT 71677
QY 157 ysValHisValAsnValSerGlyAsn-----GluLeuCysLeuMetThrSerH 173
Db 71676 GCATTCATATAATGGTAAAGGATCAATTCACAAAGAGAGCTAATATATCTAAATATAT 71617
QY 173 isLeuGluSerThr 177
Db 71616 ATGCACCAATACA 71603
RESULT 29
US-08-114-072-1
; Sequence 1, Application US/08114072
; Patent No. 5624823
; GENERAL INFORMATION:
; APPLICANT: Sachs, David,
; APPLICANT: Leguern, Christian,
; APPLICANT: Megan, Sykes,
; APPLICANT: Blancho, Gilles
; TITLE OF INVENTION: INTERLEUKIN-10 AND IMMUNOSUPPRESSION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/114,072
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965

```
; REFERENCE/DOCKET NUMBER: MGP-017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1365 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-114-072-1

Alignment Scores:
Pred. No.: 2.1 Length: 1365
Score: 79.50 Matches: 30
Percent Similarity: 42.20% Conservative: 16
Best Local Similarity: 27.52% Mismatches: 49
Query Match: 8.41% Indels: 14
DB: 2 Gaps: 3

US-10-757-745-2_COPY_54_236 (1-183) x US-08-114-072-1 (1-1365)
Qy 29 LysThrTyrValAspLeuThrAsnGluGluThrThr-----AspSerTh 43
Db 527 AAGCCATGGGTGAGTTTGACATCTTCATCAACTACATAGAACCTACATGACGATGAAGA 586
Qy 43 rThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLe 63
Db 587 TGAGGAAGAACTGAAGCATTTCTAGGGAACCAAGAAAAACCTTCCAGGATGACGACTCT 646
Qy 63 uIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArgGlyVa 83
Db 647 ACTAACTCTAGGATACAAATTTGGAGACTTTCAAAATCTGTCCAAGTTCCCGGGAGC 706
Qy 83 1-----CysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnG1 99
Db 707 AGAACCCAGCACCTGGGAACCTCTGCTACCTCTCCCTCGAGATATTTATTACCTCTGA 766
Qy 99 uValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleTh 119
Db 767 TACCTCAGCTCCCATTTCTATTATTATTTACCGAGCCTCTCTGTGAACATTATTTA----- 818
Qy 119 rGlyHisGluGluGlyTyrPheThr 127
Db 819 ----GAAGAAGAACAGTATTATACT 839

Search completed: December 4, 2005, 16:13:15
Job time : 451.302 secs

; REFERENCE/DOCKET NUMBER: MGP-017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1365 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-114-072-1

Alignment Scores:
Pred. No.: 2.1 Length: 1365
Score: 79.50 Matches: 30
Percent Similarity: 42.20% Conservative: 16
Best Local Similarity: 27.52% Mismatches: 49
Query Match: 8.41% Indels: 14
DB: 2 Gaps: 3

US-10-757-745-2_COPY_54_236 (1-183) x US-08-114-072-1 (1-1365)
Qy 29 LysThrTyrValAspLeuThrAsnGluGluThrThr-----AspSerTh 43
Db 527 AAGCCATGGGTGAGTTTGACATCTTCATCAACTACATAGAACCTACATGACGATGAAGA 586
Qy 43 rThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLe 63
Db 587 TGAGGAAGAACTGAAGCATTTCTAGGGAACCAAGAAAAACCTTCCAGGATGACGACTCT 646
Qy 63 uIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArgGlyVa 83
Db 647 ACTAACTCTAGGATACAAATTTGGAGACTTTCAAAATCTGTCCAAGTTCCCGGGAGC 706
Qy 83 1-----CysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnG1 99
Db 707 AGAACCCAGCACCTGGGAACCTCTGCTACCTCTCCCTCGAGATATTTATTACCTCTGA 766
Qy 99 uValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleTh 119
Db 767 TACCTCAGCTCCCATTTCTATTATTATTTACCGAGCCTCTCTGTGAACATTATTTA----- 818
Qy 119 rGlyHisGluGluGlyTyrPheThr 127
Db 819 ----GAAGAAGAACAGTATTATACT 839

RESULT 30
PCT-US94-09361-1
; Sequence 1, Application PC/TUS9409361
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: INTERLEUKIN-10 AND IMMUNOSUPPRESSION
; NUMBER OF SEQUENCES: 3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09361
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-017PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1365 base pairs
; TYPE: nucleic acid
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 00:41:46; Search time 3889.68 Seconds
(without alignments)
2201.217 Million cell updates/sec

Title: US-10-757-745-2_COPY_54_236

Perfect score: 945
Sequence: 1 MERNALSYFPPVPEESALER.....GNELCLMTSHLESTRGHAAE 183

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 500 summaries

Command line parameters:
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-DB=EST -OPWT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=500
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZES=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10757745 @CNC 1.1 8148 @runat_01122005_091749_10090 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOB=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hcc:*
5: gb_est4:*
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7: gb_est6:*
8: gb_est7:*
9: gb_gse1:*
10: gb_gse2:*
11: gb_gse3:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	945	100.0	583	BP262741	BP262741 BP262741
2	945	100.0	729	CN298922	CN298922 170006000
3	945	100.0	729	CN298924	CN298924 170004244
4	945	100.0	810	CX166335	CX166335 HESCC 39
5	945	100.0	870	BG740396	BG740396 602634171
6	945	100.0	870	BUI59911	BUI59911 AGENCOURT
7	945	100.0	883	BUI69945	BUI69945 AGENCOURT

8	945	100.0	883	5	BUI79107	BUI79107 AGENCOURT
9	945	100.0	948	1	AL555333	AL555333
10	945	100.0	972	3	BM468826	BM468826 AGENCOURT
11	945	100.0	981	5	BX338160	BX338160
12	945	100.0	1067	5	BX3337905	BX3337905
13	945	100.0	1081	5	BX444691	BX444691
14	945	100.0	1089	11	DQ049205	DQ049205 Homo sapi
15	945	100.0	1168	4	CR601303	CR601303 full-length
16	945	100.0	1192	3	BM553049	BM553049 AGENCOURT
17	945	100.0	1620	4	CR592636	CR592636 full-length
18	945	100.0	1894	4	CR597293	CR597293 full-length
19	945	100.0	1909	4	CR595644	CR595644 full-length
20	942	99.7	581	1	AV717253	AV717253 AV717253
21	940	99.5	1018	5	BX337141	BX337141
22	938	99.3	710	5	BUE61472	BUE61472 cl72d11.2
23	937	99.2	942	5	BX358707	BX358707 BX358707
24	937	99.2	1046	3	BM926092	BM926092 AGENCOURT
25	937	99.2	1743	4	CR602029	CR602029 full-length
26	936	99.0	767	2	B1258848	B1258848 602969663
27	936	99.0	783	5	BX365835	BX365835
28	934	98.8	701	7	CR767236	CR767236 DKF204698
29	934	98.8	846	7	CR765451	CR765451 DKF204698
30	933	98.7	780	5	BX374579	BX374579 BX374579
31	932	98.6	657	7	CN298920	CN298920 170006001
32	932	98.6	711	7	CN298923	CN298923 170006000
33	932	98.6	1103	3	BM555041	BM555041 AGENCOURT
34	926	98.0	932	2	BG740339	BG740339 602635289
35	925	97.9	904	5	BX422491	BX422491 BX422491
36	925	97.9	1035	3	BM554324	BM554324 AGENCOURT
37	923	97.7	704	3	B1334820	B1334820 602998939
38	922	97.6	1089	11	DQ049206	DQ049206 Pan trogl
39	920	97.4	906	6	CD251503	CD251503 AGENCOURT
40	914	96.7	570	3	BM172060	BM172060 imageqc_3
41	913	96.6	858	3	B1553412	B1553412 603153358
42	911	96.4	731	8	CR760857	CR760857 AGENCOURT
43	904	95.7	1097	7	CN641671	CN641671 ILLUMIGEN
44	903	95.6	927	2	BG119064	BG119064 602347589
45	899	95.1	634	6	CB157906	CB157906 K-EST0217
46	891	94.3	757	3	B1760756	B1760756 603044763
47	890	94.2	922	7	CN801806	CN801806 ILLUMIGEN
48	887	93.9	582	3	B2611141	B2611141 BP261141
49	886	93.8	838	3	B1908925	B1908925 603087028
50	883	93.4	581	3	BP270744	BP270744 BP270744
51	883	93.4	581	3	BP379659	BP379659 BP379659
52	880	93.1	739	7	CR791801	CR791801 DKF20468J
53	880	93.1	793	2	BG533717	BG533717 602562373
54	877	92.8	581	3	BP207751	BP207751 BP207751
55	873	92.4	573	3	BP261500	BP261500 BP261500
56	871	92.2	752	1	AU139147	AU139147 AU139147
57	866	91.6	774	3	B1754101	B1754101 603027659
58	860	91.0	584	3	BP263059	BP263059 BP263059
59	851	90.1	678	2	BG719113	BG719113 602699045
60	847	89.6	570	3	BP221518	BP221518 BP221518
61	845	89.4	573	3	BP221260	BP221260 BP221260
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373	153	16.2	582	3	BP194502	BP194502	BP194502	446	102	10.8	662	3	BJ524339	BJ524339
374	153	16.2	722	2	BF679649	BF679649	602154095	447	102	10.8	807	8	DR807624	ZM_BFB003
c 375	151.5	16.0	672	11	DE094838	DE094838	Oryzias 1	448	101	10.7	505	1	AV951030	AV951030
376	151	16.0	531	1	AA824213	AA824213	vy20h08.r	449	101	10.7	647	5	BW052866	BW052866
377	149.5	15.8	456	1	AA839622	AA839622	vy97e06.r	450	101	10.7	673	5	BW035002	BW035002
378	146	15.4	1030	5	BW235217	BW235217	603791177	451	101	10.7	696	5	BW031213	BW031213
c 379	145	15.3	537	7	CR774766	CR774766	DKFZP469A	452	100.5	10.6	572	3	BI406417	BI406417
380	145	15.3	637	2	BF471995	BF471995	UI-M-BH3-	453	100.5	10.6	602	8	DN743815	DN743815
381	144	15.2	570	6	CB188959	CB188959	ks27b06.y	454	100.5	10.6	691	7	CK852789	CK852789
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384	139.5	14.8	746	2	BF140146	BF140146	601786704	457	100.5	10.6	850	8	DN941734	DN941734
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389	136	14.4	833	2	BG573470	BG573470	602595261	462	99.5	10.5	781	8	DN743406	DN743406
390	135	14.3	464	5	BU788428	BU788428	il81g10.y	463	99	10.5	832	8	DN981091	DN981091
391	134	14.2	297	2	BP170990	BP170990	PCI1883.M	464	99	10.5	844	8	DN982112	DN982112
392	132	14.0	134	3	BU061261	BU061261		465	99	10.5	847	8	DN981552	DN981552
393	130	13.8	514	3	BP135431	BP135431		466	99	10.5	866	8	DN981303	DN981303
394	128	13.5	646	7	CO525830	CO525830	3530_1.17	c 467	98.5	10.4	853	9	BH525754	BH525754
395	128	13.5	723	7	CV740501	CV740501	SJAL_027	468	98	10.4	382	5	BY070423	BY070423
396	128	13.5	735	8	DR823742	DR823742	ZM_BFB006	469	98	10.4	595	7	CK555149	CK555149
397	128	13.5	738	8	DR817895	DR817895	ZM_BFB005	470	97.5	10.3	694	9	BZ015229	BZ015229
398	128	13.5	848	8	DR811846	DR811846		c 471	97.5	10.3	806	9	BH652666	BH652666
399	127.5	13.3	808	8	DN932266	DN932266	AGENCOURT	472	97.5	10.3	924	8	DR924013	DR924013
400	125.5	13.3	560	3	BI501881	BI501881	rm06c12.y	473	97	10.3	478	1	AA168965	AA168965
401	125	13.2	573	3	BP379251	BP379251		474	97	10.3	488	7	CK536224	CK536224
402	125	13.2	614	6	CB375256	CB375256	rw04e05.y	475	97	10.3	563	6	CD523817	CD523817
403	125	13.2	652	8	W02878	W02878	za06a07.r1	476	97	10.3	709	8	DR823929	DR823929
404	125	13.2	732	5	EX115672	EX115672		c 477	96.5	10.2	817	9	BH558616	BH558616
405	119.5	12.6	631	3	BM066897	BM066897	KS07019D1	478	96	10.2	707	5	BU418830	BU418830
c 406	119	12.6	781	7	CV480876	CV480876	AGENCOURT	479	96	10.2	729	8	DR704222	DR704222
407	118.5	12.5	354	2	BG949698	BG949698	RC4-BT062	480	96	10.2	736	8	DR967575	DR967575
408	118	12.5	655	8	CK034936	CK034936	1347507.N	c 481	96	10.2	835	8	DN941735	DN941735
409	117.5	12.4	559	3	BI747771	BI747771	rm44b05.y	c 482	95	10.1	198	1	AL869566	AL869566
410	115.5	12.2	532	6	CB387482	CB387482	OSTF081B1	483	95	10.1	529	9	B54478	B54478
c 411	115	12.2	517	11	DE122996	DE122996	Oryzias 1	484	95	10.1	686	7	CN789130	CN789130
412	112.5	11.9	1282	4	CNS0ADRP	CNS0ADRP		c 485	95	10.1	799	10	CZ280033	CZ280033
413	111.5	11.8	1464	4	CNS0AAVU	CNS0AAVU	Arabisdops	486	94.5	10.0	441	7	CN807482	CN807482
414	111	11.7	715	8	DR816705	DR816705	ZM_BFB004	c 487	94.5	10.0	510	9	BH900534	BH900534
415	111	11.7	741	7	CO517714	CO517714	3530_1.11	488	93.5	9.9	825	8	DR924567	DR924567
416	111	11.7	767	8	DR968669	DR968669	ZM_BFB009	489	93.5	9.9	874	8	DN982262	DN982262
417	111	11.7	786	7	CO523018	CO523018	3530_1.15	490	93.5	9.9	882	8	DR935568	DR935568
418	111	11.7	858	8	DR817985	DR817985	ZM_BFB005	491	93	9.8	506	3	BU417879	BU417879
419	111	11.7	1497	10	CL979153	CL979153	OBIFCC032	492	93	9.8	527	7	CK545252	CK545252
420	110.5	11.7	880	9	BH207435	BH207435	Sm1-45M4	493	93	9.8	536	3	BJ415166	BJ415166
421	109	11.5	431	7	CK695369	CK695369	ZF101-P00	494	93	9.8	653	7	CK543528	CK543528
c 422	107	11.3	672	1	AU500568	AU500568		495	93	9.8	777	8	DR912331	DR912331
423	106.5	11.3	566	6	CD472549	CD472549	na001-lms	c 496	92.5	9.8	545	9	BH900679	BH900679
424	106.5	11.3	1353	10	CL977639	CL977639	OBIFCC030	497	92.5	9.8	658	1	AW425258	AW425258
425	105	11.1	317	1	AV4113455	AV4113455	AV4113455	498	92.5	9.8	702	8	DR789922	DR789922
c 426	105	11.1	712	11	DE111858	DE111858	Oryzias 1	499	92	9.7	433	1	AJ398593	AJ398593
427	104.5	11.1	585	6	CB025685	CB025685	TgBST2yc8	500	92	9.7	581	7	CK515560	CK515560
428	104	11.0	311	7	CO539357	CO539357	ta131e04							
429	103.5	11.0	584	3	BU524578	BU524578								
c 430	103.5	11.0	596	9	BH650868	BH650868	BOMIG54TF							
431	103.5	11.0	651	5	BQ852542	BQ852542	QGB18E23							
432	103.5	11.0	711	5	BQ995001	BQ995001	QGRBM14.Y							
433	103	10.9	367	5	BY067359	BY067359								
434	103	10.9	522	3	BQ882055	BQ882055								
435	103	10.9	533	3	BQ006584	BQ006584								
436	103	10.9	540	3	BQ001515	BQ001515								
437	103	10.9	600	3	BQ009618	BQ009618								
438	103	10.9	615	3	BQ002736	BQ002736								
439	103	10.9	617	3	BQ003192	BQ003192								
440	103	10.9	633	3	BQ005134	BQ005134								
441	103	10.9	658	3	BQ010466	BQ010466								
442	103	10.9	676	3	BQ010795	BQ010795								
443	103	10.9	677	3	BJ705742	BJ705742								
444	103	10.9	677	3	BJ708643	BJ708643								
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ALIGNMENTS

RESULT 1	BP262741	BP262741	583 bp	mrna	linear	EST 16-SEP-2004
LOCUS	BP262741	BP262741	Sugano cDNA library,	small intestine	Homo sapiens	CDNA
DEFINITION	BP262741	BP262741	clone HS107919,	mrna	sequence.	
ACCESSION	BP262741	BP262741	GI:52177972			
VERSION	BP262741.1	BP262741.1				
KEYWORDS	EST.	EST.				
SOURCE	Homo sapiens	Homo sapiens				
ORGANISM	Homo sapiens	Homo sapiens				
	Eukaryota; Metazoa;	Eukaryota; Metazoa;				
	Mammalia; Eutheria;	Mammalia; Eutheria;				
	Chordata; Vertebrata;	Chordata; Vertebrata;				
	Primates; Catarrhini;	Primates; Catarrhini;				
REFERENCE	1	(bases 1 to 583)				

AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yszukui@ims.u-tokyo.ac.jp.

FEATURES
source
1..583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS107919"
/tissue type="small intestine"
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ORIGIN
Alignment Scores:
Pred. No.: 1.88e-105 Length: 583
Score: 945.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x BP262741 (1-583)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
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DB 30 ATGGAAGGGCTCTGAACCTCTTACCTCGAGCTCCGGTGGAGAGAGCCCTTGAACGC 89
|||||
QY 21 ArgProGluThrIleSerGluProLysTyrThrValAspLeuThrAsnGluThrThr 40
|||||
DB 90 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAAGAAACAAC 149
|||||
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
|||||
DB 150 GATTCACCACTTCTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGCGACATG 209
|||||
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
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DB 210 TTCTCTCTCATTACCTGGGAATATTGATGGATTAGATCTAAACAATCTGTGAGAGGGCT 269
|||||
QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
|||||
DB 270 CGAGGGGTGTCTCTACTAGCTTTGTACAGCCAGATGTGATATTCTACAGGAGTT 329
|||||
QY 101 IleProProTyrTyrSerTyrLeuLysArgSerSerAsnTyrGluIleIleThrGly 120
|||||
DB 330 ATTCCCCATATTATAGCTACCTAAAGAAGAGATCAAGTAATATTGAGATTATTACAGGT 389
|||||
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLysSer 140
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DB 390 CATGAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAAGAAAGC 449
|||||
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
|||||
DB 450 CAAGAGATTATTCCTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTG 509
|||||
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
|||||
DB 510 AATGTGTGAGAAATGAGCTNTGCCATTATGACATCCCATTTGGAGAGCCAGAGGGCAT 569
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QY 181 AlaAlaGlu 183
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DB 570 GCTGCGGAA 578
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RESULT 2
CN298922

LOCUS CN298922 729 bp mRNA linear EST 16-MAY-2004
DEFINITION 1700060007717 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN298922
VERSION CN298922.1 GI:47315336
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 729)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 729 Std Error: 0.00.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_lib="GRN_PREHEP"
/note="oligo dt primed, full-length enriched cDNA library
from DMSO-treated HES cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN
Alignment Scores:
Pred. No.: 2.61e-105 Length: 729
Score: 945.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x CN298922 (1-729)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
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|||||
QY 21 ArgProGluThrIleSerGluProLysTyrThrValAspLeuThrAsnGluThrThr 40
|||||
DB 212 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAAGAAACAAC 271
|||||
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
|||||
DB 272 GATTCACCACTTCTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGCGACATG 331
|||||
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
|||||
DB 332 TTCTCTCTCATTACCTGGGAATATTGATGGATTAGATCTAAACAATCTGTGAGAGGGCT 391
|||||
QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
|||||
DB 392 CGAGGGGTGTCTCTACTTACTTGTACAGCCAGATGTGATATTCTACAGGAGTT 451
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QY 101 IleProProTyrTyrSerTyrLeuLysArgSerSerAsnTyrGluIleIleThrGly 120
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DB 452 ATTCCCCATATTATAGCTTACCTTAAGAAGAGATCAAGTAATATTATGAGATTATTACAGGT 511
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Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
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Qy 141 GlnGluLeuIleProPheProSerThrLysMetMetArgAenLeuLeuCysValHisVal 160
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Db 572 CAAGAGATTATTCCTTTTCCAAGTACCAAAATGATGAGAACTTTTATGTGTGTCATGTG 631
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Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
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Db 632 AACGTGTGAGAAATAGCTTTTGCTTTATGACATCCCATTTGGAGAGACCAGAGGGCAT 691
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Qy 181 AlaAlaGlu 183
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Db 692 GCTGCGGAA 700
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RESULT 3
LOCUS CN298924
DEFINITION 17000424496911 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN298924
VERSION CN298924.1 GI:47315338
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 729)
Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
15146197
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 729 Std Error: 0.00.
Location/Qualifiers
1..729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and
H9"
/clone_lib="GRN_ES"
notes="oligo dt primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"

FEATURES
source
1..729
Location/Qualifiers

ORIGIN
Alignment Scores:
Pred. No.: 2.61e-105 Length: 729
Score: 945.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_copy_54_236 (1-183) x CN298924 (1-729)

Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
    |||||
Db 94 ATGAAAGGGCTCTGAACCTCTACTTCAGCGCTCCGTTGGAGAGCGCTTGGAAAGC 153
    |||||
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
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Db 154 CGACCTGAACCACTCTCTGAGCCCAAGACACCTATGTTGACCTAACCAATGAAGAAACAAC 213
Qy 41 AspSerThrThrSerLysLysSerProSerGluAspThrGlnGlnGluAenGlySerMet 60
    |||||
Db 214 GATTCCACCACCTCTCTAAATCAGCCCATCTCTGAAGATACCTCAGCAAGAAAAATGGCAGCATG 273
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Qy 61 PheSerLeuIleThrTrpAenIleAspGlyLeuAspLeuAenAsnLeuSerGluAtgAla 80
    |||||
Db 274 TTCTCTCTCAATACCTGGAAATATTGATGGATTAGATCTAAACAATCTGTCTGAGAGGGCT 333
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Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
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Db 334 CGAGGGGTGTCTTCTACTTCTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTT 393
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Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
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Db 394 ATTCCCCCATATTTATGACTACCTTAAAGAAGAGATCAAGTAATTAATGAGATTATTACAGGT 453
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Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
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Db 454 CATGAGAGAGATATTTTCACAGCTATATGTTGAGAAATCAAGAGTGAATATAAAGC 513
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Qy 141 GlnGluLeuIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
    |||||
Db 514 CAAGAGATTATTCCTTTTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 573
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Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
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Db 574 AACGTGTGAGAAATAGCTTTTGCTTTATGACATCCCATTTGGAGAGACCAGAGGGCAT 633
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Qy 181 AlaAlaGlu 183
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Db 634 GCTGCGGAA 642
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RESULT 4
LOCUS CX166335
DEFINITION HSC2_39_B09.g1.A035 NIH_MGC_258 Homo sapiens cDNA clone
IMAGE:7469923 5', mRNA sequence.
ACCESSION CX166335
VERSION CX166335
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 810)
NTH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: sgabs-x@mail.nih.gov
Tissue Procurement: Bresagen, Inc.
cDNA Library Preparation: Express Genomics, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
University of Georgia
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM15771 row: d column: 17
Seq primer: JENREV (CAGAAACAGCTATGACC)
High quality sequence stop: 810.
Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:7469923"

FEATURES
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1..810
Location/Qualifiers

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an early endodermal cell type"
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/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="NIH MGC 258"
/notes="Vector: pExpress-1; Site 1: NotI; Site 2: EcoRV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos and
differentiated to an early endodermal cell type. Cell line
id and NIH Registry designation is BG01. Positive for
GATA4, Mixl1, Mx1, HNF4alpha expression; negative for AFP
expression. Passage number 40. cDNA primed using oligo-dt
primer: 5'-pGACTAGTTCTAGATCGGAGCGGCCCT(T)25-3, and
cloned into the EcoRV/NotI sites of pExpress-1. This
primary library is non-normalized (normalized primary
library is NIH MGC 259). It was constructed by Express
Genomics (Frederick, MD). Sequence ends have been trimmed
to exclude vector and regions below Phred quality 16.
Three-prime sequences are presented as their reverse
complement and have been trimmed to exclude polyA. Note:
this is a Mammalian Gene Collection library."

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ORIGIN

Alignment Scores:
 Pred. No.: 3,056-105 Length: 810
 Score: 945.00 Matches: 183
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x CX166335 (1-810)

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QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
DB 117 ATGGAAAGGGCTCTGACTCTTACTTCGAGCTCCGGTGAGAGAGCGCTTGGACGC 176
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
DB 177 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACCACT 236
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 237 GATTCACCACTTCTAAATCAGCCATCTGAAGATCTCAGCAAGAAATGGCAGCATG 296
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 297 TTCTCTCTCATCTACCTGGATATTTGATGATAGATCTAAACAACTCTGTCAGAGGGCT 356
QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGluVal 100
DB 357 CGAGGGGTGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTT 416
QY 101 IleProProTyrTyrSerTyrLeuLysArgSerSerAsnTyrGluIleIleThrGly 120
DB 417 ATTCCCCCATATTTATAGCTACCTTAAAGAGAGATCAAGTAATTTATGAGATTATTACAGT 476
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
DB 477 CATGAAGAGAGATTTTTCACAGCTATATGTTGAGAGAAATCAAGATGAATTTAAAGAC 536
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
DB 537 CAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCATGTG 596
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
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QY 181 AlaAlaGlu 183
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Db 657 GCTGCGGAA 665

RESULT 5

BG740396

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

DB: 657 GCTGCGGAA 665

RESULT 5

BG740396

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

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FEATURES

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DB: 657 GCTGCGGAA 665

RESULT 5

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DEFINITION

ACCESSION

VERSION

KEYWORDS

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ORGANISM

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AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

DB: 657 GCTGCGGAA 665

RESULT 5

BG740396

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

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ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

DB: 657 GCTGCGGAA 665

RESULT 5

BG740396

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

DB: 657 GCTGCGGAA 665


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/db_xref="taxon:9606"
/clone="IMAGE:6024760"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

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ORIGIN

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Alignment Scores:
Pred. No.:      3,46e-105      Length:      883
Score:          945.00      Matches:      183
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             5      Gaps:      0

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US-10-757-745-2_COPY_54_236 (1-183) x BU169945 (1-883)

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QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
DB 40 ATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCCGGTGGAGAGAGCGCTTGAAGCG 99
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
DB 100 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTGTGACCTAACCAATGAAGAAACA 159
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 160 GATTCACACACTTTAAATATGAGCCCACTTGAAGATATCTCAGCAAGAAATGGCAGCATG 219
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 220 TTCTCTCTCATTACCTGGAATATTGATGGATTAGATCTAAACAATCTGTGAGAGGGCT 279
QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
DB 280 CGAGGGGTGTGTCTCTACTTGTGTACGCCAGATGTGATATTTCTACAGGAAGTT 339
QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
DB 340 ATTCCCAATATATAGCTACTCTAAGAAGAGATCAAGTAATATGAGATTATTACAGGT 399
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
DB 400 CATGAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATATAAAGC 459
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
DB 460 CAAGAGATTATTCCTTTTCCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 519
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
DB 520 AATGTGTGAGAAATGAGCTTTTCCCTTATGACATCCATTTGAGAGGCCAGAGGGCAT 579
QY 181 AlaAlaGlu 183
DB 580 GCTCGCGAA 588

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RESULT 8

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BU179107
LOCUS
DEFINITION BU179107 883 bp mRNA linear EST 04-SEP-2002
AGENCOURT 7984768 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6174958
5', mRNA sequence.
ACCESSION BU179107
VERSION BU179107.1 GI:22693091
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

```

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REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13548 row: 0 column: 23
High quality sequence stop: 672.
FEATURES
source
1. 883
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6174958"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."

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ORIGIN

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Alignment Scores:
Pred. No.:      3,46e-105      Length:      883
Score:          945.00      Matches:      183
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             5      Gaps:      0

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US-10-757-745-2_COPY_54_236 (1-183) x BU179107 (1-883)

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QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
DB 18 ATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCCGGTGGAGAGAGCGCTTGAAGCG 77
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 78 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTGTGACCTAACCAATGAAGAAACA 137
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 138 GATTCACACACTTTAAATATGAGCCCACTTGAAGATATCTCAGCAAGAAATGGCAGCATG 197
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 198 TTCTCTCTCATTACCTGGAATATTGATGGATTAGATCTAAACAATCTGTGAGAGGGCT 257
QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
DB 258 CGAGGGGTGTGTCTCTACTTGTGTACAGCCAGATGTGATATTTCTACAGGAAGTT 317
QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
DB 318 ATTCCCAATATATAGCTACTCTAAGAAGAGATCAAGTAATATGAGATTATTACAGGT 377
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
DB 378 CATGAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATATAAAGC 437
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
DB 438 CAAGAGATTATTCCTTTTCCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 497
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180

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|||||
498 AACGTGTCAGAAATGAGCTTTGCTTATGACATCCCATTTGGAGAGACCAGAGGGCAT 557
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Qy 181 AlalaGlu 183
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Db 558 GCTGGGAA 566

RESULT 9
AL555333 948 bp mRNA linear EST 30-MAR-2004
LOCUS AL555333 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
DEFINITION cDNA clone CS0DK007YK05 5-PRIME, mRNA sequence.
ACCESSION AL555333
VERSION AL555333.3 GI:45860070
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1. (bases 1 to 948)
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31277141.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DK007AF03QP1&c=3474.r.

FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK007YK05"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6
vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 3.84e-105 Length: 948
Score: 945.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x AL555333 (1-948)

Qy 1 MetGluArgAlaLeuAanSerTyPheGluProValGluGluSerAlaLeuGluArg 20
Db 179 ATGGAAGGGCTCTGAATCTTACTTCGAGCTCCGGTGGAGAGAGCGCTTGGAAACGC 238
Qy 21 ArgProGluThrIleSerGluProValSerTyPheGluGluSerAlaLeuGluThr 40
Db 239 CGACCTGAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACT 298
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 299 GATTCACCACTTCTAAATCAGCCCTCTGAAGATCTCAGCAAGAAATGGCAGCATG 358

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```

Qy 61 PheSerIleuThrTrpAenIleAspGlyLeuAspLeuAanLeuSerGluArgAla 80
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Db 359 TTCTCTCTCATTTACCTGGAATATTGATGGATTAGATCTAAACAATCTGTGAGAGGGCT 418
|||||
Qy 81 ArgGlyValCysSerTyPheLeuAlaLeuTyPheSerProAspValIlePheLeuGlnGluVal 100
|||||
Db 419 CGAGGGGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTT 478
|||||
Qy 101 IleProProTyPheTyPheSerTyPheLeuLysLysArgSerSerAsnTyPheGluIleThrGly 120
|||||
Db 479 ATTCCCCCATATTATATAGTACCTAAAGAAGAGATCAAGTAATATGAGATTATTACAGGT 538
|||||
Qy 121 HisGluGluGlyTyPheThrAlaIleMetLeuLysLysSerArgValLysLeuSer 140
|||||
Db 539 CATGAAGAAGGATATTTCACAGCTAATGTTGAAGAAATCAAGAGTGAATATAAAGC 598
|||||
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuValHisVal 160
|||||
Db 599 CAGAGATATTCTCTTTCCNAGTACCAAAATGATGAGAAACCTTTATGTGTGATGTG 658
|||||
Qy 161 AsnValSerGlyAenGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
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Db 659 AATGTGTGAGAAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGACCAGAGGGCAT 718
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Qy 181 AlalaGlu 183
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Db 719 GCTGGGAA 727

RESULT 10
AL555333 972 bp mRNA linear EST 05-FEB-2002
LOCUS AL555333 Homo sapiens cdna clone IMAGE:5587154
DEFINITION AGENCOURT_6445782 NIH_MGC_92 Homo sapiens
ACCESSION BM468826
VERSION BM468826.1 GI:18517868
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1. (bases 1 to 972)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI2356 row: d column: 03
High quality sequence stop: 707.
Location/Qualifiers
1..972
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5587154"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

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Alignment Scores:

Pred. No.: 3.98e-105 Length: 972
Score: 945.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x BM468826 (1-972)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluSerAlaLeuGluArg 20
DB 55 ATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCGGTGGAGGAGCGCTTGAACGC 114
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
DB 115 CGACCTGAACCACTCTGAGCCCAAGACCTATGTTGACCTTAACAATGAAGAAACAAC 174
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 175 GATTCACCACTCTTAANAATCAGCCCACTGAAGATCTCAGCAAGAAATGGCAGCATG 234
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 235 TTCTCTCTCATTTACCTGGAATATTGATGATTTAGATCTAAACAATCTGTGAGAGGGCT 294
QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
DB 295 CGAGGGGTGTGTTCTTACTTAGCTTTGACAGCCAGATGTGATATTTCTACAGGAAGTT 354
QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
DB 355 ATTCCCTCATTTATAGCTACCTAAGAAGAGATCAAGTAATATGAGATTTATACAGT 414
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
DB 415 CATGAAGAAGGATATTTACACGCTATAATGTTGAAGAAATCAAGAGTGAATTAAGAAAGC 474
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
DB 475 CAAGAGATTTATCTCTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 534
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
DB 535 AACGTGTGAGGAATGAGCTTTGCTTATGACATCCATTTGAGAGACCAAGAGGCAT 594
QY 181 AlaAlaGlu 183
DB 595 GCTGCGAA 603

RESULT 11

BX338160
LOCUS BX338160 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSODI056YC23 5-PRIME, mRNA sequence.

ACCESSION BX338160

VERSION BX338160.2 GI:46283046

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 981)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 2, 2003 this sequence version replaced gi:30345671.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3474.r

For more information about this cluster, see

<http://www.genoscope.cns.fr/cdna?c=CSODI056AB12QPI&c=3474.r>.

FEATURES

source

Location/Qualifiers

1..981

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="CSODI056YC23"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was,

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.: 4.04e-105 Length: 981
Score: 945.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x BX338160 (1-981)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluSerAlaLeuGluArg 20
DB 173 ATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCGGTGGAGGAGCGCTTGAACGC 232
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
DB 233 CGACCTGAACCACTCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 292
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 293 GATTCACCACTCTTAAATCAGCCCACTCTGAAGATCTCAGCAAGAAATGGCAGCATG 352
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 353 TTCTCTCTCATTTACTGGAATATGATGATTTAGATCTTAACAATCTGTGAGAGGGCT 412
QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
DB 413 CGAGGGGTGTGTTCTTACTTAGCTTTGACAGCCAGATGTGATATTTCTACAGGAAGTT 472
QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
DB 473 ATTCCCTCATTTATAGCTACCTAAGAAGAGATCAAGTAATATGAGATTTATACAGT 532
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
DB 533 CATGAAGAAGGATATTTACAGCTATATGTTGAAGAAATCAAGAGTGAATTAAGAAAGC 592
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
DB 593 CAAGAGATTTATCTCTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 652
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
DB 653 AATGTGTGAGGAATGAGCTTTGCTTATGACATCCATTTGAGAGACCAAGAGGCAT 712
QY 181 AlaAlaGlu 183
DB 713 GCTGCGAA 721

RESULT 12

BX337905

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LOCUS      BX337905                      1067 bp      mRNA      linear      EST 07-APR-2004
DEFINITION BX337905 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI052YN13 5-PRIME, mRNA sequence.
ACCESSION  BX337905
VERSION     BX337905.2  GI:46273926
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1 (bases 1 to 1067)
AUTHORS   Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On May 2, 2003 this sequence version replaced gi:30339657.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DI052CG07QP1&c=3474.r.
FEATURES             Location/Qualifiers
     source           1..1067
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI052YN13"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
                     was normalized."
ORIGIN
Alignment Scores:
Pred. No.:          4.57e-105      Length:      1067
Score:              945.00         Matches:    183
Percent Similarity: 100.00%        Conservative: 0
Best Local Similarity: 100.00%     Mismatches: 0
Query Match:        100.00%       Indels:      0
DB:                  5              Gaps:        0

US-10-757-745-2_COPY_54_236 (1-183) x BX337905 (1-1067)
Qy      1  MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
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        |||
        |||
Db      184  ATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCCGGTGAGGAGAGCGCTTGGAACGC 243
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        |||
        |||
Qy      21  ArgProGluThrIleSerGluProGlyThrTyrValAspLeuThrAenGluGluThr 40
        |||
        |||
        |||
Db      244  CGACCTGAACCAATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAACAAC 303
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        |||
        |||
Qy      41  AspSerThrThrSerLyIleSerProSerGluAspThrGlnGlnGluAenGlySerMet 60
        |||
        |||
        |||
Db      304  GATTCACCACTTCTAAATCAGCCCATCTGAAGATACTCAGCAAGAAATGGCAGCATG 363
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        |||
Qy      61  PheSerLeuIleThrTpAsnIleAspGlyLeuAspLeuAenAenLeuSerGluArgAla 80
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        |||
Db      364  TTCTCTCTATTACTTGAATATTGATGATTAGATTCTAAACATCTGTCTCAGAGGGCT 423
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        |||
        |||
Qy      81  ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
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        |||
        |||
Db      424  CGAGGGGTGTTCTCTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTT 483
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Qy      101  IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleThrGly 120
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```

Db      484  ATTCCCCCATATTATAGTACCTAAAGAGAGATCAAGTAATTATGAGATTATTACAGGT 543
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Qy      121  HisGluGluGlyTyrPheThrAlaIleMetLeuLysSerArgVallysLeuLysSer 140
        |||
        |||
        |||
Db      544  CATGAAGAGGATATTTCACAGCTATAATGTTCAAGAAATCAAGAGTGAAATTTAAAAAGC 603
        |||
        |||
        |||
Qy      141  GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
        |||
        |||
        |||
Db      604  CAAGAGATTATTCTCTTTCACAGTACCAAAATGATGAAACCTTTATGTGTGCATGTG 663
        |||
        |||
        |||
Qy      161  AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
        |||
        |||
        |||
Db      664  AATGTGTCAAGAAATGAGCTTTCCTTATGACATCCATTTGGAGAGACCAGAGGGCAT 723
        |||
        |||
        |||
Qy      181  AlaAlaGlu 183
        |||
        |||
        |||
Db      724  GCTGCGGAA 732
        |||
        |||
        |||
RESULT 13
BX444691
LOCUS     BX444691
DEFINITION BX444691 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
CS0DN005YN02 5-PRIME, mRNA sequence.
ACCESSION  BX444691
VERSION     BX444691.2  GI:47009162
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1 (bases 1 to 1081)
AUTHORS   Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On May 15, 2003 this sequence version replaced gi:30780264.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DN005DG01QP1&c=3474.r.
FEATURES             Location/Qualifiers
     source           1..1081
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DN005YN02"
                     /tissue_type="ADULT BRAIN"
                     /dev_stage="adult"
                     /clone_lib="Homo sapiens ADULT BRAIN"
                     /notes="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
ORIGIN
Alignment Scores:
Pred. No.:          4.66e-105      Length:      1081
Score:              945.00         Matches:    183
Percent Similarity: 100.00%        Conservative: 0
Best Local Similarity: 100.00%     Mismatches: 0
Query Match:        100.00%       Indels:      0
DB:                  5              Gaps:        0

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US-10-757-745-2_COPY_54_236 (1-183) x BX444691 (1-1081)	
QY	1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db	186 ATGGAAGGGCTCTGAATCTCTACTTCAGAGCTCCGGTGGAGAGCGCTTGAACGC 245
QY	21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db	246 CGACCTGAACCACTCTTGAGCCCAAGACCTATGTGTGACCTAACCAATGAAGAACCACT 305
QY	41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGlnAsnGlySerMet 60
Db	306 GATTCACCACTTCTAAATCAGCCATCTGAAGATACCTCAGCAAGAAAATGGCAGCATG 365
QY	61 PheSerLeuIleThrTyrPheAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db	366 TTCTCTCTCAATCTGGAATATTGATGATTTAGATCTAAACAAATCTCTCAGAGAGGGCT 425
QY	81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db	426 CGAGGGGTGTCTCTACTTACCTTTGACAGCCAGATGTGATATTTCTACAGGAAGTT 485
QY	101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db	486 ATTCCTCCATATTAATAGCTACCTAAAGAGAGATCAAGTAATATTAGATATTATACAGGT 545
QY	121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db	546 CATGAAGAAGGATATTTACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAATAAAGC 605
QY	141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysCysValHisVal 160
Db	606 CAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 665
QY	161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db	666 AATGTGTGAGGAATAGAGCTTTTGCTTATGACATCCCATTTGGAGAGCACCAGAGGGCAT 725
QY	181 AlaAlaGlu 183
Db	726 GCTGCGGAA 734
RESULT 14	
DQ049205	
LOCUS	1089 bp DNA linear GSS 02-JUN-2005
DEFINITION	Homo sapiens TTRAP gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION	DQ049205
VERSION	DQ049205.1 GI:66902404
KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo
REFERENCE	1 (bases 1 to 1089)
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civeillo,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL	(er) PLoS Biol. 3 (6), E170 (2005)
PUBMED	15869325
REFERENCE	2 (bases 1 to 1089)
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civeillo,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE	Direct Submission
JOURNAL	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
FEATURES	
source	
1. .1089	
/organism="Homo sapiens"	
/mol_type="genomic DNA"	
/db_xref="taxon:9606"	
/chromosome="6"	
<1..>1089	
/gene="TTRAP"	
/locus_tag="HC17203"	
ORIGIN	
Alignment Scores:	
Pred. No.: 4.71e-105 Length: 1089	
Score: 945.00 Matches: 183	
Percent Similarity: 100.00% Conservative: 0	
Best Local Similarity: 100.00% Mismatches: 0	
Query Match: 100.00% Indels: 0	
DB: 11 Gaps: 0	
US-10-757-745-2_COPY_54_236 (1-183) x DQ049205 (1-1089)	
QY	1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db	160 ATGGAAGGGCTCTGAATCTCTACTTCAGAGCTCCGGTGGAGAGCGCTTGAACGC 219
QY	21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db	220 CGACCTGAACCACTCTGAGCCCAAGACCTATGTGTGACCTAACCAATGAAGAACCACT 279
QY	41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGlnAsnGlySerMet 60
Db	280 GATTCACCACTTCTAAATCAGCCATCTGAAGATACCTCAGCAAGAAAATGGCAGCATG 339
QY	61 PheSerLeuIleThrTyrPheAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db	340 TTCTCTCTCAATCTGGAATATTGATGATTTAGATCTAAACAAATCTCTCAGAGAGGGCT 399
QY	81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db	400 CGAGGGGTGTCTCTACTTACCTTTGACAGCCAGATGTGATATTTCTACAGGAAGTT 459
QY	101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db	460 ATTCCTCCATATTAATAGCTACCTAAAGAGAGATCAAGTAATATTAGATATTATACAGGT 519
QY	121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db	520 CATGAAGAAGGATATTTACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAATAAAGC 579
QY	141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysCysValHisVal 160
Db	580 CAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 639
QY	161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db	640 AACGTGTGAGGAATAGAGCTTTTGCTTATGACATCCCATTTGGAGAGCACCAGAGGGCAT 699
QY	181 AlaAlaGlu 183
Db	700 GCTGCGGAA 708
RESULT 15	
CR601303	
LOCUS	1168 bp mRNA linear HTC 21-JUL-2004
DEFINITION	full-length cDNA clone CS0DN005YN02 of Adult brain of Homo sapiens (human).
ACCESSION	CR601303
VERSION	CR601303.1 GI:50482110
KEYWORDS	HTC; CNSLT_cDNA.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

665 AACGTGTCAGGAATAGCTTTTCCTTATGCATCCCATTTGGAGAGCACCAGAGGCAT 720

181 AlaAlaGlu 183
|||||
725 GCTGCGAA 733

RESULT 16
BM553049
LOCUS
DEFINITION
5', mRNA sequence.
AGENCOURT_6542413 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742798
BM553049
BM553049.1 GI:18791437
EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1. (bases 1 to 1192)
NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12761 row: i column: 07
High quality sequence stop: 747.
FEATURES
source
1..1192
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5742798"
/tissue_type="medulla"
/lab_host="DH108"
/clone_lib="NIH_MGC_119"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note
this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 5.38e-105 Length: 1192
Score: 945.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_54_236 (1-183) x BM553049 (1-1192)
QY 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
DB 217 ATGGAAGGCTCTGAACTCTACTTCGAGCTCCGGTGGAGGAGAGCGCCTTGGAGCGC 276
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 277 CGACCTGAACCACTCTCTGAGCCCAAGACCTATCTTGACCTTACCATGAAGAAACAAC 336
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60

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337 GATTCACCACTTCTAATAACAGCCACTGAGATACCTCAGCAGAAAATGGCAGCATG 396
Qy 61 PheSerLeuIleThrTTPAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 397 TTCTCTCTCATACCTGGAATATTGATGATTAGATCTAAACAATCTGTCAGAGAGGCT 456
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 457 CGAGGGGTGTGTTCTTACTTGTACAGCCAGATGTGATATTCTACAGGAAGTT 516
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 517 ATTCCCCCATATATAGCTACCTAAAGAAGAGATCAAGTAATATGAGATTATACAGGT 576
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 577 CATGAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATAAAAAAGC 636
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuCysValHisVal 160
Db 637 CAAGAGATTATTCTTTTCCAGTAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 696
Qy 161 AnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 697 ATGTGTACAGGAATGAGCTTTGCCTTATGACATCCCATTTGAGAGCACCAGAGGGCAT 756
Qy 181 AlaAlaGlu 183
Db 757 GCTGCGGAA 765

RESULT 17
CR592636 1620 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DM007YE11 of Fetal liver of Homo sapiens
DEFINITION (human).
ACCESSION CR592636
VERSION CR592636.1 GI:50473443
KEYWORDS HTC; CNSLT CDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1620)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1620)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. .1620
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM007YE11"
/tissue_type="Fetal liver"
/plasmid="pCMVSPORT_6"

FEATURES
source

ORIGIN
Alignment Scores :
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Pred. No.: 8.45e-105 Length: 1620
Score: 945.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-757-745-2_COPY_54_236 (1-183) x CR592636 (1-1620)
Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 103 ATGGAAGGGGTCTGAACTCTTCTTCTGAGGCTCCGGTGGAGGAGCGCTTTGGAAGC 162
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db 163 CGACTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACT 222
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 223 GATTCACCACTTCTAAAATCAGCCATCTGAAGATCTCAGCAAGAAAATGGCAGCATG 282
Qy 61 PheSerLeuIleThrTTPAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 283 TTCTCTCTCATACCTGGAATATTGATGATTAGATCTAAACAATCTGTCAGAGAGGCT 342
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 343 CGAGGGGTGTGTTCTTACTTGTACAGCCAGATGTGATATTCTACAGGAAGTT 402
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 403 ATTCCCCCATATATAGCTACCTAAAGAAGAGATCAAGTAATATGAGATTATACAGGT 462
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 463 CATGAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATAAAAAAGC 522
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuCysValHisVal 160
Db 523 CAAGAGATTATTCTTTTCCAGTAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 582
Qy 161 AnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 583 AACGTGTGAGGAATGAGCTTTGCCTTATGACATCCCATTTGAGAGCACCAGAGGGCAT 642
Qy 181 AlaAlaGlu 183
Db 643 GCTGCGGAA 651

RESULT 18
CR597293 1894 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DK007YK05 of HeLa cells Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR597293
VERSION CR597293.1 GI:50478100
KEYWORDS HTC; CNSLT CDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1894)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1894)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
```

BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES

Location/Qualifiers
source
1. 1894
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK007YK05"
/tissue_type="Hela cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:
Pred. No.: 1.06e-104 Length: 1894
Score: 945.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x CR597293 (1-1894)

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Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 178 ATGGAAGGGCTCTGAACCTCTACTTCGAGCTCCGGTGGAGGAGCGCTTGGAAACG 237
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db 238 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATCTGTG 297
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAenGlySer 60
Db 298 GATTCACCATCTTCTAAATCAGCCCATCTGAGAGATCTCAGCAAGAAATGGCAG 357
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAenLeuSerGluArgAla 80
Db 358 TTCTCTCTCAATCACTCGAATATTGATGATTAGATTAGATCTAACAATCTGTG 417
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 100
Db 418 CGAGGGGTGTCTCTACTTACCTTGTACAGCCCATGTGTATTTCTACAGGAAGT 477
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThr 120
Db 478 ATCCCCCATATTATAGCTACTTAAGAGAGATCAAGTATATTAGATTTATACAGGT 537
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuSer 140
Db 538 CATGAAGAAGGATATTTACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAAGA 597
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHis 160
Db 598 CAAGAGATATTATCTCTTTTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGT 657
Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGly 180
Db 658 AACGTGTGAGGAATGAGCTTTGCTTATGATCATCCCATTTGGAGAGACCAAGG 717
Qy 181 AlaAlaGlu 183
Db 718 GCTGGGAA 726
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RESULT 19

CR595644
LOCUS
DEFINITION
full-length cDNA clone CS0DI052YN13 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION
CR595644

VERSION
KEYWORDS
SOURCE

CR595644.1 GI:50476451
HTC; CNSUT_CDNA.

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK

1 (bases 1 to 1909)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue

REFERENCE
AUTHORS
TITLE
JOURNAL

2 (bases 1 to 1909)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr)

COMMENT

- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES

Location/Qualifiers
source
1. 1909
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI052YN13"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:
Pred. No.: 1.08e-104 Length: 1909
Score: 945.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x CR595644 (1-1909)

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Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 184 ATGGAAGGGCTCTGAACCTCTACTTCGAGCTCCGGTGGAGGAGCGCTTGGAAACG 243
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db 244 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACAATCTGTG 303
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAenGlySer 60
Db 304 GATTCACCATCTTCTAAATCAGCCCATCTGAGAGATCTCAGCAAGAAATGGCAG 363
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAenLeuSerGluArgAla 80
Db 364 TTCTCTCTCAATCACTCGAATATTGATGATTAGATTAGATCTAACAATCTGTG 423
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 100
Db 424 CGAGGGGTGTGTCTCTACTTGTACAGCCCATGTGTATTTCTACAGGAAGT 483
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThr 120
Db 484 ATTCCCCCATATTATAGCTACTTAAGAGAGATCAAGTATATTAGATTTATACAG 543
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuSer 140
Db 544 CATGAAGAAGGATATTTACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAAGA 603
```


Alignment Scores:

Pred. No.: 1.76e-104 Length: 1018
Score: 940.00 Matches: 182
Percent Similarity: 99.45% Conservative: 0
Best Local Similarity: 99.45% Mismatches: 1
Query Match: 99.47% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x BX337141 (1-1018)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 150 ATGGAAGGGCTCTGAACCTCTACTTCGAGCTCGGTGGAGGAGCGCTTGAACGC 209
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 210 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTGTACCTTAACCAATGAAGAACAAC 269
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 270 GATTCACCACTTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATG 329
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 330 TTCTCTCATCTACCTGGAATATTGATGATTAGATTCTAAACATCTGTCTCAGAGGGCT 389
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 390 CGAGGGGTGTCTCTACTTACCTTGTACAGCCAGATGTGTATTTCTACAGGAAGTT 449
Qy 101 IleProProTyrTyrSerTyrLeuLysIleArgSerSerAsnTyrGluIleIleThrGly 120
Db 450 ATTCCCCATATTATAGCTACTTAAGAGAGATCAAGTAATTAAGATTATTACAGGT 509
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 510 CATGAGAAGATATTTACAGCTATAATGTGAGAAATCAAGAGTGAATTAAGAAGC 569
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db 570 CAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAACTTTTATGTGTGATGTG 629
Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 630 AATGTGTGAGAAATGAGCTTTGCTTATGATCATCCCATTTGGAGAGCAGAGGGCAT 689
Qy 181 AlaAlaGlu 183
Db 690 GCTGGGAA 698

RESULT 22

BU661472

LOCUS

BU661472 710 bp mRNA linear EST 30-SEP-2002
cl72dl1.z1 Hembase; Erythroid Precursor Cells (LCB:cl library) Homo

sapiens cdna clone cl72dl1 5', mRNA sequence.

ACCESSION

BU661472.1

VERSION

EST.

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 710)

Gubin,A.N., Lee,Y.T., Bouffard,G.G. and Miller,J.L.

Gene Expression in Human Erythroid Precursor Cells

Unpublished (2002)

Contact: Jeffery L. Miller

Laboratory of Chemical Biology

National Institute of Diabetes

Building 10, Room 9B17, National Institutes of Health, Bethesda, MD

20892, USA

Tel: 301 402 2373

Fax: 301 435 5148

Email: jn7fenih.gov

The 'cl' library was constructed by Alexander Gubin, Ph.D. in the Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing and/or analyses by National Institutes of Health Intramural Sequencing Center (NISC). More information available at: <http://hembase.nidk.nih.gov>

Plate: 72 row: d column: 11

Seq primer: 5' lambda-Triplex2 Sequencing Primer.

FEATURES

source

1. 710
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="cl72dl1"
/sex="unknown"
/tissue_type="blood"
/cell_type="Erythroid Precursor Cells"
/contig_line="Primary Culture of Peripheral Blood Mononuclear Cells"
/dev_stage="Precursor erythroblasts; GPA++"
/lab_host="DH5alpha"
/clone_lib="Hembase; Erythroid Precursor Cells (LCB:cl library)"
/notes="Organ: blood; Vector: pTriplex2; Site:1: SfiI; Site:2: SfiI; A complementary DNA (cDNA) library from human erythroid precursor cells was constructed using SMART PCR (polymerase chain reaction) cDNA Library Construction Kit (Clontech, Palo Alto, CA) according to the manufacturer's directions, but with slight modifications. Briefly, reverse transcription was performed in the presence of 1 umol/l peptide nucleic acid (PNA) oligos (N-terminal) -biotin-GTC-CAC-AAG-CTT-G- (C-terminal) and (N-terminal) -biotin-C(T/C)T-GAA-GTT-CTC-AGG-A- (C-terminal) . Synthesized cDNA was digested with SfiI and size-selected on a 1% agarose gel (>800bp). Large-scale sequencing of the library was performed by the NIH Intramural Sequencing Center (NISC;
<http://www.nisc.nih.gov/>) ."

ORIGIN

Alignment Scores:
Pred. No.: 1.82e-104 Length: 710
Score: 938.00 Matches: 182
Percent Similarity: 99.45% Conservative: 0
Best Local Similarity: 99.45% Mismatches: 1
Query Match: 99.26% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x BU661472 (1-710)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 76 ATGGAAGGGCTCTGAACCTCTACTTCGAGCTCGGTGGAGGAGCGCTTGAACGC 135
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 136 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTGTACCTTAACCAATGAAGAACAAC 195
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 196 GATTCACCACTTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATG 255
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 256 TTCTCTCATCTACCTGGAATATTGATGATTAGATTCTAAACCAATCTGTCTCAGAGGGCT 315
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 316 CGAGGGGTGTCTCTACTTACCTTTGTACAGCCAGATGTGTATTTCTTACAGGAAGTT 375
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120

Db 376 ATTCCCCCATATATAGCTACCTAAGAGAGATCAAGTAATATGAGATTATACAGGT 435
 QY 121 HsGluGluGlyTyrPheThrAlaIleMetLeuLysSerArgValLysLeuLysSer 140
 Db 436 CATGAAGAAGGATATTTACAGCTATATATGTTGAAGAAATCAAGAGTGAATTAAGC 495
 QY 141 GlnGluIleProPheProSerThrLysMetMetArgAenLeuLysValHisVal 160
 Db 496 CAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCCCTTTATGTGTGATGTG 555
 QY 161 AenValSerGlyAenGluLysCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
 Db 556 AACGTGTGAGGAATGAGCTTTCCTTATGACATCCATTTGGAGAGACCAAGGGCAT 615
 QY 181 AlaAlaGlu 183
 Db 616 GCTGCGAA 624

RESULT 23
 BX358707 942 bp mRNA linear EST 08-APR-2004
 LOCUS BX358707 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CSODI042YL19 5-PRIME, mRNA sequence.

ACCESSION BX358707 GI:46306560
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 5, 2003 this sequence version replaced gi:30378261.

Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 3474.r

For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?8=CSODI042CF10QP1&c=3474.r.

FEATURES

source
 Location/Qualifiers
 1..942
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODI042YL19"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /notes="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 3 67e-104 Length: 942
 Score: 937.00 Matches: 181
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.45% Mismatches: 0
 Query Match: 99.15% Indels: 0
 DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x BX358707 (1-942)

QY 2 GluArgAlaLeuAenSerTyrPheGluProProValGluGluSerAlaLeuGluArgArg 21
 Db 32 CAGAGGGCTCTGAACCTCTACTTCGAGCCTCCGGTGGAGGAGAGCGCTTGGAAACGCCGA 91
 QY 22 ProGluThrIleSerGluProLysThrTyrValAspLeuThrAenGluGluThrThrAsp 41
 Db 92 CCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAACCAACTGAT 151
 QY 42 SerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAenGlySerMetPhe 61
 Db 152 TCCACCACCTCTTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATGTTC 211
 QY 62 SerLeuIleThrTrpAenIleAspGlyLeuAspLeuAenAenLeuSerGluArgAlaArg 81
 Db 212 TCTCTATTACTTGGATATTTGATGGATTAGATCTTAAACAATCTGTGAGAGGGCTCGA 271
 QY 82 GlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIle 101
 Db 272 GGGGTGTGTTCTTACTTGTACAGCCCATGATGATATTTCTACAGGAAGTTATT 331
 QY 102 ProproTyrTyrSerTyrLeuLysLysArgSerSerAenTyrGluIleIleThrGlyHis 121
 Db 332 CCCCATATTATAGCTACCTTAAAGAGAGATCAAGTAATATGAGATTATTACAGTCAAT 391
 QY 122 GluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGln 141
 Db 392 GAAGAGGATATTTACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAAGAACCCAA 451
 QY 142 GluIleIleProPheProSerThrLysMetMetArgAenLeuLysCysValHisValAen 161
 Db 452 GAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTAAT 511
 QY 162 ValSerGlyAenGluLysCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAla 181
 Db 512 GTGTGAGAAATGAGCTTTGCTTATGACATCCCATTTGGAGAGACCCAGAGGGCATGCT 571
 QY 182 AlaGlu 183
 Db 572 GCGGAA 577

RESULT 24

LOCUS

BM926092 1046 bp mRNA linear EST 12-MAR-2002
 AGENCOURT 5649780 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5764440
 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 1046)
 NIH-MGC http://mgi.mci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgsbbs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12817 row: o column: 01
 High quality sequence start: 4
 High quality sequence stop: 632.

FEATURES

source

1..1046
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"

/db_xref="taxon:9606"
 /clone="IMAGE:5764440"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_114"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
 male brains, age range 23-27 yo. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.5 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 019. Note:
 this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 4,28e-104 Length: 1046
 Score: 937.00 Matches: 181
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.45% Mismatches: 0
 Query Match: 99.15% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x BM926092 (1-1046)

Qy	2	GluArgAlaLeuAenSerTyrPheGluProValGluSerAlaLeuGluArg	21
Db	36	CAGAGGGCTCTGAATCTCTACTTCGAGCCTCCGGTGAGGAGCGCCTTGGAAACGCCGA	95
Qy	22	ProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrAsp	41
Db	96	CCTGNAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAACCTGAT	155
Qy	42	SerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPhe	61
Db	156	TCCACCATCTTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGCATGTTTC	215
Qy	62	SerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArg	81
Db	216	TCTCTCATTCCTGGAAATATTGATGGATTAGATCTAAACAATCTGTGAGAGGGCTCGA	275
Qy	82	GlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIle	101
Db	276	GGGTGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATATTCTACAGGAAGTTATT	335
Qy	102	ProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIlelleThrGlyHis	121
Db	336	CCCCCATATTATAGCTACCTAAGAAGAGATCAAGTAATATTAGATATTATTACAGGTCT	395
Qy	122	GluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValIysLeuLysSerGln	141
Db	396	GAAGAAGGATATTTACAGCTATTAATGTGTAAGAAATCAAGAGTGAATTTAAAGAAGCAA	455
Qy	142	GluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsn	161
Db	456	GAGATTATCTCTTCCAGTACCAATATGATGAGAACTTTTATGTGTCATGTGAAT	515
Qy	162	ValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAla	181
Db	516	GTGTGAGGAATGAGCTTTGCTTATGATCATCCCATTTGGAGAGCACCAGAGGGCATGCT	575
Qy	182	AlaGlu 183	
Db	576	CGGAA 581	
RESULT 25			
LOCUS	CR602029	1743 bp	mRNA linear HTC 21-JUL-2004
DEFINITION	full-length cDNA clone CSODI042YL19 of Placenta Cot 25-normalized		
	of Homo sapiens (human).		
ACCESSION	CR602029		
VERSION	CR602029.1	GI:50482836	
KEYWORDS	HTC; CNSLT_cDNA.		

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1743)
 AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
 Faraday Avenue
 REFERENCE 2 (bases 1 to 1743)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail: segref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr
 COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 FEATURES Location/Qualifiers
 source
 1..1743
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODI042YL19"
 /issue_type="Placenta Cot 25-normalized"
 /plasmid="pCMVSPORT_6"
 ORIGIN
 Alignment Scores:
 Pred. No.: 9,08e-104 Length: 1743
 Score: 937.00 Matches: 181
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.45% Mismatches: 0
 Query Match: 99.15% Indels: 0
 DB: 4 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x CR602029 (1-1743)

Qy	2	GluArgAlaLeuAenSerTyrPheGluProValGluSerAlaLeuGluArg	21
Db	32	CAGAGGGCTCTGAATCTCTACTTCGAGCCTCCGGTGAGGAGCGCCTTGGAAACGCCGA	91
Qy	22	ProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrAsp	41
Db	92	CCTGNAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAACCTGAT	151
Qy	42	SerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPhe	61
Db	152	TCCACCATCTTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGCATGTTTC	211
Qy	62	SerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArg	81
Db	212	TCTCTCATTCCTTCCAGTACCAATATGATGGATTAGATCTAAACAATCTGTGAGAGGGCTCGA	271
Qy	82	GlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIle	101
Db	272	GGGTGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATATTCTACAGGAAGTTATT	331
Qy	102	ProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIlelleThrGlyHis	121
Db	332	CCCCCATATTATAGCTACCTAAGAAGAGATCAAGTAATATTAGATATTATTACAGGTCT	391
Qy	122	GluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValIysLeuLysSerGln	141
Db	392	GAAGAAGGATATTTACAGCTATTAATGTGTAAGAAATCAAGAGTGAATTTAAAGAAGCAA	451
Qy	142	GluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsn	161

Db 452 GAGATTATTCTCTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGTCATGTGAAC 511
Qy 162 ValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAla 181
Db 512 GTGTGAGGAAATGAGCTTTGGCTTATGACATCCCATTTGGAGAGACCAAGAGGGCATGCT 571
Qy 182 AlaGlu 183
Db 572 GCGGAA 577

RESULT 26
BI258848 767 bp mRNA linear EST 17-JUL-2001
LOCUS 602969663F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109303 5',
DEFINITION mRNA sequence.
ACCESSION BI258848
VERSION BI258848.1 GI:14815606
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 767)

REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Arrayed by: Incyte Genomics, Inc.
CDNA Sequencing by: Incyte Genomics, Inc.
DNA Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL1264 row: m column: 16
High quality sequence stop: 758.
Location/Qualifiers

FEATURES

source
1..767
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5109303"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH MGC 12"
/notes="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.4 kb. Library prepared by Life
Technologies.."

ORIGIN

Alignment Scores:
Pred. No.: 3.6e-104 Length: 767
Score: 936.00 Matches: 181
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.05% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x BI258848 (1-767)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 97 ATGGAAGGCTCTGAACCTCTACTTCGACCTCCGCTGGAGAGAGCGCTTGGAAACGC 156
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 157 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAAGAAACAAC 216
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60

Db 217 GATTCCACCACCTCTAAATCAGCCCATCTGAAGATACTCAGCAAGAAAAATGGCAGCATG 276
Qy 61 PheSerLeuIleThrTTPAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 277 TTCTCTCTCATCTGGAATATTGATGGATTAGATCTTAACATCTCTCAGAGAGGGCT 336
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 337 CGAGGGGTGTCTCTACTTGTGTACAGCCAGATGTGATATTCTACAGGAAGTT 396
Qy 101 IleProProTyrTyrSerTyrLeuIleLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 397 ATTCCCCCATATTATAGCTACCTAAAGAGAGATCAAGTAATTATGAGATATTACAGT 456
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 457 CATGAAGAAGGATATTTCCAGCTATAATGTTGAAGAAATCAAGAGTGAATTAAGG 516
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db 517 CAAGAGATTATCTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTG 576
Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 577 AATGTGTGAGAAATGAGCTTTGCCTTATGACATCCCATTTGGAGAGCACCAAGAGGGCAT 636
Qy 181 Ala 181
Db 637 GCT 639

RESULT 27

BI258848

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

783 bp mRNA linear EST 08-APR-2004
BX365835 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
CDNA clone CSODB007YB11 5-PRIME, mRNA sequence.
BX365835
BX365835.2 GI:46288859
EST.
Homo sapiens (human)
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 783)
Li W.B., Gruber C., Jessee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30370946.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CS1DB0022F03QPl&c=3474.r>.
Location/Qualifiers

FEATURES

source

1..783

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODB007YB11"

/tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"

/clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"

/notes="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

```
Alignment Scores:      3.71e-104      Length:      783
Pred. No.:            936.00      Matches:      181
Score:                99.45%      Conservative: 1
Percent Similarity:   98.91%      Mismatches:  1
Best Local Similarity: 99.05%      Indels:      0
Query Match:         5           Gaps:        0
DB:

US-10-757-745-2_COPY_54_236 (1-183) x BX365835 (1-783)

Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 172 ATGGAAGGGCTCTGAACCTCTACTTCGAGGCTCGGTGGAGAGAGCGCTTGGAAAGC 231
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db 232 CGACTGAACCACTCTCTGAGCCCAAAACCTATTTGACCTAACCAATGAAGAAACAACT 291
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAenGlySerMet 60
Db 292 GATTCCACCACTCTTAAATCAGCCCATCTGAAGATATCTCAGCAAGAAATGGCAGCAT 351
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAenSerGluArgAla 80
Db 352 TTCTCTCATATCTCTGAATATTGATGGATTAGATCTTAAACATCTGTCAGAGGGCT 411
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 412 CGAGGGGTGTCTCTACTTACCTTGTGACAGCCAGATGTGATATTCTACAGGAAGTT 471
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleThrGly 120
Db 472 ATTCCCCCATATTATAGCTACCTAAGAAGAGATCAAGTAAATATGAGATTATTACAGGT 531
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 532 CATGAGAGAGATATTTCACAGCTATATATGTTGAAGAAATCAAGAGTGAATTTAAAGC 591
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db 592 CAAGAGATTATTCCTTTTCCAAATACCAAAATGATGAGAAACCTTTTATGTGTCATGTG 651
Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 652 AACGTGTGAGAAATGAGCTTTGCTTATGACATCCCATTTGGAGAGACCAGAGGGCAT 711
Qy 181 AlaAlaGlu 183
Db 712 CTGCGGGA 720

RESULT 28
CR767236
LOCUS
DEFINITION DKFZp469E1236 r1 469 (synonym: pkid1) Pongo pygmaeus cdna clone
CR767236
ACCESSION CR767236.1 GI:52609173
VERSION
KEYWORDS
SOURCE
ORGANISM Pongo pygmaeus (orangutan)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pongo.
1 (bases 1 to 701)
Ansoerge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
Wiemann,S.
Pongo pygmaeus mRNA (Ansoerge,W., Krieger,S., Regiert,T., et al.)
JOURNAL Unpublished (2004)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
```

This is the 5' sequence of the clone insert. Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; rlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469E1236
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.

FEATURES

source
1..701
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp469E1236"
/tissue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="469 (synonym: pkid1)"
/notes="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"

ORIGIN

Alignment Scores: 5.56e-104 Length: 701
Pred. No.: 934.00 Matches: 181
Score: 99.45% Conservative: 1
Percent Similarity: 98.91% Mismatches: 1
Best Local Similarity: 98.84% Indels: 0
Query Match: 7 Gaps: 0
DB:

US-10-757-745-2_COPY_54_236 (1-183) x CR767236 (1-701)

Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 88 ATGGAAGGGCTCTGAACCTCTACTTCGAGGCTCGGTGGAGAGAGCGCTTGGAAAGC 147
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db 148 CGCCTGAAACCACTCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACT 207
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAenGlySerMet 60
Db 208 GATTCCACCACTCTTAAATCAGCCCATCTGAAGATATCTCAGCAAGAAATGGCAGCATG 267
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAenSerGluArgAla 80
Db 268 TTCTCTCATATCTCTGAATATTGATGGATTAGATCTTAAACATCTGTCAGAGGGCT 327
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 328 CGAGGGGTGTCTCTACTTACCTTGTACAGCCAGATGTGATATTCTACAGGAAGTT 387
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleThrGly 120
Db 388 ATTCCCCCATATTATAGCTACCTTAAAGAGAGTTCAAGTAAATATGAGATTATTACAGGT 447
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 448 CATGAGAGAGGATATTTCACAGCTATCATGTTGAGAAATCAAGAGTGAATTTAAAGC 507
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db 508 CAAGAGATTATTCCTTTTCCAAATACCAAAATGATGAGAAACCTTTTATGTGTCATGTG 567
Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 568 AGTGTGTGAGAAATGAGCTTTGCTTATGACATCCCATTTGGAGAGACCAGAGGGCAT 627
Qy 181 AlaAlaGlu 183
Db 628 GCTGCGGGA 636

RESULT 29
CR765451
LOCUS
CR765451 846 bp mRNA linear EST 23-SEP-2004

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DEFINITION DKEP2469E2434.r1.469 (synonym: pkid1) Pongo pygmaeus cDNA clone
ACCESSION DKEP2469E2434.5, mRNA sequence.
VERSION CR765451.1 GI:52605526
SOURCE EST.
ORGANISM Pongo pygmaeus (orangutan)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pongo.
REFERENCE 1 (bases 1 to 846)
AUTHORS Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Schaipp, A.,
Mewes, H.W., Weill, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
Wiemann, S.
TITLE Pongo pygmaeus mRNA (Ottenwaelder, B., Obermaier, B.,
Deutschenbaur, S., et al.)
JOURNAL Unpublished (2004)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@kfz-heidelberg.de; sequenced by Medigenomix
(Martinried/Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKEP2469E2434) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKEP2469E2434
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
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         /dev_stage="adult"
         /lab_host="DH10B"
         /clone_lib="469 (synonym: pkid1)"
         /note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"

ORIGIN
Alignment Scores:
Pred. No.: 7.33e-104 Length: 846
Score: 934.00 Matches: 181
Percent Similarity: 99.45% Conservative: 1
Best Local Similarity: 98.91% Mismatches: 1
Query Match: 98.84% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x CR765451 (1-846)

Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluSerAlaLeuGluAq 20
Db 63 ATGGAAGGCTCTGAACCTCTGAGCTCCCGTGGAGAGAGCCCTTGGACCC 122
Qy 21 ArgProGluThrIleSerGluProLysTyrTyrValAspLeuThrAsnGluGluThr 40
Db 123 CGCCCTGAACCACTCTCGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACA 182
Qy 41 AspSerThrThrSerLysIleSerProSerGluApsThrGlnGlnGluAsnGlySerMet 60
Db 183 GATTCACCACTCTCTAAATCAGCCCATCTGAAGATACTCAGCAAGAAAATGCGCAGCATG 242
Qy 61 PheSerLeuIleThrTrpAnileAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 243 TTCTCTCTCATTACCTGGAAATATGATGGATTAGATCTAAACAATCTGTCAGAGAGGCT 302
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 303 CGAGGGGGTGTTCCTACTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTT 362

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Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 363 ATTCCTCCCATATTATAGCTACCTTAAGAGAGAGTTCAAGTAATTATGAGATTATTACAGGT 422
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 423 CATGAAGAAGGGTATTTTCACAGACTATCATGTGTGAAGAAATCAAGAGTGAAATTAAGAACG 482
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db 483 CAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 542
Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 543 AGTGTGTGAGAAATGAGCTTTGCTTATGATCATCCCATTTGGAGAGCACCAGAGGCGCAT 602
Qy 181 AlaAlaGlu 183
Db 603 GCTGCGGAA 611

RESULT 30
BX374579 780 bp mRNA linear EST 27-APR-2004
LOCUS BX374579 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
DEFINITION CNA clone CS0DB007YB11 5-PRIME, mRNA sequence.
ACCESSION BX374579
VERSION BX374579.2 GI:46618956
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
REFERENCE 1 (bases 1 to 780)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 8, 2003 this sequence version replaced gi:30452317.
Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DB007CA06QP1&c=3474.r.
FEATURES             Location/Qualifiers
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     1..780
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         /db_xref="taxon:9606"
         /clone="CS0DB007YB11"
         /tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
         /clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
         /note="1st strand cDNA was primed with a NotI-oligo(dT)
         primer. Five prime end enriched, double-strand cDNA was
         digested with Not I and EcoR V sites of the pCMVSPORT 6 vector.
         Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 8.64e-104 Length: 780
Score: 933.00 Matches: 181
Percent Similarity: 98.91% Conservative: 0
Best Local Similarity: 98.91% Mismatches: 2
Query Match: 98.73% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x BX374579 (1-780)

```

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Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db |||||||
172 ATGAAAAGGGCTCTGAACCTCTACTTCAGGCTCCGGTGGAGGAGCGCTTGGAACGC 231
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db |||||||
232 CGACCTGNAACCATCTCTGAGCCCAARACCTATATTGACCTAACCAATGAAGAAACAACT 291
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db |||||||
292 GATTCACACCTTCTAAAAATCAGCCCATCTGAAGATACTCAGCAAGAAAAATGGCAGCATG 351
Qy 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db |||||||
352 TTCTCTCTCATTTACCTGGAATATTGATGGATTATTAACAATCTGTCTAGARAGGGCT 411
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db |||||||
412 CGAGGGGTGTGTTCTACTTAGCTTTGTACAGCCACAGATGTGATATTTCTACAGGAAGTT 471
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db |||||||
472 ATCCCCCATATTATAGCTACCTAAAGAAGAGATCAAGTAATTATGAGATTATTACAGGT 531
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db |||||||
532 CATGAAGAAGGATATTTACACAGCTATAATGTGTAAGAAATCAGAGGTCAAAATTTAAAAAGC 591
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db |||||||
592 CAAGAGATTATTCCTTTCCAAAGTACCMAAATGATGAGAAACCTTTTATGTGCAATGTG 651
Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db |||||||
652 AACGTGTCAGGAAATGAGCTTTGCCTTATGACATCCCATTTGGAGAGCACCAGAGGGCAT 711
Qy 181 AlaAlaGlu 183
Db |||||||
712 GCTCGGAA 720
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Search completed: December 4, 2005, 15:32:22
Job time : 3904.68 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 3, 2005, 23:33:41 ; Search time 568.047 Seconds
(without alignments)
2147.074 Million cell updates/sec

Title: US-10-757-745-2_COPY_54_236

Perfect score: 945

Sequence: 1 MERALNSYFPPVPSALR.....GNELCLMTSHLESTRGHAHE 183

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 500 summaries

Command line parameters:

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-O=/cgn2.1/USPTO.spool/US10757745/runat_01122005_091747_10071/app.query.fasta.1.981
-DB=N_Geneseq -OFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=500
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10757745 @CNG 1.1 1072 @runat_01122005_091747_10071 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPE=6
-FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database : N_Geneseq_21.*

1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002as.*
7: Geneseq2002bs.*
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9: Geneseq2003bs.*
10: Geneseq2003cs.*
11: Geneseq2003ds.*
12: Geneseq2004as.*
13: Geneseq2004bs.*
14: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	945	100.0	1920	3	Az47118 Human CD4
2	945	100.0	1936	10	AD19013 Human dis
3	945	100.0	1936	13	ADP25361 PRO polyp
4	945	100.0	1940	14	ADX06356 Cyclin-de

5	945	100.0	1948	4	AAI58997	AAI58997 Human pol
6	945	100.0	1948	5	ADQ99219	ADQ99219 DNA encod
7	945	100.0	1948	9	ADB48979	ADB48979 Novel hum
8	945	100.0	1958	4	AAI60783	AAI60783 Human pol
9	945	100.0	2499	2	AXA28153	AXA28153 Toposome
10	945	100.0	3152	9	ADA10970	ADA10970 Human cDN
11	937	99.2	1296	3	AAAC98160	AAAC98160 Human col
12	936	99.0	1898	4	AAH15146	AAH15146 Human cDN
13	871	92.2	752	4	AAH08073	AAH08073 Human cDN
14	623.5	66.0	1312	3	AAZ47119	AAZ47119 Mouse CD4
15	585.5	62.0	602	10	ADD34376	ADD34376 Mouse mit
16	559	59.2	483	2	AAAX40590	AAAX40590 Human sec
17	542	57.4	553	11	ADT95464	ADT95464 Colon can
18	542	57.4	553	11	ADX41946	ADX41946 Human cDN
19	540	57.1	401	11	ADT95844	ADT95844 Colon can
20	540	57.1	401	11	ADX42326	ADX42326 Human cDN
21	540	57.1	625	11	ADT95512	ADT95512 Colon can
22	540	57.1	625	11	ADX41994	ADX41994 Human cDN
23	540	57.1	633	11	ADT95565	ADT95565 Colon can
24	540	57.1	633	11	ADX42047	ADX42047 Human cDN
25	540	57.1	644	11	ADT95551	ADT95551 Colon can
26	540	57.1	644	11	ADX42033	ADX42033 Human cDN
27	540	57.1	674	11	ADT95548	ADT95548 Colon can
28	540	57.1	674	11	ADX42030	ADX42030 Human cDN
29	531	56.2	1088	5	AA886254	AA886254 DNA encod
30	525	55.6	1079	2	AA84209	AA84209 DNA encod
31	525	55.6	1079	3	AACT79438	AACT79438 cDNA sequ
32	525	55.6	1079	6	ABK28982	ABK28982 Human bre
33	522	55.2	625	11	ADT95029	ADT95029 Colon can
34	522	55.2	625	11	ADX41511	ADX41511 Human cDN
35	414	43.8	391	11	ADT95307	ADT95307 Colon can
36	414	43.8	391	11	ADX41789	ADX41789 Human cDN
37	352	37.2	1227	5	AA886255	AA886255 DNA encod
38	328	34.1	774	10	ADD34375	ADD34375 Mouse mit
39	292	31.5	176	6	ABK27684	ABK27684 Human col
40	298	31.5	176	6	ABV95959	ABV95959 Human pan
41	298	31.5	179	6	ABL36461	ABL36461 Human col
42	182.5	19.3	444	4	AAI15311	AAI15311 Probe #52
43	182.5	19.3	444	4	AAI124484	AAI124484 Probe #14
44	116.5	12.3	525	13	ACN59762	ACN59762 Cotton gy
45	114	12.1	725	6	ABQ34465	ABQ34465 Oligonucle
46	114	12.1	725	6	ABQ34464	ABQ34464 Oligonucle
47	113	12.0	258	2	AAAC41008	AAAC41008 Human sec
48	111.5	11.8	1566	3	AAAC47239	AAAC47239 Arabidops
49	111.5	11.8	1806	3	AAAC41089	AAAC41089 Arabidops
50	103	10.9	37741	14	ABE47090	ABE47090 Chimpanze
51	101	10.7	60	6	ABN41860	ABN41860 Human spl
52	91.5	9.7	3532	10	ADE15671	ADE15671 Human str
53	91.5	9.7	3640	6	AA899915	AA899915 Polynucle
54	91.5	9.7	3640	12	ADL13159	ADL13159 Human ste
55	91.5	9.7	3875	13	ADR24178	ADR24178 Breast ca
56	91.5	9.7	3950	14	AEA19702	AEA19702 Novel hum
57	91.5	9.7	4058	14	AEA19701	AEA19701 Novel hum
58	91.5	9.7	4061	4	AAI58478	AAI58478 Human pol
59	91.5	9.7	4061	5	ADQ98693	ADQ98693 DNA encod
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61	91.5	9.7	4150	4	AAK51922	AAK51922 Human pol
62	91.5	9.7	4176	4	AAK52905	AAK52905 Human pol
63	91.5	9.7	4176	4	AAK52906	AAK52906 Human pol
64	91.5	9.7	4176	4	AAI60264	AAI60264 Human pol
65	91.5	9.7	4176	14	AEA20688	AEA20688 Novel hum
66	91.5	9.7	4176	14	AEA20689	AEA20689 Novel hum
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69	91.5	9.7	5077	14	ADX07700	ADX07700 Cyclin-de
70	91.5	9.7	5077	14	ADZ49482	ADZ49482 Insulin s
71	88.5	9.4	110000	2	AAK20248_03	Continuation (24 o
72	88.5	9.4	110000	2	ABQ69245_23	Continuation (24 o
73	88.5	9.4	213251	6	ABQ67193	ABQ67193 Listeria
74	88	9.3	8718	6	ABL33273	ABL33273 Human imm
75	87.5	9.3	727	3	AAZ97418	AAZ97418 Human pro
76	87.5	9.3	748	3	AAZ97417	AAZ97417 Human pro
77	87.5	9.3	762	13	AD559554	AD559554 Bacterial

KW immunosuppressive; antiinflammatory; immunosuppressive; antiallergic;
 KW human; CD40 receptor associated protein; CRAP; cytoplasmic domain;
 KW tumour necrosis factor; TNF; receptor; superfamily; CD30; homology;
 KW TNF receptor associated factor; TRAF; modulator; signalling pathway;
 KW diagnosis; NF-kappaB; Jun; kinase; atherosclerosis; multiple sclerosis;
 KW arthritis; systemic lupus erythematosus; graft rejection; allergy;
 KW graft versus host disease; autoimmune disease; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO9955859-A2.
 XX
 XX 04-NOV-1999.
 XX
 XX 28-APR-1999; 99WO-EP003025.
 XX
 XX 29-APR-1998; 98EP-00201392.
 XX
 XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 XX
 XX Pype SMC, Remacle JEFJG, Huybroeck DFE;
 XX
 XX WPI; 2000-062029/05.
 XX
 XX P-PSDB; AAY56019.
 XX
 PT Novel proteins used to treat inflammatory diseases, NF-kappaB related
 PT diseases and for improvement of anti-tumor treatments.
 XX
 XX Claim 9; Page 37-39; 48pp; English.
 XX
 CC This sequence represents the gene encoding human CD40 receptor associated
 CC protein (CRAP). CRAP is a functional protein capable of interacting with
 CC the cytoplasmic domain of CD40 and/or other receptors of the tumour
 CC necrosis factor (TNF) receptor superfamily such as CD30 and TNF receptor
 CC 1, where the protein has no homology to TNF receptor associated factor
 CC (TRAF)-proteins. The CD40 binding proteins can be used as modulators of
 CC the CD40 signalling pathway, especially to diagnose and treat TRAF-
 CC related, CD40-related, NF-kappaB related and/or Jun (kinase)-related
 CC diseases, and for the improvement of anti-tumour diseases. Diseases which
 CC may be treated include atherosclerosis, arthritis, multiple sclerosis,
 CC systemic lupus erythematosus, graft rejection, graft versus host disease,
 CC allergy, and autoimmune disease. The proteins can be used to sensitize
 CC tumour cells to anti-tumour treatments and to screen for compounds which
 CC interfere with the interaction of the proteins with other protein
 CC components of the TRAF, CD40 or NF-kappaB related pathway
 XX
 XX Sequence 1920 BP; 599 A; 327 C; 435 G; 557 T; 0 U; 2 Other;
 XX
 Alignment Scores:
 Pred. No.: 1.07e-104 Length: 1920
 Score: 945.00 Matches: 183
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-10-757-745-2_COPY_54_236 (1-183) x AAZ47118 (1-1920)
 QY 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
 Db 179 ATGGAAAGGCTCTGAACCTCTACTTCCGCTCCGGTGGAGGAGCGCTTGGACGC 238
 QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAenGluThrThr 40
 Db 239 CGACCTGAAACCATCTCGAGCCCAAGACCTATGTGACCTAAACCAATGAAGAAACAAC 298
 QY 41 AspSerThrThrSerIlylleSerProSerGluAspThrGlnGluAenGlySerMet 60
 Db 299 GATTCCACCACTCTCTAAATCAGCCCATCTGAAGATACTCAGCAAGAAAATGGCAGATG 358
 QY 61 PheSerLeuIleThrTyrAenIleAspGlyLeuAspLeuAenLeuSerGluArgAla 80
 Db 359 TTCTCTCTATTACCTGGATATGTGATTAGATTAAACATCTGTCTCAGAGAGGGCT 418

QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
 Db 419 CGAGGGGTGTCTCTACTTACGCTTGTACAGCCAGATGTGATATTTCTACAGGAAGTT 478
 QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
 Db 479 ATTCGCCCATATTATAGCTACCTAAAGAAGAGATCAAGTAATATGAGATTATTACAGGT 538
 QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
 Db 539 CATGAAGAAGGATATTTTACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAAGAAGC 598
 QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
 Db 599 CAAGAGATATATCTCTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCATGTG 658
 QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
 Db 659 AATGTGTCAGGAATGAGCTTTCCTTATGACATCCCATTTTGGAGAGCACCAGAGGCAT 718
 QY 181 AlaAlaGlu 183
 Db 719 GCTGCGGAA 727
 RESULT 2
 ADD19013
 ID ADD19013 standard; DNA; 1936 BP.
 XX
 XX AC ADD19013;
 XX
 XX DT 15-JAN-2004 (first entry)
 XX
 XX DE Human disease related protein DNA sequence SeqID502.
 XX
 XX KW human; disease state; cytostatic; antiinflammatory; ophthalmological;
 KW antiarteriosclerotic; vulnary; gene therapy;
 KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
 KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
 KW glucose transportation; catecholamine synthesis; iron transport;
 KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
 KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
 KW inflammatory condition; wound healing; gene; ds.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO2003018621-A2.
 XX
 XX PD 06-MAR-2003.
 XX
 XX PF 23-AUG-2002; 2002WO-GB003892.
 XX
 XX PR 23-AUG-2001; 2001GB-00020558.
 XX
 XX PR 05-OCT-2001; 2001GB-00024037.
 XX
 XX PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX
 XX PI Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
 XX
 XX DR WPI; 2003-290046/28.
 XX
 XX DR P-PSDB; ADD19012.
 XX
 XX PT New substantially purified polypeptide, useful for diagnosing or treating
 XX a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
 XX injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
 XX wound healing.
 XX
 XX PS Claim 27; SEQ ID NO 502; 424pp; English.
 XX
 XX CC This invention relates to novel human genes and gene product which are
 XX implicated in certain disease states. Compounds which modulate the
 XX proteins of the invention may have cytostatic, antiinflammatory, the
 XX ophthalmological, antiarteriosclerotic or vulnerary activities. The

CC sequences of the invention may be useful for gene therapy. The invention
CC may be useful for diagnosing or treating a hypoxia-regulated condition,
CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
CC erythropoiesis, or the biological response to hypoxia conditions
CC including processes such as glycolysis, gluconeogenesis, glucose
CC transportation, catecholamine synthesis, iron transport or nitric oxide
CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
CC inflammatory conditions or wound healing. The present sequence is that of
CC a disease related protein encoding DNA sequence of the invention.
XX
XX

SQ Sequence 1936 BP; 617 A; 330 C; 431 G; 558 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.08e-104 Length: 1936
Score: 945.00 Matches: 183
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x ADD19013 (1-1936)

Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 176 ATGGAAGGGCTCTGAACTCTTCTGAGCTCGGTGGAGAGCGCTTGGACGC 235
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db 236 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAAC 295
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 296 GATTCCACCATCTTAAATCAGCCCATCTGAAGATATCTCAGCAAGAAATGGCAGCATG 355
Qy 61 PheSerLeuIleThrTTPAsnIleAspGlyLeuAspLeuAenSerGluArgAla 80
Db 356 TTCTCTCTCATCTGGAATATTGATGGATTAGATTAACAATCTGTACAGAGGGCT 415
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 416 CGAGGGGTGTCTCTACTAGCTTTGTACAGCCAGATGTGATATTCTACAGGAAGTT 475
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 476 ATTCCTCCATATTATAGCTACCTAAGAAGAGATCAAGTAATTATGATATTATACAGGT 535
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 536 CATGAGNAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGGTGAATTTAAAGC 595
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCyValHisVal 160
Db 596 CAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 655
Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 656 AACGTGTGAGAAATGAGCTTTGCTTATGATCATCCCATTTGGAGAGCAGAGGGCAT 715
Qy 181 AlaAlaGlu 183
Db 716 GCTGGGAA 724

RESULT 3

ADP25361

ID ADP25361 standard; cDNA; 1936 BP.

XX ADP25361;

AC ADP25361;

XX 18-NOV-2004 (first entry)

XX PRO polypeptide encoding cDNA SEQ ID NO:475.
XX

KW ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
KW immunosuppressive; osteopathic; antidiabetic; dermatological;
KW antiproliferative; antiallergic; antiasthmatic; hepatotropic; respiratory;
KW gene therapy; immune system.
XX Unidentified.

XX WO2004041170-A2.

XX 21-MAY-2004.

XX 30-OCT-2003; 2003WO-US034312.

XX 01-NOV-2002; 2002US-0423394P.

XX (GETH) GENENTECH INC.

XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WT;

XX Wu TD;

XX WPI; 2004-419628/39.

XX P-PSDB; ADP25362.

XX New PRO polypeptides and polynucleotides, useful for treating e.g.

XX erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
XX renal disease, or demyelinating diseases of the central or peripheral
XX nervous system.

XX Claim 1; SEQ ID NO 475; 2940pp; English.

XX The invention relates to a novel isolated nucleic acid and the PRO

XX polypeptide encoded by it. A protein of the invention has

XX antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,

XX osteopathic, antidiabetic, dermatological, antiproliferative, antiallergic,

XX antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide

XX of the invention may have a use in gene therapy. The PRO polypeptide, its

XX agonist, antagonist, or antibody that specifically binds to the

XX polypeptide is useful for treating an immune related disorder such as

XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,

XX juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an

XX idiopathic inflammatory myopathy, Sjogren's syndrome, systemic

XX vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune

XX thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal

XX disease, a demyelinating disease of the central or peripheral nervous

XX system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,

XX a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary

XX disease, infectious or autoimmune chronic active hepatitis, primary

XX biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,

XX inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's

XX disease, an autoimmune or immune-mediated skin disease, a bullous skin

XX disease, erythema multiforme, contact dermatitis, psoriasis, an allergic

XX disease, asthma, allergic rhinitis, atopic dermatitis, food

XX hypersensitivity, urticaria, an immunologic disease of the lung,

XX eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity

XX pneumonitis, a transplantation associated disease, graft rejection or

XX graft-versus-host disease. The present sequence encodes a PRO protein of

XX the invention.

XX SQ Sequence 1936 BP; 617 A; 330 C; 431 G; 558 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.08e-104 Length: 1936

Score: 945.00 Matches: 183

Percent Similarity: 100.00% Conservativeness: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 13 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x ADP25361 (1-1936)

Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20

Db 176 ATGGAAGGGCTCTGAACTCTTCTGAGCTCGGTGGAGAGCGCTTGGACGC 235

QY 21 ArgProGluThrIleSerGluProIlyThrTyValAspLeuThrAsnGluThrThr 40
DB 236 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAAC 295
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 236 GATTCACACACTTCTAAATACGCCCATCTGAAGATATCTCAGCAAGAAATGGCAGCATG 355
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 356 TTCTCTCTCATACCTGGAATATTGATGATAGATCTAAACAATCTGTCTCAGAGAGGCT 415
QY 81 ArgGlyValCysSerTyLeuAlaLeuTySerProAspValIlePheLeuGlnGluVal 100
DB 416 CGAGGGGTGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATATTCTCAGGAAGTT 475
QY 101 IleProProTyTySerTyLeuLysLysArgSerSerAsnTyGluIleIleThrGly 120
DB 476 ATTCCTCCATATTATAGCTTACCTTAAGAAGAGATCAAGTAATTATGAGATTATTACAGGT 535
QY 121 HisGluGluGlyTyPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
DB 536 CATGAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAAGAAAGC 595
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
DB 596 CAAGAGATTATTCTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 655
QY 161 AsnValSerGlyAsnGluLeuCysValLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
DB 656 AACGTGTGAGGAATAGAGCTTTGCTTATGACATCCATTTGGAGAGACCAAGAGGGCAT 715
QY 181 AlaAlaGlu 183
DB 716 GCTGCGGAA 724
RESULT 4
ADX06356
ID ADX06356 standard; DNA; 1940 BP.
XX AC ADX06356;
XX DT 21-APR-2005 (first entry)
XX DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 921.
XX KW cytostatic; cyclin-dependent kinase; cdk; biomarker; gene; ds.
XX OS Homo sapiens.
XX PN W02005012875-A2.
XX PD 10-FEB-2005.
XX PF 29-JUL-2004; 2004WO-US024424.
XX PR 29-JUL-2003; 2003US-0490890P.
XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX WPI; 2005-163068/17.
XX P-PSDB; ADX06357.
XX PT Biomarkers useful for predicting or determining the response of a mammal
XX to a cancer treatment comprising administration of a modulator of cyclin-
XX dependent kinase activity.
XX PS Claim 5; SEQ ID NO 921; 141pp; English.
XX CC This invention describes a novel method of predicting or determining

CC whether a mammal will respond or is responding to an anti-cancer agent
CC that modulates cyclin-dependent kinase (cdk) activity. The method
CC comprises measuring the level of one or more biomarkers selected from
CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
CC NO.1246 (Genbank EST W28729) is especially preferred). The method of the
CC invention is utilized in a kit for determining or predicting whether
CC patient would be susceptible or resistant to treatment by an agent
CC modulating cdk activity. The invention also describes a method for
CC utilizing individualized genetic profiles for treating diseases and
CC disorders based on patient's response and molecular level, specialized
CC microarrays comprising the biomarkers described, antibodies directed
CC against the biomarkers and a cell culture model to identify biomarkers.
CC The cdk modulator is preferably N-5-[(5-(1,1-Dimethylethyl)-2-
CC oxazolyl)methyl]chlo-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
CC tartaric acid salt. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_sequences. This
CC sequence encodes a biomarker used in the method of the invention.
XX SQ Sequence 1940 BP; 613 A; 330 C; 439 G; 558 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.09e-104 Length: 1940
Score: 945.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps:
US-10-757-745-2_COPY_54_236 (1-183) x ADX06356 (1-1940)
QY 1 MetGluArgAlaLeuAsnSerTyPheGluProValGluGluSerAlaLeuGluArg 20
DB 185 ATGGAAGGGCTCTGAACTCTTCTGAGCTTCGGTGGAGAGAGCGCTTGGNACGC 244
QY 21 ArgProGluThrIleSerGluProIlyThrTyValAspLeuThrAsnGluThrThr 40
DB 245 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAAC 304
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 305 GATTCACACACTTCTAAATATCAAGCCATCTGAAGATATCTCAGCAAGAAATGGCAGCATG 364
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 365 TTCTCTCTCATACCTGGAATATTGATGATAGATTAGATCTAAACAATCTGTCTCAGAGGGCT 424
QY 81 ArgGlyValCysSerTyLeuAlaLeuTySerProAspValIlePheLeuGlnGluVal 100
DB 425 CGAGGGGTGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATATTCTACAGGAAGTT 484
QY 101 IleProProTyTySerTyLeuLysLysArgSerSerAsnTyGluIleIleThrGly 120
DB 485 ATTCCTCCATATTATAGCTTACCTTAAGAAGAGATCAAGTAATTATGAGATTATTACAGGT 544
QY 121 HisGluGluGlyTyPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
DB 545 CATGAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTAAGAAAGC 604
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
DB 605 CAAGAGATTATTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 664
QY 161 AsnValSerGlyAsnGluLeuCysValMetThrSerHisLeuGluSerThrArgGlyHis 180
DB 665 AACGTGTGAGGAATAGAGCTTTGCTTATGACATCCATTTGGAGAGACCAAGAGGGCAT 724
QY 181 AlaAlaGlu 183
DB 725 GCTGCGGAA 733
RESULT 5
AAI58997

ID	AAI58997 standard; cDNA; 1948 BP.	US-10-757-745-2_COPY_54_236 (1-183) x AAI58997 (1-1948)	
XX	AAI58997;		
XX	22-OCT-2001 (first entry)		
XX	Human polynucleotide SEQ ID NO 1200.		
XX	Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;		
KW	peripheral nervous system; neuropathy; central nervous system; CNS;		
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;		
KW	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;		
KW	chemokinetic; thrombolytic; drug screening; arthritis; inflammation;		
KW	leukaemia; BS.		
XX	Homo sapiens.		
OS	WO200153312-A1.		
XX	26-JUL-2001.		
XX	26-DEC-2000; 2000WO-US034263.		
XX	23-DEC-1999; 99US-00471275.		
PR	21-JAN-2000; 2000US-00488725.		
PR	23-APR-2000; 2000US-00552317.		
PR	20-JUN-2000; 2000US-00598042.		
PR	19-JUL-2000; 2000US-00620312.		
PR	03-AUG-2000; 2000US-00653450.		
PR	14-SEP-2000; 2000US-00662191.		
PR	19-OCT-2000; 2000US-00693036.		
PR	29-NOV-2000; 2000US-00727344.		
XX	(HYSE-) HYSEQ INC.		
XX	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;		
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;		
PI	Zhou F, Goodrich R, Drmanac RT;		
XX	WPI; 2001-442253/47.		
DR	P-PSDB; AAM39841.		
XX	Novel nucleic acids and polypeptides, useful for treating disorders such		
PT	as central nervous system injuries.		
XX	Claim 1; SEQ ID NO 1200; 10078pp; English.		
XX	The invention relates to human nucleic acids (AAI57798-AAI61369) and the		
CC	encoded polypeptides (AAM38642-AAM42213) with nootropic,		
CC	immunosuppressant and cytostatic activity. The polynucleotides are useful		
CC	in gene therapy. A composition containing a polypeptide or polynucleotide		
CC	of the invention may be used to treat diseases of the peripheral nervous		
CC	system, such as peripheral nervous injuries, peripheral neuropathy and		
CC	centralised neuropathies and central nervous system diseases, such as		
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic		
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the		
CC	utilisation of the activities such as: immune system suppression,		
CC	Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic		
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,		
CC	assays for receptor activity, arthritis and inflammation, leukaemias and		
CC	C.N.S disorders. Note: The sequence data for this patent did not form		
CC	part of the printed specification		
XX	Sequence 1948 BP; 614 A; 335 C; 436 G; 563 T; 0 U; 0 Other;		
SQ			
XX	Alignment Scores:		
Pred. No.:	1-09e-104	Length:	1948
Score:	945.00	Matches:	183
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0
DB:			
Qy	1 MetGluArgAlaLeuAenSerTyrPheGluProProValGluGluSerAlaLeuGluArg	20	
Db	198 ATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCCGGTGAGGAGCGCCTTTGGAAACGC	257	
Qy	21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAenGluGluThrThr	40	
Db	258 CGACCTGAAACCAATCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAAGAACAAC	317	
Qy	41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAenGlySerMet	60	
Db	318 GAITCCACCACTTCTAAATCAGCCCATCTGAAAGATACTCAGCAAGAAAATGGCAGCATG	377	
Qy	61 PheSerLeuIleThrTrpAenIleAspGlyLeuAspLeuAenLeuSerGluArgAla	80	
Db	378 TTCTCTCTCATTTACCTGGAATATTGATGGATTAGATCTAAACAATCTGTGAGAGGGCT	437	
Qy	81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal	100	
Db	438 CGAGGGGTGTCTTCTACTTAGCTTTGTACAGCCCATGTGATATTCTACAGAAAGTT	497	
Qy	101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleThrGly	120	
Db	498 ATTCCCCCATATTATAGTACCTAAGAAGAGATCAAGTAATTATGAGATTATTACAGGT	557	
Qy	121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer	140	
Db	558 CATGAAGAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAAAGC	617	
Qy	141 GlnGluIleIleProPheProSerThrLysMetMetArgAenLeuLysValHisVal	160	
Db	618 CAAGAGATTATTCTTTTCCAAAGTACCATAATGATGAGAAACCTTTTATGTGTCATGTG	677	
Qy	161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis	180	
Db	678 AATGTGTGAGAAATGAGCTTTTGCTTATGACATCCCATTTGGAGAGACCCAGAGGGCAT	737	
Qy	181 AlaAlaGlu	183	
Db	738 GCTGCGGAA	746	
XX	RESULT 6		
ADQ99219	ADQ99219 standard; cDNA; 1948 BP.		
XX	ADQ99219;		
XX	23-SEP-2004 (first entry)		
DE	DNA encoding human GPCR-like protein seqid 889.		
XX	ophthalmological; immunomodulatory; cytostatic; antiatherosclerotic;		
KW	antidiabetic; GPCR-like protein; ophthalmic disorder;		
KW	neurological disorder; immunological disorder; nephritic disorder;		
KW	hormonal dysfunction; cancer; atherosclerosis; diabetes;		
KW	molecular weight marker; food supplement; human; ss.		
OS	Homo sapiens.		
PN	US6569662-B1.		
XX	27-MAY-2003.		
XX	19-JUL-2000; 2000US-00620312.		
PR	21-JAN-2000; 2000US-00488725.		
XX	25-APR-2000; 2000US-00552317.		
PA	(HYSE-) HYSEQ INC.		
XX	Tang YT, Zhou P, Drmanac RT;		
XX			

DR WPI; 2001-442255/47.
XX New G-protein-coupled receptor-like polypeptides and polynucleotides,
PT useful for treating diseases of ophthalmic, neurological, immunological
PT and nephritic systems and hormonal dysfunction, cancer, atherosclerosis
PT and diabetes.
XX
XX Example 2; SEQ ID NO 889; 92pp; English.
PS
XX The invention describes an isolated polynucleotide (I) comprising a fully
CC defined (S1) of 749, 3188, 2484, 1169, 2936, 1467, 5773, 5714, 4041,
CC 1372, 3996, 3945, 2735, 1788, 585, 1782, 927, 5714 or 2282 nucleotides as
CC given in the specification, its translated or protein coding portion, its
CC extracellular portion or its active domain. The GPCR-like polypeptides
CC and polynucleotides are useful for the treatment of diseases of
CC ophthalmic, neurological, immunological and nephritic systems. They may
CC also be used to treat hormonal dysfunction, cancer, atherosclerosis and
CC diabetes. The antibodies are useful for detecting or quantitating the
CC polypeptide in tissue. The polypeptides can also be used as molecular
CC weight markers and as a food supplement. This sequence represents a human
CC polynucleotide of the invention.
XX
SQ Sequence 1948 BP; 614 A; 335 C; 436 G; 563 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.09e-104 Length: 1948
Score: 945.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x ADO99219 (1-1948)

QY 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluSerAlaLeuGluArg 20
DB 198 ATGGAAGGCTCTGAACCTCTACTTCGAGCCTCCGGTGGAGAGAGCGCTTGGAAACG 257
QY 21 ArgProGluThrIleSerGluProLysThrValAspLeuThrAenGluThrThr 40
DB 258 CGACCTGAAACCATCTCGAGCCCAAGACCTATGTGACCTAACCAATGAAGAAACAACT 317
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGluAenGlySerMet 60
DB 318 GATTCCACCACTCTCTAAATCAGCCCACTGGAAGATACTCAGCAAGAAAATGCCAGCATG 377
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAenSerGluArgAla 80
DB 378 TTCTCTCTATACCTGGATATATGATGGATTAGATTAACTAATCTGTCAGAGAGGGCT 437
QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
DB 438 CGAGGGGTGTCTCTACTTACTTGTACAGCCCAAGATGTGATATTTCTACAGGAAGTT 497
QY 101 IleProProTyrTyrSerTyrLeuLysValArgSerSerAenTyrGluIleThrGly 120
DB 498 ATTCCTCCATATATATAGCTACCTAAAGAGAGATCAAGTATATATGATATATACAGGT 557
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
DB 558 CATGAAGAGAGATATTTACAGCTATATATGTTGAAGAAATCAAGAGTGAATTAAGAAAG 617
QY 141 GlnIleIleLeuProPheProSerThrLysMetMetMetArgAenLeuLysValHisVal 160
DB 618 CAAGAGATATATCTCTTCCAAATGATGAGAAACCTTTTATGTGTGATGTG 677
QY 161 AsnValSerGlyAenGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
DB 678 AATGTGTGAGAAATGAGCTTTGCTTTATGACATCCCATTTGGAGAGACCAAGAGGGCAT 737
QY 181 AlaAlaGlu 183
DB 738 GCTCCGGA 746

RESULT 7

ID ADB48979 standard; cDNA; 1948 BP.
XX ADB48979;
AC ADB48979;
XX 04-DEC-2003 (first entry)
DT
XX
DE Novel human cDNA SEQ ID NO 889.
XX
XX ss; cancer; neurodegenerative disease; human.
XX
XX Homo sapiens.
OS
XX US2003104529-A1.
PN
XX
XX 05-JUN-2003.
PD
XX 04-JAN-2002; 2002US-00037270.
PF
XX 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 19-JUL-2000; 2000US-00620312.
XX
XX (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R T.
XX
XX Zhou P, Tang YT, Liu C, Asundi V, Drmanac RT;
XX WPI; 2003-678194/64.
DR
XX New polynucleotide, useful for treating diseases e.g., cancer or
PT neurodegenerative diseases.
XX
XX Claim 1; SEQ ID NO 889; 99pp; English.
PS
XX The invention relates to a polynucleotide comprising a sequence given in
CC the specification, or its mature protein-coding portion, or its
CC complement. The polynucleotide is useful for treating diseases e.g.,
CC cancer or neurodegenerative diseases and many others listed in the
CC specification. The present sequence represents a novel human cDNA. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=20030104529.
XX
SQ Sequence 1948 BP; 614 A; 335 C; 436 G; 563 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.09e-104 Length: 1948
Score: 945.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x ADB48979 (1-1948)

QY 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluSerAlaLeuGluArg 20
DB 198 ATGGAAGGCTCTGAACCTCTACTTCGAGCCTCCGGTGGAGAGAGCGCTTGGAAACG 257
QY 21 ArgProGluThrIleSerGluProLysThrValAspLeuThrAenGluThrThr 40
DB 258 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAAGAAACAACT 317
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGluAenGlySerMet 60
DB 318 GATTCCACCACTCTCTAAATCAGCCCACTCTGAGAGATACTCAGCAAGAAAATGGCAGCATG 377

Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 378 TTCTCTCTCATCTGAAATATTGATGGATTAGATCTAAACAATCTGTCAGAGGGCT 437
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 438 CGAGGGGTGTCTCTACTTACCTTGTACAGCCAGATGTGATATTTCTACAGGAGTT 497
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 498 ATTCCTCCCATATTATAGCTTACCTAAAGAAAGAGATCAAGTAATATTGAGATTATTACAGGT 557
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 558 CATGAAGAAGGATATTTCACAGCTATAATGTGAAGAAATCAAGAGTGAATATAAAGC 617
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysValHisVal 160
Db 618 CAAGAGATTATTCCTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 677
Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 678 AATGTGTGAGGAAATGAGCTTTGCCTTATGACATCCCATTTGGAGAGCACCAGAGGGCAT 737
Qy 181 AlaAlaGlu 183
Db 738 GCTGCGGAA 746
RESULT 8
AAI60783
ID AAI60783 standard; cDNA; 1958 BP.
XX AC AAI60783;
XX DT 22-OCT-2001 (first entry)
XX DE Human polynucleotide SEQ ID NO 4772.
XX KW Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX OS Homo sapiens.
XX PN WO200153312-A1.
XX PD 26-JUL-2001.
XX PF 26-DEC-2000; 2000WO-US034263.
XX PR 23-DEC-1999; 99US-00471275.
XX PR 21-JAN-2000; 2000US-00488725.
XX PR 25-APR-2000; 2000US-00552317.
XX PR 20-JUN-2000; 2000US-00598042.
XX PR 19-JUL-2000; 2000US-00620312.
XX PR 03-AUG-2000; 2000US-00653450.
XX PR 14-SEP-2000; 2000US-00662191.
XX PR 19-OCT-2000; 2000US-00693036.
XX PR 29-NOV-2000; 2000US-00727344.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX WPI; 2001-442253/47.
XX DR P-PSDB; AAM41627.
XX PT Novel nucleic acids and polypeptides, useful for treating disorders such

as central nervous system injuries.
XX Claim 1; SEQ ID NO 4772; 10078pp; English.
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with neurotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX SQ Sequence 1958 BP; 613 A; 339 C; 442 G; 564 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.1e-104 Length: 1958
Score: 945.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-757-745-2_COPY_54_236 (1-183) x AAI60783 (1-1958)
Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 210 ATGGAAGGGCTCTGAACTCTCTACCTCGAGCTCCGGTGGAGAGCGCTTGGAAAGC 269
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db 270 CGACTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAAC 329
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 330 GATTCACCACTTCTTAAATCAGCCCATCTCAAGATACTCAGCAAGAAATGGCAGCATG 389
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 390 TTCTCTCTCATCTGAAATATTGATGGATTAGATCTAAACAATCTGTCAGAGGGCT 449
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 450 CGAGGGGTGTCTCTACTTACCTTGTACAGCCAGATGTGATATTTCTACAGGAGTT 509
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 510 ATTCCTCCCATATTATAGCTTACCTAAAGAAAGAGATCAAGTAATATTGAGATTATTACAGGT 569
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 570 CATGAAGAAGGATATTTCACAGCTATAATGTGTGAAGAAATCAAGAGTGAATATAAAGC 629
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysValHisVal 160
Db 630 CAAGAGATTATTCCTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 689
Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 690 AATGTGTGAGGAAATGAGCTTTGCCTTATGACATCCCATTTGGAGAGCACCAGAGGGCAT 749
Qy 181 AlaAlaGlu 183
Db 750 GCTGCGGAA 758
RESULT 9

```
AA28153
ID AAX28153 standard; DNA; 2499 BP.
AC AAX28153;
DT 16-JUN-1999 (first entry)
XX Topoisomerase II binding protein 1 coding sequence.
DE Topoisomerase II binding protein; TopBP; anticancer agent; ds.
KW Topoisomerase II binding protein; TopBP; anticancer agent; ds.
OS Homo sapiens.
XX JP11075856-A.
PN 23-MAR-1999.
PD 17-SEP-1997; 97JP-00251544.
PF 17-SEP-1997; 97JP-00251544.
PR 17-SEP-1997; 97JP-00251544.
XX (TSURUO T.
PA (CHUS ) CHUGAI PHARM CO LTD.
XX WPI; 1999-257704/22.
DR P-PSDB; AAY03182.
XX New Topoisomerase II- binding protein - useful as an anticancer agent.
PT Disclosure; Page 18-19; 28pp; Japanese.
PS This sequence encodes the topoisomerase II binding protein (TopBP) of the
CC invention. The TopBP protein is useful as an anticancer agent. TopBP can
CC be used as the target molecule for anticancer agent
XX SQ Sequence 2499 BP; 720 A; 505 C; 587 G; 687 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.56e-104 Length: 2499
Score: 945.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x AAX28153 (1-2499)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 641 ATGGAAGGCTCTGAACCTCTACTTCGAGCCTCCCGTGAGGAGCGCTTGGAAACG 700

QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 701 CGACCTGAACCATCTCGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 760

QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 761 GAITCCACCACTTCTAAATCAGCCCATCTGAAGATACTCAGCAAGAAAATGGCAGCATG 820

QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 821 TTCTCTCTCATACCTGGAATATTTGATGGATTAGATCTAAACAAATCTGTACAGAGGGCT 880

QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
DB 881 CGAGGGGTGTCTCTACTTAGCTTTGTACAGCCAGAGTGTATATTCTACAGGAAGTT 940

QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
DB 941 ATTCGCCCATATTATAGTCTACCTAAAGAGAGATCAAGTAATTTATGAGATTATTACAGGT 1000

QY 121 HisGluGluClyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
DB 121 ATTCGCCCATATTATAGTCTACCTAAAGAGAGATCAAGTAATTTATGAGATTATTACAGGT 1000

Db 1001 CATGAAGAAGGATATTTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAAATTAAGAGC 1060
QY 141 GlnGluIleIleProPheProSerThrIleMetMetArgAsnLeuLeuCysValHisVal 160
DB 1061 CAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 1120
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
DB 1121 AATGTGTAGGAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCACCAGAGGCAT 1180
QY 181 AlaAlaGlu 183
DB 1181 GCTGCGGAA 1189

RESULT 10
ADA10970
ID ADA10970 standard; cDNA; 3152 BP.
XX AC ADA10970;
XX DT 06-NOV-2003 (first entry)
XX DE Human cDNA differentially expressed in colon cancer #60.
XX KW ss; differential expression; colon cancer; cancer; human.
XX OS Homo sapiens.
XX PN US2002160382-A1.
XX PD 31-OCT-2002.
XX PF 11-OCT-2001; 2001US-00981353.
XX PR 11-OCT-2000; 2000US-0239841P.
XX PA (LASEK/) LASEK A W.
XX PA (JONES/) JONES D A.
XX PI Lasek AW, Jones DA;
XX WPI; 2003-265756/26.
XX PT New combination comprising cDNAs that are differentially expressed in
PT colon disorder, useful for diagnosing, treating, staging or monitoring
PT treatment for colon cancers.
XX Claim 1; SEQ ID NO 88; 231pp; English.
XX The invention relates to a combination comprising cDNAs that are
XX differentially expressed in colon disorder. The methods and compositions
XX of the present invention are useful for diagnosing, treating, staging or
XX monitoring treatment for colon cancer. They are also useful in high
XX throughput methods for using cDNAs to detect differential expression of
XX nucleic acids in a sample, screening molecules or compounds to identify a
XX ligand which specifically binds a cDNA and using a protein to screen
XX molecules or compounds to identify at least one ligand which specifically
XX binds the protein. The present sequence represents a human cDNA
XX differentially expressed in colon cancer.
SQ Sequence 3152 BP; 875 A; 643 C; 707 G; 926 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 2.17e-104 Length: 3152
Score: 945.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x ADA10970 (1-3152)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
```

|||||
Db 1411 ATGGAAGGCTCTGAATCTTACTTCAGGCTCCGGTGGAGGAGCGCTTGGACGC 1470
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db 1471 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAACAAC 1530
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 1531 GATTCCACCACCTTCTAAATCAGCCATCTGAAGATCTCAGCAAGAAATGGCAGCATG 1590
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 1591 TTCTCTCATTAATCTGGAATATTGATGATAGTAAACATCTCTCAGAGGGCT 1650
Qy 81 ArgGlyValCysSerThrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 1651 CGAGGGGTGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTT 1710
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 1711 ATTCCCCATATTATAGTACTTAAGAGAGATCAAGTAATTATGAGATTATTACAGGT 1770
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 1771 CATGAAGAGGATATTTCCAGCTATTAATGTTGAAGAAATCAAGAGTGAATTTAAAGC 1830
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db 1831 CAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 1890
Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 1891 AATGTGTGAGGAATGAGCTTTGCTTATGACATCCCATTTGGAGAGACCAGAGGGCAT 1950
Qy 181 AlaAlaGlu 183
Db 1951 GCTGCGGAA 1959
RESULT 11
AAC98160
ID AAC98160 standard; cDNA; 1296 BP.
XX
AC AAC98160;
XX
XX
XX 09-MAR-2001 (first entry)
XX
XX Human colon cancer antigen nucleotide sequence SEQ ID NO:170.
DE
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW identification; cytostatic; cardioactive; neuroprotective; vulnary;
KW immunomodulatory; muscular; gynaecological; gastrointestinal;
KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;
KW neural disorder; immune system disorder; muscular disorder;
KW reproductive disorder; gastrointestinal disorder; renal disorder;
KW infectious disease; cardiovascular disorder; ss.
XX
XX Homo sapiens.
OS
XX WO200055351-A1.
PN
XX
XX 21-SEP-2000.
PD
XX
XX 08-MAR-2000; 2000WO-US005883.
PF
XX
XX 12-MAR-1999; 99US-0124270P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Ruben SM;
PI
XX
XX WPI; 2000-587534/55.
DR
XX
XX P-PSDB; AAB53403.

XX
PT Colon cancer associated gene sequences, referred to as colon cancer
PT antigens, useful for the treatment, prevention, and diagnosis of colon
PT disorders such as colon cancer.
XX
PS Claim 1; Page 597; 2104pp; English.
XX
CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
CC vulnary, nephrotropic, antiinfective and antibacterial activities, and
CC can be used in gene therapy. The colon cancer antigen polynucleotides,
CC proteins and antibodies to the proteins are useful for the prevention,
CC treatment and diagnosis of colon disorders, such as colon cancer. The
CC polynucleotides may be used in diagnostics and research, such as for
CC chromosome identification, and as hybridisation probes. The proteins may
CC also be used to prevent diseases such as neural disorders, immune system
CC disorders, muscular disorders, reproductive disorders, gastrointestinal
CC disorders, wounds, renal disorders, infectious diseases, and
CC cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 1296 BP; 376 A; 250 C; 326 G; 333 T; 0 U; 11 Other;
Alignment Scores:
Pred. No.: 5.78e-104 Length: 1296
Score: 937.00 Matches: 182
Percent Similarity: 99.45% Conservative: 0
Best Local Similarity: 99.45% Mismatches: 1
Query Match: 99.15% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_54_236 (1-183) x AAC98160 (1-1296)
Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 183 ATGGAAGGCTCTGAATCTTACTTTCAGGCTCCGGTGGAGGAGCGCTTGGACGC 242
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db 243 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAACAAC 302
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 303 GATTCCACCCTCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAACAAC 362
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 363 TTCTCTCTCATTAATCTGGAATATTGATGATAGTAAACATCTGTGAGAGGGCT 422
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 423 CGAGGGGTGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTT 482
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120
Db 483 ATTCCCCATATTATAGTACTTAAGAGAGATCAAGTAATTATGAGATTATTACAGGT 542
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 543 CATGAAGAGGAKATTTCCAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAGC 602
Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisVal 160
Db 603 CAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 662
Qy 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 663 AATGTGTGAGGAATGAGCTTTGCTTATGACATCCCATTTGGAGAGACCAGAGGGCAT 722
Qy 181 AlaAlaGlu 183
|||||


```
Db          723 GCTGCGGAA 731
RESULT 12
ID AAH15146 standard; cDNA; 1898 BP.
AC AAH15146;
XX
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:13209.
XX
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
XX Homo sapiens.
XX
XX EP1074617-A2.
XX
XX 07-FEB-2001.
XX
XX 28-JUL-2000; 2000EP-00116126.
XX
XX 29-JUL-1999; 99JP-00248036.
XX
XX 27-AUG-1999; 99JP-00300253.
XX
XX 11-JAN-2000; 2000JP-00118776.
XX
XX 02-MAY-2000; 2000JP-00183767.
XX
XX 09-JUN-2000; 2000JP-00241899.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-
XX length cDNAs defined in the specification, and for the detection and/or
XX diagnosis of the abnormality of the proteins encoded by the full-length
XX cDNAs.
XX
XX Claim 8; SEQ ID NO 13209; 2537pp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesising 5602 full-
XX length cDNAs defined in the specification. Where a primer set comprises:
XX (a) an oligo-dT primer and an oligonucleotide complementary to the
XX complementary strand of a polynucleotide which comprises one of the 5602
XX nucleotide sequences defined in the specification, where the
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 5'-end
XX sequence and an oligonucleotide comprising a sequence complementary to a
XX polynucleotide which comprises a 3'-end sequence, where the
XX oligonucleotide comprises at least 15 nucleotides and the combination of
XX the 5'-end sequence/3'-end sequence is selected from those defined in the
XX specification. The primer sets can be used in antisense therapy and in
XX gene therapy. The primers are useful for synthesising polynucleotides,
XX particularly full-length cDNAs. The primers are also useful for the
XX detection and/or diagnosis of the abnormality of the proteins encoded by
XX the full-length cDNAs. The primers allow obtaining of the full-length
XX cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
XX AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
XX represent human amino acid sequences; and AAH13629 to AAH13632 represent
XX oligonucleotides, all of which are used in the exemplification of the
XX present invention
XX
XX Sequence 1898 BP; 590 A; 327 C; 426 G; 555 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 1.32e-103 Length: 1898
XX Score: 936.00 Matches: 182
XX Percent Similarity: 99.45% Conservative: 0
XX Best Local Similarity: 99.45% Mismatches: 1
XX Query Match: 99.05% Indels: 0
```

DB: 4 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x AAH15146 (1-1898)

QY 1 MetGluArgAlaLeuAasnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20

160 ATGGAAGGGCTCTGAACCTCCTGCTTCGAGCCCTCGGTGGAGGAGCGCTTGAACGC 219

QY 21 ArgProGluThrIleSerGluProLysThrTyrValaAspLeuThrAenGluGluThrThr 40

220 CGACCTGAACCACTCTCTGAGCCCAAGACCTATGTTGACCTAAACCAATGAAGAACAACACT 279

QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGlnGlnGlnGlnGln 60

280 GATTCACCACTTCTTAATTCAGCCCATCTGAAGTACTCAGCAAGAAAATGGCAGCATG 339

QY 61 PheSerLeuIleThrTirAsnIleAspGlyLeuAspLeuAasnLeuSerGluArgAla 80

340 TTCTCTCTCATTCCTGAATATTGATGATTTAGATCTAAACAATCTGTCTCAGAGGGCT 399

QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100

400 CGAGGGGTGCTCTCTACTTGTACAGCCAGATGTGATATTCTCAGGAAGTT 459

QY 101 IleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGly 120

460 ATTCCCTCATTTATGATGCTTACCTAAAGAGAGATCAAGTAATTATGAGATTTATTACAGCT 519

QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140

520 CATGAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAGAC 579

QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAasnLeuLeuCysValHisVal 160

580 CAAGAGATTTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTG 639

QY 161 AenValSerGlyAasnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180

640 AACGTGTGAGGAATGAGCTTTGCTTTATGACATCCCATTTTGAGAGACCAAGAGGCAT 699

QY 181 AlaAlaGlu 183

700 GCTGCGGAA 708

RESULT 13

AAH08073

ID AAH08073 standard; cDNA; 752 BP.

XX AC AAH08073;

XX DT 26-JUN-2001 (first entry)

XX DE Human cDNA clone (5'-primer) SEQ ID NO:4908.

XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX OS Homo sapiens.

XX PN EP1074617-A2.

XX PD 07-FEB-2001.

XX PF 28-JUL-2000; 2000EP-00116126.

XX PR 29-JUL-1999; 99JP-00248036.

XX PR 27-AUG-1999; 99JP-00300253.

XX PR 11-JAN-2000; 2000JP-00118776.

XX PR 02-MAY-2000; 2000JP-00183767.

XX PR 09-JUN-2000; 2000JP-00241899.

XX (HELI-) HELIX RES INST.

XX PA Ota T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;

PI

Pred. No.:	1,08e-65	Length:	1312
Score:	623.50	Matches:	122
Percent Similarity:	80.22%	Conservative:	24
Best Local Similarity:	67.03%	Mismatches:	35
Query Match:	65.98%	Indels:	1
DB:	3	Gaps:	1
US-10-757-745-2_COPY_54_236 (1-183) x AAZ47119 (1-1312)			
QY	2	GluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArgArg	21
DB	317	CAGAAAGCCCTGAGCGCTACTTCGAGCTGCCAGAGACCAAGGGTGGCGGCCAG	376
QY	22	ProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThrAsp	41
DB	377	CTCTCCACCTCCTTCAGAGTCCGAGGCTATGTGTATCTAACCAACGAGGATCAATGAT	436
QY	42	SerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPhe	61
DB	437	ACAAACCATTTTGAAGCCAGTCCATCT--GGAACTCCTCTAGAAGATAGCAGCACTATT	493
QY	62	SerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArg	81
DB	494	TCITTCATTACCTGGAAATATTGATGATGATGATGATGATGATGATGATGATGATGAT	553
QY	82	GlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheIleGlnGluValIle	101
DB	554	GGGGTGTGTTCCCTGCTAGCTTTGTATAGTCCAGATGTGGTATTTCTACAGGAAGTTATC	613
QY	102	ProProTyrTyrSerTyrLeuLysLysAspGlySerSerAsnTyrGluIleThrGlyHis	121
DB	614	CCCCCATCTGCTGCTACCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	673
QY	122	GluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGln	141
DB	674	GAAGAGGATATTTCACAGCTATCTATTTCAGAAAGAGAGAGAGAGAGAGAGAGAGAG	733
QY	142	GluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsn	161
DB	734	GAGATTATTCTCTTTTCCAAATACCAAAATGATGAGAAACCTGCTATGCGTAAATGTGAT	793
QY	162	ValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAla	181
DB	794	TTGGTGGAAATGAATTTTCCCTTATGACATCCATTTTGGAGAGCACCAGAGACATTCT	853
QY	182	AlaGlu 183	
DB	854	GCGGAA 859	
RESULT 15			
ID	ADD34376	standard; DNA; 602 BP.	
XX	AC	ADD34376;	
XX	AC	ADD34376;	
DT	15-JAN-2004	(first entry)	
XX	XX	Mouse mitochondrial DNA sequence SEQ ID NO:2154.	
DE	XX	ds; mouse; array; mitochondrial; hybridisation; energy-metabolism;	
KW	XX	mitochondrial disease; oxidative phosphorylation dysfunction;	
KW	XX	oxidative stress; apoptosis; aging.	
OS	XX	Mus musculus.	
XX	XX	W02003020220-A2.	
PN	XX	13-MAR-2003.	
PD	XX	30-AUG-2002; 2002WO-US027886.	
PF	XX	30-AUG-2001; 2001US-0316323P.	
XX	XX	31-AUG-2001; 2001CA-02356540.	
PR	XX		

XX	(UYEM-) UNIV EMORY.		
PA	Wallace DC, Levy S, Kerstann K, Procaccio V;		
XX	WPI; 2003-300821/29.		
XX	Array containing probes for genes involved in mitochondrial biology,		
PT	useful for determining mitochondrial biology gene expression profiles for		
PT	use in diagnosing pathologies and identifying biochemical pathways.		
XX	Claim 2; SEQ ID NO 2154; 201pp; English.		
XX	The invention relates to a novel array comprising at least two isolated		
CC	nucleotide molecules, each molecule having a sequence capable of uniquely		
CC	hybridising to a nucleic acid molecule which is an expression product of		
CC	a gene involved in mitochondrial biology. The array comprises two or more		
CC	isolated nucleic acid molecules or spots, each molecule having a sequence		
CC	chosen from sequence of 994 human probes and 2046 mouse probes. An array		
CC	of the invention is useful for determining an expression profile of a		
CC	mouse or human sample containing nucleic acid, by contacting the array		
CC	with the sample under conditions allowing selective hybridisation, and		
CC	measuring hybridisation of nucleic acid in the sample to the array to		
CC	produce an expression profile. The array is also useful for determining		
CC	an expression profile of a first labelled sample containing nucleic acid		
CC	relative to a second, differently labelled sample containing nucleic		
CC	acid. The second sample is a reference or a standard. An array is useful		
CC	for determining an expression profile diagnostic of an energy-metabolism-		
CC	related physiological condition. An array of the invention is useful for		
CC	determining mitochondrial biology gene expression profiles of organisms,		
CC	such as human, mice and closely related species, tissue and organs of		
CC	such organisms, which are useful for determining expression profiles		
CC	diagnostic of energy metabolism-related physiological conditions.		
CC	Diagnosing such physiological conditions, identifying biochemical		
CC	pathways, genes, and mutations involved in such physiological conditions,		
CC	identifying therapeutic agents useful for preventing and/or treating such		
CC	physiological conditions, evaluating and/or monitoring the efficacy of		
CC	such therapies, and creating and identifying animal models of human		
CC	energy metabolism-related physiological conditions. An array is also		
CC	useful for defining expression signatures or profiles for mitochondrial		
CC	diseases, as well as distinguishing clinical disorders that result from		
CC	oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress,		
CC	apoptosis and aging. An array of the invention contains probes of genes		
CC	not previously recognised to participate in mitochondrial biology. The		
CC	sequences shown in ADD33224-ADD35260 represent murine mitochondrial DNA		
CC	clones used to make the probes of the invention. Some sequences are not		
CC	present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905,		
CC	1906, 2408 and 2643.		
XX	Sequence 602 BP; 194 A; 119 C; 134 G; 155 T; 0 U; 0 Other;		
SQ			
Alignment Scores:			
Pred. No.:	1.54e-61	Length:	602
Score:	585.50	Matches:	115
Percent Similarity:	82.32%	Conservative:	20
Best Local Similarity:	70.12%	Mismatches:	28
Query Match:	61.96%	Indels:	1
DB:	10	Gaps:	1
US-10-757-745-2_COPY_54_236 (1-183) x ADD34376 (1-602)			
QY	20	ArgArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThr	39
DB	15	CGCCAGCCTCCACGCTCTTCAAGTCCGAGGCTTGTGTATCTAACCAACGAGGATGCA	74
QY	40	ThrAspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnAsnGlySer	59
DB	75	AATGATACACCACTTTTAGAGCCAGTCCATCT--GGAACCTCTCTAGAGATAGCAGC	131
QY	60	MetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArg	79
DB	132	ACTATTCTTTTCACTTACCTGGAAATATTGATGGATTAGATGCAATCTGCCCGAGG	191

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Qy 80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99
Db 192 GCTGAGGGGGTGTCTCGCTAGCTTGTATAGTCGAGATGGTATTCTACAGAA 251
Qy 100 ValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThr 119
Db 252 GTTATCCCCCTACTGTGCTACTCTAAAGAGAGAGCAGCAGCTTACACAATTATTACA 311
Qy 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLys 139
Db 312 GGTAAATGAAGAAGGATATTTTCACAGCTATATCTTGAAGAAAGGAGAGTGAATTTAAA 371
Qy 140 SerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHis 159
Db 372 AGTCAGGAGATATTCCTTTTCCAAATACCAAATGATGAGAGCCTGCTATGCTTAAT 431
Qy 160 ValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGly 179
Db 432 GTGAGTTTGGGTGGAAATGAATTTTGCCTTATGACATCCCATTTTGGAGAGCACCAGAGAA 491
Qy 180 HisAlaAlaGlu 183
Db 492 CATTCGCGGAA 503
RESULT 16
AAAX40590
ID AAAX40590 standard; cDNA; 483 BP.
XX
AC AAAX40590;
XX
DT 18-JUN-1999 (first entry)
XX
DE Human secreted protein 5' EST SEQ ID No: 190.
XX
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide; prostate;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
OS Homo sapiens.
XX
PN WO9906550-A2.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98WO-IB001232.
XX
PR 01-AUG-1997; 97US-00905144.
XX
PA (GBST ) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Lacroix B;
XX
DR WPI; 1999-153780/13.
XX
DR P-PSDB; AAY11868.
XX
PT New isolated prostate-derived nucleic acids - used to develop products
PT which may have cytokine, immune regulatory, haematopoiesis regulating,
PT anti-inflammatory or tumour inhibition activity.
XX
PS Claim 1; Page 298; 675pp; English.
XX
CC AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins expressed in prostate, and encode the proteins
CC given in AAY11716 to AAY11993 respectively. The proteins given represent
CC the signal peptide and an N-terminal fragment of a secreted protein. The
CC nucleic acid sequences can be used for producing secreted human gene
CC products. They can also be used to develop products for diagnosis and
CC therapy. The proteins obtained may have cytokine activity, cell
CC proliferation and differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
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CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptides can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell
XX
SQ Sequence 483 BP; 123 A; 111 C; 139 G; 110 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.94e-58 Length: 483
Score: 559.00 Matches: 108
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 59.15% Indels: 0
DB: 2 Gaps: 0
US-10-757-745-2_COPY_54_236 (1-183) x AAX40590 (1-483)
Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 160 ATGGAAAGGGCTCTGAACCTCTACTTCGAGCCTCCGCTGGAGGAGCGCTTGGAAACGC 219
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 220 CGACCTTGAACCACTCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAAC 279
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 280 GATTCCACCACTTCTAAATCAGCCCATCTGAAGATACTCAGCAAGAAAATGGCAGCATG 339
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 340 TTCTCTCTCATCTACCTGGAATATTGATGGATTAGATCTAAACAATCTGTGTCAGAGGGCT 399
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 400 CGAGGGGTGTGTTCTCTACTTAGCTTTGTACAGCCAGATGTGATATTCTTACAGGAAGTT 459
Qy 101 IleProProTyrTyrSerTyrLeu 108
Db 460 ATTCCCCCATATTATAGTACTACCTA 483
RESULT 17
ADT95464
ID ADT95464 standard; cDNA; 553 BP.
XX
AC ADT95464;
XX
DT 16-DEC-2004 (first entry)
XX
DE Colon cancer associated human cDNA sequence #983.
XX
KW Colon cancer; T cell; tumour protein; C6345; C635S; C637S; C640S; C636S;
KW humoral immune response; cellular immune response; cytostatic;
KW immunostimulant; human; ss.
XX
OS Homo sapiens.
XX
PN US2003087818-A1.
XX
PD 08-MAY-2003.
XX
PP 01-FEB-2002; 2002US-00066543.
XX
PR 02-FEB-2001; 2001US-0267400P.
PR 07-FEB-2001; 2001US-0267382P.
PR 11-MAY-2001; 2001US-0290322P.
PR 12-JUL-2001; 2001US-0305265P.
PR 16-AUG-2001; 2001US-0313077P.
XX
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PA (CORI-) CORIXA CORP.
XX Jiang Y, Chenault RA, Xu J, Indrias CY, Lodes MJ, Secretist H;
PI Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;
XX WPI; 2003-040540/03.
XX
XX New isolated nucleic acids and polypeptides capable of eliciting a
PT humoral and/or cellular immune response, useful for diagnosing,
PT preventing or treating cancer, particularly colon cancer.
XX
XX Claim 1; SEQ ID NO 983; 87pp; English.
PS
XX The invention relates to polynucleotide and polypeptide sequences
CC associated with cancer, particularly colon cancer. Also disclosed are (i)
CC an expression vector comprising the polynucleotide, (ii) a host cell
CC transformed or transfected with the expression vector, (iii) an isolated
CC antibody, or its antigen-binding fragment, which specifically binds to
CC the polypeptide, (iv) a method of detecting or determining the presence
CC of cancer in a patient, (v) a fusion protein comprising at least one of
CC the polypeptides, (vi) an oligonucleotide that hybridizes to the
CC polynucleotide sequence under highly stringent conditions, and (vii) a
CC method of stimulating and/or expanding T cells specific for a tumour
CC protein. The polypeptide specifically comprises the amino acid sequence
CC of C634S, C635S, C637S, C640S, C636S or one of the potential open reading
CC frames (ORFs) of C636S. These polypeptides are encoded by the
CC polynucleotide sequences, where both are capable of eliciting a humoral
CC and/or cellular immune response. The polynucleotides, polypeptides, and
CC antibodies are useful for diagnosing, preventing or treating cancer,
CC particularly colon cancer. The polynucleotide and polypeptide sequences
CC are also useful in DNA strand invasion, antisense inhibition, mutational
CC analysis, nucleic acid purification, isolation of transcriptionally
CC active genes, blocking or transcription factor binding, genome cleavage
CC or in situ hybridization, and as enhancers of transcription or
CC biomarkers. This sequence represents a human colon cancer associated
CC cDNA. Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at seqdata.uspto.gov
XX
SQ Sequence 553 BP; 181 A; 94 C; 125 G; 151 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.: 2,79e-56 Length: 553
Score: 542.00 Matches: 105
Percent Similarity: 97.22% Conservative: 0
Best Local Similarity: 97.22% Mismatches: 3
Query Match: 57.35% Indels: 0
DB: 11 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x ADT95464 (1-553)
Qy 76 LeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIle 95
Db 30 CTCTANATGTCATGCTCGAGGGGTGTCTTCTACTTAGCTTTGTACAGCCAGATGTGATA 89

Qy 96 PheLeuGlnGluValIleProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyr 115
Db 90 TTTCTACAGAAAGTATTTCCTCCCATATTATAGCTACCTTAAGAAGAGATCAAGTAATAT 149

Qy 116 GluIleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArg 135
Db 150 GAGNTTATTACAGTCTATGAAGAGGATATTTCACAGCTATTAATGTTGAAGAATCAAGA 209

Qy 136 ValLysLeuLysSerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeu 155
Db 210 GTGAAATTAAGCAAGCAAGATATTTCCTTTTCCAAGTACCAAAATGATGAGAAACCTT 269

Qy 156 LeuCysValHisValAnValSerGlyAsnGluLeuLysLeuMetThrSerHisLeuGlu 175
Db 270 TTATGTGTGATGTAATGTGTACGAAATGAGCTTTGCGCTTATGATCCCATTTGGAG 329

Qy 176 SerThrArgGlyHisAlaAlaGlu 183
Db 330 AGCACAGAGGGCATGCTGCGAA 353

RESULT 18
ADX41946
ID ADX41946 standard; cDNA; 553 BP.
XX
XX AC ADX41946;
XX
XX 21-APR-2005 (first entry)
XX
XX Human cDNA encoding colon cancer protein SEQ ID NO 983.
XX
XX Cytostatic; Immunostimulant; therapy; diagnosis; colon cancer; neoplasm;
KW ss; gene.
XX
XX Homo sapiens.
OS
XX WO200274156-A2.
PN
XX 26-SEP-2002.
PD
XX 01-FEB-2002; 2002WO-US002870.
PF
XX 02-FEB-2001; 2001US-0267400P.
PR
XX 07-FEB-2001; 2001US-0267382P.
PR
XX 11-MAY-2001; 2001US-0290322P.
PR
XX 12-JUL-2001; 2001US-0305265P.
PR
XX 16-AUG-2001; 2001US-0313077P.
PR
XX (CORI-) CORIXA CORP.
PA
XX Jiang Y, Chenault RA, Xu J, Indrias CY, Lodes MJ, Secretist H;
PI Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;
XX WPI; 2003-040540/03.
XX
XX New isolated nucleic acids and polypeptides capable of eliciting a
PT humoral and/or cellular immune response, useful for diagnosing,
PT preventing or treating cancer, particularly colon cancer.
XX
XX Claim 1; SEQ ID NO 983; 244pp; English.
PS
XX The invention relates to a new isolated nucleic acid. The nucleic acids,
CC polypeptides, antibodies are useful for diagnosing, preventing or
CC treating cancer, particularly colon cancer. The nucleic acid and
CC polypeptides are also useful in DNA strand invasion, antisense
CC inhibition, mutational analysis, nucleic acid purification, isolation of
CC transcriptionally active genes, blocking or transcription factor binding,
CC genome cleavage or in situ hybridization, and as enhancers of
CC transcription or biomarkers. The kits are useful for detecting antibody
CC binding. The present sequence represents a human cDNA encoding a colon
CC cancer protein.
XX
SQ Sequence 553 BP; 181 A; 94 C; 125 G; 151 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.: 2,79e-56 Length: 553
Score: 542.00 Matches: 105
Percent Similarity: 97.22% Conservative: 0
Best Local Similarity: 97.22% Mismatches: 3
Query Match: 57.35% Indels: 0
DB: 11 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x ADX41946 (1-553)
Qy 76 LeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIle 95
Db 30 CTCTANATGTCATGCTCGAGGGGTGTCTTCTACTTAGCTTTGTACAGCCAGATGTGATA 89

Qy 96 PheLeuGlnGluValIleProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyr 115
Db 90 TTTCTACAGAAAGTATTTCCTCCCATATTATAGCTACCTTAAGAAGAGATCAAGTAATAT 149

Qy 116 GluIleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArg 135
Db 150 GAGNTTATTACAGTCTATGAAGAGGATATTTCACAGCTATTAATGTTGAAGAATCAAGA 209

Qy 136 ValLysLeuLysSerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeu 155
Db 210 GTGAAATTAAGCAAGCAAGATATTTCCTTTTCCAAGTACCAAAATGATGAGAAACCTT 269

Qy 156 LeuCysValHisValAnValSerGlyAsnGluLeuLysLeuMetThrSerHisLeuGlu 175
Db 270 TTATGTGTGATGTAATGTGTACGAAATGAGCTTTGCGCTTATGATCCCATTTGGAG 329

Qy 176 SerThrArgGlyHisAlaAlaGlu 183
Db 330 AGCACAGAGGGCATGCTGCGAA 353

|||||
150 GAGATTATACAGTCATGAAGAGGATATTTACAGCTATATGTTGGAAGAAATCAAGA 209
|||||
136 VallysLeuLysSerGlnGluIleleProPheProSerThrLysMetMetArgAsnLue 155
|||||
210 GTGAATTTAAAAAGCCAAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTT 269
|||||
156 LeuCysValHisValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGlu 175
|||||
270 TTATGTGTGCATGTGAATGTGTACAGAAATGAGCTTTGCCTTATGACATCCCATTTGGAG 329
|||||
176 SerThrArgGlyHisAlaAlaGlu 183
|||||
330 AGCACCAGAGGCGATGCTGCGGAA 353
RESULT 19
ADT95844
ID ADT95844 standard; cDNA; 401 BP.
XX
AC ADT95844;
XX
DT 16-DEC-2004 (first entry)
XX
XX Colon cancer associated human cDNA sequence #1363.
XX
XX Colon cancer; T cell; tumour protein; C634S; C635S; C637S; C640S; C636S;
KW humoral immune response; cellular immune response; cytostatic;
KW immunostimulant; human; ss.
XX
XX Homo sapiens.
XX
XX US2003087818-A1.
XX
XX PD 08-MAY-2003.
XX
XX PF 01-FEB-2002; 2002US-00066543.
XX
XX PR 02-FEB-2001; 2001US-0267400P.
PR 07-FEB-2001; 2001US-0267382P.
PR 11-MAY-2001; 2001US-0290322P.
PR 12-JUL-2001; 2001US-0305265P.
PR 16-AUG-2001; 2001US-0313077P.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Jiang Y, Chenault RA, Xu J, Indirias CY, Lodes MJ, Secrist H;
PI Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;
XX
XX DX WPI; 2003-040540/03.
XX
XX PT New isolated nucleic acids and polypeptides capable of eliciting a
PT humoral and/or cellular immune response, useful for diagnosing,
PT preventing or treating cancer, particularly colon cancer.
XX
XX PS Claim 1; SEQ ID NO 1363; 87pp; English.
XX
XX CC The invention relates to polynucleotide and polypeptide sequences
CC associated with cancer, particularly colon cancer. Also disclosed are (i)
CC an expression vector comprising the polynucleotide, (ii) a host cell
CC transformed or transfected with the expression vector, (iii) an isolated
CC antibody, or its antigen-binding fragment, which specifically binds to
CC the polypeptide, (iv) a method of detecting or determining the presence
CC of cancer in a patient, (v) a fusion protein comprising at least one of
CC the polypeptides, (vi) an oligonucleotide that hybridises to the
CC polynucleotide sequence under highly stringent conditions, and (vii) a
CC method of stimulating and/or expanding T cells specific for a tumour
CC protein. The polypeptide specifically comprises the amino acid sequence
CC of C634S, C635S, C637S, C640S, C636S or one of the potential open reading
CC frames (ORFs) of C636S. These polypeptides are encoded by the
CC polynucleotide sequences, where both are capable of eliciting a humoral
CC and/or cellular immune response. The polynucleotides, polypeptides, and
CC antibodies are useful for diagnosing, preventing or treating cancer,
CC particularly colon cancer. The polynucleotide and polypeptide sequences

CC are also useful in DNA strand invasion, antisense inhibition, mutational
CC analysis, nucleic acid purification, isolation of transcriptionally
CC active genes, blocking or transcription factor binding, genome cleavage
CC or in situ hybridisation, and as enhancers of transcription or
CC biomarkers. This sequence represents a human colon cancer associated
CC cDNA. Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at seqdata.uspto.gov

SQ Sequence 401 BP; 132 A; 67 C; 89 G; 113 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3.09e-56	Length:	401
Score:	540.00	Matches:	104
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	57.14%	Indels:	0
DB:	11	Gaps:	0

US-10-757-745-2_COPY_54_236 (1-183) x ADT95844 (1-401)

Qy	80	AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGluGlu	99
Db	19	GCTCGAGGGGTGTTCTCTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAA	78
Qy	100	VallileProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThr	119
Db	79	GTTATTTCCCATATTTATAGCTACTAAAGNAGAGATCAAGTATATTAGATTTATTACA	138
Qy	120	GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLys	139
Db	139	GGTCATGAAGAAGGATATTTTCCAGCTATATATGTTGAAGAAATCAAGAGTCAAAATTA	198
Qy	140	SerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHis	159
Db	199	AGCCAAGAGATTATTTCTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTG	258
Qy	160	ValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGly	179
Db	259	GTGAATGTGTGAGAAATGAGCTTTGCTTATGATCATCCCATTTTGAGAGACCCAGAGGG	318
Qy	180	HisAlaAlaGlu 183	
Db	319	CATGCTGCGGAA 330	

RESULT 20

ADX42326
ID ADX42326 standard; cDNA; 401 BP.

XX AC ADX42326;

XX DT 21-APR-2005 (first entry)

XX DE Human cDNA encoding colon cancer protein SEQ ID NO 1363.

XX DX Cytostatic; Immunostimulant; therapy; diagnosis; colon cancer; neoplasia;
KW ss; gene.

XX OS Homo sapiens.

XX PN WO200274156-A2.

XX PD 26-SEP-2002.

XX PF 01-FEB-2002; 2002WO-US002870.

XX PR 02-FEB-2001; 2001US-0267400P.

PR 07-FEB-2001; 2001US-0267382P.

PR 11-MAY-2001; 2001US-0290322P.

PR 12-JUL-2001; 2001US-0305265P.

PR 16-AUG-2001; 2001US-0313077P.

XX (CORI-) CORIXA CORP.

XX

PI Jiang Y, Chenault RA, Xu J, Indrias CV, Lodes MJ, Secretist H;
PI Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;
XX WPI; 2003-040540/03.
XX
XX New isolated nucleic acids and polypeptides capable of eliciting a
PT humoral and/or cellular immune response, useful for diagnosing,
PT preventing or treating cancer, particularly colon cancer.
XX
XX Claim 1; SEQ ID NO 1363; 244pp; English.
XX
XX The invention relates to a new isolated nucleic acid. The nucleic acids,
CC polypeptides, antibodies are useful for diagnosing, preventing or
CC treating cancer, particularly colon cancer. The nucleic acid and
CC polypeptides are also useful in DNA strand invasion, antisense
CC inhibition, mutational analysis, nucleic acid purification, isolation of
CC transcriptionally active genes, blocking or transcription factor binding,
CC genome cleavage or in situ hybridization, and as enhancers of
CC transcription or biomarkers. The kits are useful for detecting antibody
CC binding. The present sequence represents a human cDNA encoding a colon
CC cancer protein.
XX
SQ Sequence 401 BP; 132 A; 67 C; 89 G; 113 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.09e-56 Length: 401
Score: 540.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.14% Indels: 0
DB: 11 Gaps:

US-10-757-745-2_COPY_54_236 (1-183) x ADX42326 (1-401)

QY 80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99
Db 19 GCTCGAGGGGTGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATATTCTTACAGGAA 78
QY 100 ValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThr 119
Db 79 GTTATTCCCCCATATTATAGTACTACCTAAAGAGAGATCAAGTAATTTATGAGATTATTACA 138
QY 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValIleLys 139
Db 139 GGCATGAAGAGAGATATTTCACAGCTATTAATGTTGAAGAAATCAAGAGTGAATTTAAA 198
QY 140 SerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysValHis 159
Db 199 AGCCAGAGATTATTCCTTTTCCAGTACCACCAATGATGAGAAACCTTTTATGTGTCAT 258
QY 160 ValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGly 179
Db 259 GTCAATGTGTGAGAAATGAGCTTTCCTTATGACATCCCATTTGGAGAGCACCAGAGGG 318
QY 180 HisAlaAlaGlu 183
Db 319 CATGCTGCGGAA 330

RESULT 21

ADT95512

ID ADT95512 standard; cDNA; 625 BP.

XX

AC ADT95512;

XX

DT 16-DEC-2004 (first entry)

XX

DE Colon cancer associated human cDNA sequence #1031.

XX

KW Colon cancer; T cell; tumour protein; C634S; C635S; C637S; C640S; C636S;

KW humoral immune response; cellular immune response; cytostatic;

KW immunostimulant; human; ss.

XX

OS Homo sapiens.

XX
PN US2003087818-A1.
XX
PD 08-MAY-2003.
XX
XX 01-FEB-2002; 2002US-00066543.
PF
XX 02-FEB-2001; 2001US-0267400P.
PR
XX 07-FEB-2001; 2001US-0267382P.
PR
XX 11-MAY-2001; 2001US-0290322P.
PR
XX 12-JUL-2001; 2001US-0305265P.
PR
XX 16-AUG-2001; 2001US-0313077P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Jiang Y, Chenault RA, Xu J, Indrias CV, Lodes MJ, Secretist H;
PI Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;
PI
XX WPI; 2003-040540/03.
XX
XX New isolated nucleic acids and polypeptides capable of eliciting a
PT humoral and/or cellular immune response, useful for diagnosing,
PT preventing or treating cancer, particularly colon cancer.
XX
XX Claim 1; SEQ ID NO 1031; 87pp; English.

XX The invention relates to polynucleotide and polypeptide sequences
XX associated with cancer, particularly colon cancer. Also disclosed are (i)
CC an expression vector comprising the polynucleotide, (ii) a host cell
CC transformed or transfected with the expression vector, (iii) an isolated
CC antibody, or its antigen-binding fragment, which specifically binds to
CC the polypeptide, (iv) a method of detecting or determining the presence
CC of cancer in a patient, (v) a fusion protein comprising at least one of
CC the polypeptides, (vi) an oligonucleotide that hybridizes to the
CC polynucleotide sequence under highly stringent conditions, and (vii) a
CC method of stimulating and/or expanding T cells specific for a tumour
CC protein. The polypeptide specifically comprises the amino acid sequence
CC of C634S, C635S, C637S, C640S, C636S or one of the potential open reading
CC frames (ORFs) of C636S. These polypeptides are encoded by the
CC polynucleotide sequences, where both are capable of eliciting a humoral
CC and/or cellular immune response. The polynucleotides, polypeptides, and
CC antibodies are useful for diagnosing, preventing or treating cancer,
CC particularly colon cancer. The polynucleotide and polypeptide sequences
CC are also useful in DNA strand invasion, antisense inhibition, mutational
CC analysis, nucleic acid purification, isolation of transcriptionally
CC active genes, blocking or transcription factor binding, genome cleavage
CC or in situ hybridisation, and as enhancers of transcription or
CC biomarkers. This sequence represents a human colon cancer associated
CC cDNA. Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at seqdata.uspto.gov

SQ Sequence 625 BP; 202 A; 104 C; 144 G; 174 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 5.83e-56 Length: 625
Score: 540.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.14% Indels: 0
DB: 11 Gaps:

US-10-757-745-2_COPY_54_236 (1-183) x ADT95512 (1-625)

QY 80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99
Db 42 GCTCGAGGGGTGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATATTCTTACAGGAA 101
QY 100 ValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThr 119
Db 102 GTTATTCCCCCATATTATAGTACTACCTAAAGAGAGATCAAGTAATTTATGAGATTATTACA 161
QY 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValIleLys 139

CC antibody, or its antigen-binding fragment, which specifically binds to
 CC the polypeptide, (iv) a method of detecting or determining the presence
 CC of cancer in a patient, (v) a fusion protein comprising at least one of
 CC the polypeptides, (vi) an oligonucleotide that hybridizes to the
 CC polynucleotide sequence under highly stringent conditions, and (vii) a
 CC method of stimulating and/or expanding T cells specific for a tumour
 CC protein. The polypeptide specifically comprises the amino acid sequence
 CC of C634S, C635S, C637S, C640S, C636S or one of the potential open reading
 CC frames (ORFs) of C636S. These polypeptides are encoded by the
 CC polynucleotide sequences, where both are capable of eliciting a humoral
 CC and/or cellular immune response. The polynucleotides, polypeptides, and
 CC antibodies are useful for diagnosing, preventing or treating cancer,
 CC particularly colon cancer. The polynucleotide and polypeptide sequences
 CC are also useful in DNA strand invasion, antisense inhibition, mutational
 CC analysis, nucleic acid purification, isolation of transcriptionally
 CC active genes, blocking or transcription factor binding, genome cleavage
 CC or in situ hybridisation, and as enhancers of transcription or
 CC biomarkers. This sequence represents a human colon cancer associated
 CC cDNA. Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at seqdata.uspto.gov
 XX
 SQ Sequence 633 BP; 205 A; 108 C; 144 G; 175 T; 0 U; 1 Other;

Alignment Scores:
 Pred. No.: 5,93e-56 Length: 633
 Score: 540.00 Matches: 104
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 57.14% Indels: 0
 DB: 11 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x ADT95565 (1-633)

QY 80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99
 DB 34 GCTCGAGGGGTGTGTTCTTACTTGTACAGCCAGATGTGATATTCTTACAGGAA 93
 QY 100 ValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGlulIleThr 119
 DB 94 GTTATTCCCCCATATTATATAGCTACCTTAAAGAGAGATCAAGTAAATATGAGATTATTA 153
 QY 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValHis 139
 DB 154 GGTCAATGTGTGAGGAAATGAGCTTTGCTTATGACATCCATTTGGAGAGCACCAGGG 213
 QY 140 SerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuValHis 159
 DB 214 AGCCNAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCAT 273
 QY 160 ValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGly 179
 DB 274 GTGAATGTGTGAGGAAATGAGCTTTGCTTATGACATCCATTTGGAGAGCACCAGGG 333
 QY 180 HisAlaAlaGlu 183
 DB 334 CATGCTGCGGAA 345

RESULT 24

ADX42047
 ID ADX42047 standard; cDNA; 633 BP.

AC ADX42047;

XX 21-APR-2005 (first entry)

DE Human cDNA encoding colon cancer protein SEQ ID NO 1084.

XX Cytostatic; Immunostimulant; therapy; diagnosis; colon cancer; neoplasm;
 KW ss; gene.

XX Homo sapiens.

XX WO200274156-A2.

XX 26-SEP-2002.
 PD 01-FEB-2002; 2002WO-US002870.
 XX 02-FEB-2001; 2001US-0267400P.
 PR 07-FEB-2001; 2001US-0267382P.
 PR 11-MAY-2001; 2001US-0290322P.
 PR 12-JUL-2001; 2001US-0305265P.
 PR 16-AUG-2001; 2001US-0313077P.
 XX (CORI-) CORIXA CORP.
 PA Jiang Y, Chenault RA, Xu J, Indirias CY, Lodes MJ, Secretist H;
 PI Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;
 PI WPI; 2003-040540/03.
 XX New isolated nucleic acids and polypeptides capable of eliciting a
 DR humoral and/or cellular immune response, useful for diagnosing,
 PT preventing or treating cancer, particularly colon cancer.
 XX Claim 1; SEQ ID NO 1084; 244pp; English.
 XX The invention relates to a new isolated nucleic acid. The nucleic acids,
 CC polypeptides, antibodies are useful for diagnosing, preventing or
 CC treating cancer, particularly colon cancer. The nucleic acid and
 CC polypeptides are also useful in DNA strand invasion, antisense
 CC inhibition, mutational analysis, nucleic acid purification, isolation of
 CC transcriptionally active genes, blocking or transcription factor binding,
 CC genome cleavage or in situ hybridization, and as enhancers of
 CC transcription or biomarkers. The kits are useful for detecting antibody
 CC binding. The present sequence represents a human cDNA encoding a colon
 CC cancer protein.
 XX
 SQ Sequence 633 BP; 205 A; 108 C; 144 G; 175 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 5,93e-56 Length: 633
 Score: 540.00 Matches: 104
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 57.14% Indels: 0
 DB: 11 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x ADX42047 (1-633)

QY 80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99
 DB 34 GCTCGAGGGGTGTGTTCTTACTTGTACAGCCAGATGTGATATTCTTACAGGAA 93
 QY 100 ValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGlulIleThr 119
 DB 94 GTTATTCCCCCATATTATATAGCTACCTTAAAGAGAGATCAAGTAAATATGAGATTATTA 153
 QY 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValHis 139
 DB 154 GGTCAATGTGTGAGGAAATGAGCTTTGCTTATGACATCCATTTGGAGAGCACCAGGG 213
 QY 140 SerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuValHis 159
 DB 214 AGCCNAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCAT 273
 QY 160 ValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGly 179
 DB 274 GTGAATGTGTGAGGAAATGAGCTTTGCTTATGACATCCATTTGGAGAGCACCAGGG 333
 QY 180 HisAlaAlaGlu 183
 DB 334 CATGCTGCGGAA 345
 RESULT 25
 ADT95551

CC genome cleavage or in situ hybridization, and as enhancers of
CC transcription or biomarkers. The kits are useful for detecting antibody
CC binding. The present sequence represents a human cDNA encoding a colon
CC cancer protein.
SQ Sequence 644 BP; 206 A; 110 C; 148 G; 180 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 6.08e-56 Length: 644
Score: 540.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.14% Indels: 0
DB: 11 Gaps: 0
US-10-757-745-2_COPY_54_236 (1-183) x ADX42033 (1-644)
QY 80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99
DB 32 GCTCGAGGGGTGTCTTCTACTTAGCTTTGTACAGCCAGATGTGATATTCTTACAGGAA 91
QY 100 ValIleProProTyrTyrSerTyrLeuLysLysLysSerSerSerSerSerSerSerSer 119
DB 92 GTTATTCCCCCATATTATAGCTACCTAAAGAGAGATCAAGTAAATTATGAGATTATTACA 151
QY 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLys 139
DB 152 GGTGATGAAGAGAGATATTTCACAGCTATTAATGTTGAAGAAATCAAGAGTGAATAA 211
QY 140 SerGlnGluIleIleProPheProSerThrLysMetMetMetMetMetMetMetMetMet 159
DB 212 AGCCAGAGATTATTCCTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTCAT 271
QY 160 ValAsnValSerGlyAsnGluLeuLysLeuMetThrSerHisLeuGluSerThrArgGly 179
DB 272 GTGAATGTGTGAGAAATGAGCTTTCCTTATGACATCCCATTTGGAGAGCACCAGAGGG 331
QY 180 HisAlaAlaGlu 183
DB 332 CATGCTGCGGAA 343
RESULT 27
ADT95548
ID ADT95548 standard; cDNA; 674 BP.
AC ADT95548;
XX
DT 16-DEC-2004 (first entry)
XX
DE Colon cancer associated human cDNA sequence #1067.
XX
KW Colon cancer; T cell; tumour protein; C634S; C635S; C637S; C640S; C636S;
KW humoral immune response; cellular immune response; cytostatic;
KW immunostimulant; human; ss.
XX
OS Homo sapiens.
XX
PN US2003087818-A1.
XX
PD 08-MAY-2003.
XX
PF 01-FEB-2002; 2002US-0006543.
XX
PR 02-FEB-2001; 2001US-0267400P.
PR 07-FEB-2001; 2001US-0267382P.
PR 11-MAY-2001; 2001US-0290322P.
PR 12-JUL-2001; 2001US-0305265P.
PR 16-AUG-2001; 2001US-0313077P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Jiang Y, Chenault RA, Xu J, Indirias CY, Lodes MJ, Secret H;
PI Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;

XX WPI; 2003-040540/03.
DR
XX
PT New isolated nucleic acids and polypeptides capable of eliciting a
PT humoral and/or cellular immune response, useful for diagnosing,
PT preventing or treating cancer, particularly colon cancer.
XX
PS Claim 1; SEQ ID NO 1067; 87pp; English.
XX
XX The invention relates to polynucleotide and polypeptide sequences
CC associated with cancer, particularly colon cancer. Also disclosed are (i)
CC an expression vector comprising the polynucleotide, (ii) a host cell
CC transformed or transfected with the expression vector, (iii) an isolated
CC antibody, or its antigen-binding fragment, which specifically binds to
CC the polypeptide, (iv) a method of detecting or determining the presence
CC of cancer in a patient, (v) a fusion protein comprising at least one of
CC the polypeptides, (vi) an oligonucleotide that hybridizes to the
CC polynucleotide sequence under highly stringent conditions, and (vii) a
CC method of stimulating and/or expanding T cells specific for a tumour
CC protein. The polypeptide specifically comprises the amino acid sequence
CC of C634S, C635S, C637S, C640S, C636S or one of the potential open reading
CC frames (ORFs) of C636S. These polypeptides are encoded by the
CC polynucleotide sequences, where both are capable of eliciting a humoral
CC and/or cellular immune response. The polynucleotides, polypeptides, and
CC antibodies are useful for diagnosing, preventing or treating cancer,
CC particularly colon cancer. The polynucleotide and polypeptide sequences
CC are also useful in DNA strand invasion, antisense inhibition, mutational
CC analysis, nucleic acid purification, isolation of transcriptionally
CC active genes, blocking or transcribing factor binding, genome cleavage
CC or in situ hybridisation, and as enhancers of transcription or
CC biomarkers. This sequence represents a human colon cancer associated
CC cDNA. Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at seqdata.uspto.gov
XX
SQ Sequence 674 BP; 213 A; 114 C; 152 G; 191 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.: 6.49e-56 Length: 674
Score: 540.00 Matches: 104
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 57.14% Indels: 0
DB: 11 Gaps: 0
US-10-757-745-2_COPY_54_236 (1-183) x ADT95548 (1-674)
QY 80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99
DB 18 GCTCGAGGGGTGTCTTCTACTTAGCTTTGTACAGCCAGATGTGATATTCTTACAGGAA 77
QY 100 ValIleProProTyrTyrSerTyrLeuLysLysLysSerSerSerSerSerSerSerSer 119
DB 78 GTTATTCCCCCATATTATAGCTACCTAAAGAGAGATCAAGTAAATTATGAGATTATTACA 137
QY 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLys 139
DB 138 GGTGATGAAGAGAGATATTTCACAGCTATAATGTTCAAGAAATCAAGAGTGAATAA 197
QY 140 SerGlnGluIleIleProPheProSerThrLysMetMetMetMetMetMetMetMetMet 159
DB 198 AGCCAGAGATTATTCCTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTCAT 257
QY 160 ValAsnValSerGlyAsnGluLeuLysLeuMetThrSerHisLeuGluSerThrArgGly 179
DB 258 GTGAATGTGTGAGAAATGAGCTTTTCCTTATGACATCCCATTTGGAGAGCACCAGAGGG 317
QY 180 HisAlaAlaGlu 183
DB 318 CATGCTGCGGAA 329

RESULT 28
ADX42030
ID ADX42030 standard; cDNA; 674 BP.


```
Alignment Scores:
Pred. No.: 1,61e-54 Length: 1088
Score: 531.00 Matches: 102
Percent Similarity: 99.04% Conservative: 1
Best Local Similarity: 98.08% Mismatches: 1
Query Match: 56.19% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x AAS86254 (1-1088)
QY 80 AlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGlu 99
Db 1 GCTCGAGGGGTGGTCTTACTTAGCTTTGTACAGCCAGATGTGATATTCTACAGGAA 60

QY 100 ValIleProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleThr 119
Db 61 GTTATTCCCCCATATTATATAGCTACCTTAAAGAGAGATCAAGTAATTATGAGATTATTACA 120

QY 120 GlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLys 139
Db 121 GGTGATGAGAGAGAGATATTTCACAGCTATATGTTGAAGAAATCAAGATGAATTAACA 180

QY 140 SerGlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHis 159
Db 181 AGCCAGAGATTATTCCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTCAT 240

QY 160 ValAsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGly 179
Db 241 GTGAATGTGTGAGAAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGACCAAGGG 300

QY 180 HisAlaAlaGlu 183
Db 301 CATGCTGCGGAA 312

RESULT 30
AAX84209/c
ID AAX84209 standard; cDNA; 1079 BP.
XX
AC AAX84209;
XX
DT 08-SEP-1999 (first entry)
XX
DE DNA encoding human breast tumour protein immunogenic fragment.
XX
KW Breast tumour protein; immunogenic fragment; vaccine; detection;
KW breast cancer development; therapy; ss.
XX
OS Homo sapiens.
XX
PN W09933869-A2.
XX
PD 08-JUL-1999.
XX
PF 22-DEC-1998; 98WO-US027416.
XX
PR 24-DEC-1997; 97US-00998253.
PR 24-DEC-1997; 97US-00998255.
PR 17-JUL-1998; 98US-00118554.
PR 17-JUL-1998; 98US-00118627.
XX
PA (CORI-) CORIXA CORP.
XX
PI Reed SG, Xu J;
XX
WP1; 1999-405486/34.
XX
PT New breast tumor protein genes used, in vaccines for immunotherapy, or
PT for diagnosis of breast cancer.
XX
PS Claim 3; Page 60; 70pp; English.
XX
CC This sequence encodes a human breast tumour protein immunogenic fragment
CC of the invention. The polypeptides or nucleic acids encoding them are
```

```
CC useful in vaccines and pharmaceutical compositions for manufacture of
CC medicaments for inhibiting the development of breast cancer in a patient.
CC They can also be used to treat breast cancer. Antibodies against these
CC polypeptides can be used to detect and monitor progression of breast
CC cancer in patients. Primers and probes derived from the polynucleotides
CC encoding the breast proteins are useful for detection of breast cancer.
CC Peripheral blood cells from a patient incubated in the presence of at
CC least one polypeptide, such that T cells proliferate, are useful in
CC manufacture of a medicament for treating breast cancer in a patient.
CC Antigen presenting cells incubated in the presence of at least one
CC polypeptide are also useful for treating breast cancer
XX
SQ Sequence 1079 BP; 327 A; 229 C; 177 G; 346 T; 0 U; 0 Other;
```

```
Alignment Scores:
Pred. No.: 8.6e-54 Length: 1079
Score: 525.00 Matches: 101
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 55.56% Indels: 0
DB: 2 Gaps: 0
```

```
US-10-757-745-2_COPY_54_236 (1-183) x AAX84209 (1-1079)
QY 83 ValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIlePro 102
Db 1077 GGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATATTCTACAGGAAGTTATCCC 1018

QY 103 ProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleThrGlyHisGlu 122
Db 1017 CCATATTATAGCTACCTAAAGAGAGATCAAGTAATTATGAGATTATTACAGGTCATGAA 958

QY 123 GluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGlnGlu 142
Db 957 GAAGGATATTTCACAGCTATAATGTGAAAGAAATCAAGAGTGAATTAATAAGCCCAAGAG 898

QY 143 IleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsnVal 162
Db 897 ATTATTCCTTTTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTGAATGTG 838

QY 163 SerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAla 182
Db 837 TCAGGAAATGAGCTTTGCCCTTATGACATCCCATTTTGGAGAGACCAGAGGGCATGCTGCG 778

QY 183 Glu 183
Db 777 GAA 775
```

Search completed: December 4, 2005, 09:03:56
Job time : 594.047 secs

ms ruge blank (uspto)

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 3, 2005, 23:34:21 ; Search time 4821.86 Seconds
(without alignments)
2157.330 Million cell updates/sec

Title: US-10-757-745-2_COPY_54_236

Perfect score: 945
Sequence: 1 MERALNSYFPPVBSALER.....GNELCLMTSLHSTRGHAE 183

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

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4: gb_om.*
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7: gb_ph.*
8: gb_pr.*
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12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	945	100.0	1261	8 AF201687	AF201687 Homo sapi
2	945	100.0	1920	6 BD205490	BD205490 CD40-Inte
3	945	100.0	1920	6 AR594294	AR594294 Sequence

4	945	100.0	1920	6 AX011599	AX011599 Sequence
5	945	100.0	1921	8 HSA269473	HSA269473 Homo sapi
6	945	100.0	1936	8 AF223469	AF223469 Homo sapi
7	945	100.0	1948	6 AR339398	AR339398 Sequence
8	945	100.0	1952	6 BC017553	BC017553 Homo sapi
9	945	100.0	2499	6 E23195	E23195 Topoisomera
10	936	99.0	1898	6 BD157138	BD157138 Primer fo
11	936	99.0	1898	6 AX878304	AX878304 Sequence
12	936	99.0	1898	6 AK002168	AK002168 Homo sapi
13	871	92.2	752	6 BD150065	BD150065 Primer fo
14	871	92.2	752	6 AX870003	AX870003 Sequence
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16	785.5	83.1	2151	8 HSA420495	HSA420495 Homo sapi
17	623.5	66.0	1312	6 BD205491	BD205491 CD40-Inte
18	623.5	66.0	1312	6 AR594295	AR594295 Sequence
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21	586	62.0	1236	5 CR761829	CR761829 Xenopus c
22	559	59.2	483	6 BD076937	BD076937 5' EST of
23	525	55.6	1079	6 BD139846	BD139846 Compounds
24	525	55.6	1079	6 AR202950	AR202950 Sequence
25	525	55.6	1079	6 AR208051	AR208051 Sequence
26	525	55.6	1079	6 AX429924	AX429924 Sequence
27	495.5	52.4	858	6 CQ726600	CQ726600 Sequence
28	463	49.0	1451	5 BC083404	BC083404 Dario rer
29	443	46.9	1455	5 BC097117	BC097117 Dario rer
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BD139846 Compounds
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AUTHORS
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JOURNAL
OncoGene 22 (18), 2699-2709 (2003)
PUBMED
12743594
2 (bases 1 to 1261)
REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (03-NOV-1999) Center for Molecular and Structural
Biology, Department of Medicine, and Hollings Cancer Center,
Medical University of South Carolina, 86 Jonathan Lucas St.,
Charleston, SC 29425, USA
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Best Local Similarity: 100.00% Mismatches: 0
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ACCESSION
BD205490
VERSION
BD205490.1 GI:33015260
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JP 2002512796-A/1.
SOURCE
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ORGANISM
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 1920)
AUTHORS
PYPE,S.M.C., Ghislaian,J.E.F.J., Remacle and Huylebroeck,D.F.E.
TITLE
CD40-Interacting and TRAF-Interacting protein
JOURNAL
Patent: JP 2002512796-A 1 08-MAY-2002;
VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE VZW
COMMENT
OS Homo sapiens (human)
PN JP 2002512796-A/1
PD 08-MAY-2002
PF 28-APR-1999 JP 2000546003
PR 29-APR-1998 EP 98201392.2
PI STEFAN MARIA CHRISTIAAN PYPE,
PI JACQUES EMILE FERNAND JOSIANE GHISLAIN REMACLE, PI DANNY
FRANCOIS EVELINE HUYLEBROECK
PC C12N15/09,A61K38/00,A61P9/10,A61P19/02,A61P25/00,A61P35/00, PC
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Score: 945.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
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DEFINITION Sequence 1 from patent US 6812203.
ACCESSION AR594294
VERSION   AR594294.1 GI:56643900
KEYWORDS   "Unknown."
SOURCE     Unknown.
ORGANISM   Unclassified.

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REFERENCE
AUTHORS   Pype,S.M.C., Remacle,J.E.F. and Huylebroeck,D.F.E.
TITLE      CD40-Interacting and TRAF-Interacting proteins
JOURNAL    Patent: US 6812203-A 1 02-NOV-2004;
           Vlaams Interuniversitair Instituut voor Biotechnologie VZW;
           Zwijnhaarde;
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Alignment Scores:

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Score:              945.00           Matches:          183
Percent Similarity: 100.00%          Conservative: 0
Best Local Similarity: 100.00%       Mismatches:      0
Query Match:        100.00%          Indels:          0
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US-10-757-745-2_COPY_54_236 (1-183) x AR594294 (1-1920)

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ACCESSION AX011599
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KEYWORDS   "Homo sapiens (human)"
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

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REFERENCE
AUTHORS   Remacle,J.E., Huylebroeck,D.F. and Pype,S.M.
TITLE      Cd40-interacting and traf-interacting proteins
JOURNAL    Patent: WO 9955859-A 1 04-NOV-1999;
           REMACLE JACQUES EMILE FERNAND (BE); VLAAMS INTERUNIV INST BIOTECH
           (BE); HUYLEBROECK DANNY FRANCOIS EVE (BE); PYPE STEFAN MARIA
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ORIGIN

Alignment Scores:

Pred. No.:	1-26e-90	Length:	1920
Score:	945.00	Matches:	183
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

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Db	359	TTCTCTCTATACCTGGAATATTGATGATTAGATCTAAACAATCTGTACAGAGGGCT	418
Qy	81	ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal	100
Db	419	CGAGGGGTGTCTCTACTAGCTTTGTACAGCCAGATGTGATATTCTACAGGAAGTT	478
Qy	101	IleProProTyrTyrSerTyrLeuLysLysArgSerAsnTyrGluIleIleThrGly	120
Db	479	ATTCCTCCCATTTATAGCTACCTTAAGAAAGATCAAGTAATTATGATATTACAGGT	538
Qy	121	HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer	140
Db	539	CATGAGAAGGATATTTTACAGCTATAATGTTGAAGAAATCAAGAGTGAATAATTAAGC	598
Qy	141	GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLysValHisVal	160
Db	599	CAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGCGATGTG	658
Qy	161	AsnValSerGlyAsnGluLeuLysLysMetThrSerHisLeuGluSerThrArgGlyHis	180
Db	659	AATGTGTGAGAAATGAGCTTTCCTTATGACATCCCATTTTGGAGACCAAGAGGGCAT	718
Qy	181	AlaAlaGlu	183
Db	719	GCTGGCGAA	727

RESULT 5
HSA269473
LOCUS
DEFINITION
Homo sapiens mRNA for TRAF and TNF receptor associated protein (ttrap gene).
ACCSSION
AJ269473.1 GI:8247253
VERSION
KEYWORDS
TRAF and TNF receptor associated protein; ttrap gene.
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1
Pepe, S., Declercq, W., Ibrahim, A., Michiels, C., Van Rietshoren, J.G., Dewulf, N., de Boer, M., Vandenaabeele, P., Huybroeck, D., and Remacle, J.E.
TRAP, a novel protein that associates with CD40, tumor necrosis factor (TNF) receptor-75 and TNF receptor-associated factors (TRAFs), and that inhibits nuclear factor-kappa B activation
J. Biol. Chem. 275 (24), 18586-18593 (2000)
10764746
2 (bases 1 to 1921)
Pepe, S.

TITLE
JOURNAL
PUBMED
AUTHORS

Direct Submission
Submitted (08-SEP-1999) Pype S., VIB07, Dept. Cell Growth, Differentiation and Development, Flanders Interuniversity Institute for Biotechnology, CELGEN, K.U.Leuven, Gasthuisberg Campus, Herestraat 49, B-3000 Leuven, BELGIUM
Related sequence: AL031775.
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
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Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
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Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerAsnTyrGluIleIleThrGly 120
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Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140

Submitted (08-SEP-1999) Pype S., VIB07, Dept. Cell Growth, Differentiation and Development, Flanders Interuniversity Institute for Biotechnology, CELGEN, K.U.Leuven, Gasthuisberg Campus, Herestraat 49, B-3000 Leuven, BELGIUM
Related sequence: AL031775.
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Score: 945.00 Matches: 183
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
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Db 181 ATGGAAGGGCTCTGAACCTCTTCCGAGCCTCCGCTGGAGAGCGCTTTGGAACGC 240
Qy 21 ArgProGluThrIleSerGluProLysThrValAspLeuThrAsnGluGluThrThr 40
Db 241 CGACCTGAAACCATCTCTGAGCCAGACCTATGTGACCTAACCAATGAGAAACACT 300
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
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Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 361 TTCTCTCTATACCTGGAATATTGATGATTAGATCTAAACAATCTGTACAGAGGGCT 420
Qy 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 421 CGAGGGGTGTCTCTACTAGCTTTGTACAGCCAGATGTGATATTCTACAGGAAGTT 480
Qy 101 IleProProTyrTyrSerTyrLeuLysLysArgSerAsnTyrGluIleIleThrGly 120
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Db      601 CAAGAGATTATTTCTCTTTTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGTCATGTG 660
Qy      161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db      661 AACGTGTGAGAAATAGACTTTGCTTATGACATCCCATTTGGAGAGCACCAGAGGGGAT 720
Qy      181 AlaAlaGlu 183
Db      721 GCTGGGAA 729

RESULT 6
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LOCUS      AF223469      1936 bp      mRNA      linear      PRI 17-APR-2000
DEFINITION Homo sapiens AD022 protein (AD022) mRNA, complete cds.
ACCESSION  AF223469
VERSION     AF223469.1  GI:7578788
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1 (bases 1 to 1936)
AUTHORS    Song,H., Gao,G., Peng,Y., Ren,S., Chen,Z. and Han,Z.
TITLE      A novel gene expressed in human adrenal gland
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 1936)
AUTHORS    Song,H., Gao,G., Peng,Y., Ren,S., Chen,Z. and Han,Z.
TITLE      Direct Submission
JOURNAL    Submitted (12-JAN-2000) Chinese National Human Genome Center at
            Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
            Shanghai 201203, China
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Pred. No.:      1.27e-90      Length:      1936
Score:          945.00      Matches:      183
Percent Similarity: 100.00%      Conservative: 0
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DEFINITION Sequence 889 from patent US 6569662.
ACCESSION  AR339398
VERSION     AR339398.1  GI:33726255
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SOURCE      Unknown.
ORGANISM    Unclassified.
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            Tang,Y.T., Zhou,P. and Drmanac,R.T.
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            Patent: US 6569662-A 889 27-MAY-2003;
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RESULT 8
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BC017553
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BC017553 1952 bp mRNA linear PRI 29-JUN-2004
BC017553
BC017553.2 GI:34782842
MGC.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 1952)
Srausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Siemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
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Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Udell, T.B., Toehiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

JOURNAL
PUBMED
12477932
REFERENCE
2 (bases 1 to 1952)
Srausberg, R.
AUTHORS
TITLE
Direct Submission

JOURNAL

REMARK
COMMENT

Submitted (19-NOV-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Sep 16, 2003 this sequence version replaced gi:17028464.
Contact: MGC help desk
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC/DCD/DTDP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth
Featherstone, Malachi Griffith, Osi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Anara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angeliue Schnerch, Ursula Skalska,
Duane Smalios, Jeff Stott, Miranda Tsai, George Yang, Jacqueie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK plate: 15 Row: m Column: 16
This clone was selected for full length sequencing because it
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gene

CDS

ORIGIN

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Query Match: 100.00% Indels: 0
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PC
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PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
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FT CDS
Location/Qualifiers
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QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
DB 400 CGAGGGGTGCTCTCTACTTAGCTTGACGCCCAAGATGTGATATTTCTACAGGAAT 459
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QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
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DB 400 CGAGGGGTGCTCTCTACTTAGCTTGACGCCCAAGATGTGATATTTCTACAGGAAT 459
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DB 460 ATTCCCCCATATTATAGTACCTTAAAGAGAGATCAAGTAATTTATGAGATTATTACAGGT 519
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DB 520 CATGAAGAAGGATATTTACAGCTATATTTGATGGATAGATCTAAACAATCTGTGAGAGAGGCT 399
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QY 181 AlaAlaGlu 183
DB 700 GCTGCGGAA 708
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AX878304
LOCUS AX878304 1898 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 13209 from Patent EP1074617.
ACCESSION AX878304
VERSION AX878304.1 GI:40033040
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Ota, T., Isegai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
Primers for synthesizing full-length cDNA and their use
Patent: EP 1074617-A 13209 07-FEB-2001;
JOURNAL Research Association for Biotechnology (JP)
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Qy 101 AlalaGlu 183
|||||

Db 700 GCTGGGAA 708

RESULT 12

AK002168 1898 bp mRNA linear PRI 30-JAN-2004

LOCUS Homo sapiens cDNA FLJ11306 fis, clone PLACE1010031.

DEFINITION AK002168

ACCESSION AK002168

VERSION AK002168.1 GI:7023882

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1

REFERENCE

AUTHORS Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Oobayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yasuda, T., Watanabe, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yanashita, H., Hirakawa, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Muesashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshioka, Y., Matsunawa, H., Ichihara, T., Shichata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujisawa, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigetani, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.

Complete sequencing and characterization of 21,243 full-length human cDNAs

Nat. Genet. 36 (1), 40-45 (2004)

14702039

2

Isogai, T., Ota, T., Hayaashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H., Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahara, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T.

NEDO human cDNA sequencing project

Unpublished

3 (bases 1 to 1898)

Isogai, T. and Otsuki, T.

Direct Submission

Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@helix.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- and 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

101 AlalaGlu 183
|||||

700 GCTGGGAA 708

RESULT 12

AK002168 1898 bp mRNA linear PRI 30-JAN-2004

LOCUS Homo sapiens cDNA FLJ11306 fis, clone PLACE1010031.

DEFINITION AK002168

ACCESSION AK002168

VERSION AK002168.1 GI:7023882

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1

REFERENCE

AUTHORS Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Oobayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yasuda, T., Watanabe, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yanashita, H., Hirakawa, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Muesashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshioka, Y., Matsunawa, H., Ichihara, T., Shichata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujisawa, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigetani, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.

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Isogai, T., Ota, T., Hayaashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H., Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahara, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T.

NEDO human cDNA sequencing project

Unpublished

3 (bases 1 to 1898)

Isogai, T. and Otsuki, T.

Direct Submission

Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@helix.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- and 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center

etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

FEATURES

source

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ORIGIN

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Score: 936.00 Matches: 182

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Best Local Similarity: 99.45% Mismatches: 1

Query Match: 99.05% Indels: 0

DB: 8 Gaps: 0

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Db 700 GCTCGGAA 708
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LOCUS Primer for synthesizing full-length cDNA and use thereof.
DEFINITION BD150065
ACCESSION BD150065
VERSION BD150065.1 GI:27855823
KEYWORDS JP 2002191363-A/4908.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 4908 09-JUL-2002;
KEYWORDS HELIX RESEARCH INSTITUTE
SOURCE OS Homo sapiens (human)
ORGANISM PN JP 2002191363-A/4908
COMMENT PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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Score: 871.00
Percent Similarity: 95.14% Conservative: 1
Best Local Similarity: 94.59% Mismatches: 7
Query Match: 92.17% Indels: 2
DB: 6 Gaps: 0
US-10-757-745-2_COPY_54_236 (1-183) x BD150065 (1-752)
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Db 160 ATGGAAGGGCTCTGAACCTCTGCTTCGAGCTCCGGTGGAGGAGCGCTTGGACGC 219
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Db 400 CGAGGGGTGCTCTCTACTAGCTTTGTACAGCCCAAGATGTGATATTCTTACAGGAAGTT 459
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Db 460 ATTTCCCATATTATAGCTACCTAAAGAGAGATCAAGTAATTATGAGATTATTACAGCT 519
Qy 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
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Qy 141 GlnGluIleIleProPheProSerThrLysMetMetArg-AsnLeuLeuCysValHisVa 160
Db 580 CAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAAACCTTTTATGTGTGATGT 639
Qy 160 IasnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeu-GluSerThrArgGlyH 180
Db 640 GAACGTGTTCAGAAATGAGCTTTGCTTAAAGACATCCCAATTTGGGGAACACACANAGGC 699
Qy 180 isAlaAlaGlu 183
Db 700 ATCTCGGGAA 710
RESULT 14
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LOCUS Sequence 4908 from Patent EP1074617.
DEFINITION AX870003
ACCESSION AX870003
VERSION AX870003.1 GI:40024866
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
TITLE Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
JOURNAL Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
PATENT: EP 1074617-A 4908 07-FEB-2001;
KEYWORDS Research Association for Biotechnology (JP)
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Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores: 3.28e-83 Length: 752
Pred. No.: 871.00 Matches: 175
Score: 871.00
Percent Similarity: 95.14% Conservative: 1
Best Local Similarity: 94.59% Mismatches: 7
Query Match: 92.17% Indels: 2
DB: 6 Gaps: 0
US-10-757-745-2_COPY_54_236 (1-183) x AX870003 (1-752)
Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 160 ATGGAAGGGCTCTGAACCTCTGCTTCGAGCTCCGGTGGAGGAGCGCTTGGACGC 219
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db 220 CGACCTGAACCACTCTCGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACA 279
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAenGlySerMet 60
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Qy 61 PheSerLeuIleThrTpaAniLeAspGlyLeuAspLeuAenLeuSerGluArgAla 80
Db 340 TTCTCTCTCATTTACCTGAATATTGATGGATTAGATCTAAACAATCTGTCTCAGAGGGCT 399
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Qy      121 HisGluGluGlyTyRPhoTherAlaileMetleuLySArgVallyLeuLySser 140
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Qy      141 GlnGluileileProPheProSerThryLysMetMetArg-AenLeuLeuCySValHieVa 160
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Db      580 CAAGAGATTATTCCTTTTCCAGTACCAAAATGATGAGAAAACCTTTTATGTGTGCATGT 639
Qy      160 laSnValSerGlyAenGluLeuCyLeuMetThSerHisLeu-GluSerThrArgGlyH 180
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Db      640 GAACGTGTCAAGAAATGAGCTTTCCTTAAAGACATCCCAATTTGGGNGAACACCANAGGCG 699
Qy      180 isAlaAlaGlu 183
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RESULT 15
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ordered pieces.
ACCESSION AC152027
VERSION   HTG; HTGS PHASE2; HTGS DRAFT.
KEYWORDS Dasyus novemcinctus (nine-banded armadillo)
SOURCE   Dasyus novemcinctus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Xenarthra; Dasypodidae; Dasypus.
REFERENCE
  1 (bases 1 to 150344)
  Antonellis,A., Avele,K., Benjamin,B., Blakesley,R.W., Boakye,A.,
  Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,H.,
  Engle,J., Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N.,
  Ho,S.-L., Hu,P., Hurlb,B., Idol,J.R., Jones,C., Kwong,P., Laric,P.,
  Larson,S., Lee-Lin,S.-Q., Legaspi,R., Madden,M., Maduro,Q.L.,
  Maddulo,V.B., Marquies,E.H., Mastello,C., Maskeri,B., McDowell,J.,
  Mullikin,J.C., Oestreicher,J.S., Park,M., Portunoy,M.E., Prasad,A.,
  Puri,O., Reddix-Dugue,N., Rosas,B., Schandler,K., Schueler,M.G.,
  Shan,K., Sison,C., Stantirpop,S., Stephen,E., Thomas,J.W.,
  Thomas,P.J., Tshipouri,V., Vogt,J.L., Wetherby,K.D., Young,A. and
  Green,E.D.
  NISC Comparative Sequencing Initiative
  Unpublished
  2 (bases 1 to 150344)
  Green,E.D.
  Direct Submission
  Submitted (21-OCT-2004) NIH Intramural Sequencing Center, 8717
  Grovemont Circle, Gaithersburg, MD 20877, USA
  3 (bases 1 to 150344)
  Green,E.D.
  Direct Submission
  Submitted (11-NOV-2004) NIH Intramural Sequencing Center, 5625
  Fishers Lane, Rockville, MD 20852, USA
  On Nov 11, 2004 this sequence version replaced gi:54312159.
  ----- Genome Center
  Center: NIH Intramural Sequencing Center
  Center code: NISC
  Web site: http://www.nisc.nih.gov
  Contact: nisc_zoo@nhgri.nih.gov
  ----- Project Information
  -----
  Center project name: ifi
  Center clone name: 012D21

```

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring

clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 149480 bases at least Q40
 Consensus quality: 149754 bases at least Q30
 Consensus quality: 149909 bases at least Q20
 Insert size: 155000; agarose-fp
 Insert size: 149944; sum-of-contigs
 Quality coverage: 9.52x in Q20 bases; agarose-fp
 Quality coverage: 9.84x in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 5 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submittor.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.

```

* 1 36273: contig of 36273 bp in length
* 36274 36373: gap of unknown length
* 36374 55049: contig of 18676 bp in length
* 55050 55149: gap of unknown length
* 55150 101939: contig of 46790 bp in length
* 101940 102039: gap of unknown length
* 102040 114806: contig of 12767 bp in length
* 114807 114906: gap of unknown length
* 114907 150344: contig of 35438 bp in length.

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FEATURES

Location/Qualifiers

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  /clone_lib="VMRC5"
  /note="BAC resource: http://bacpac.chori.org/"
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  clone_end:SP6
  vector_side:left"
misc_feature
  1. .23736
  /note="clone overlaps with GenBank Accession Number
  AC152029 clone VMRC5-168B11 (center project name ifj)"
  36274. .36373
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  36374. .55049
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  55050. .55149
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  55150. .101939
  /note="assembly_fragment"
  101940. .102039
  /estimated_length=unknown
  102040. .114806
  /note="assembly_fragment"
  114807. .114906
  /estimated_length=unknown
  114907. .150344
  /note="assembly_fragment
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  vector_side:right"

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ORIGIN

Alignment Scores:

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Pred. No.: 2,93e-72 Length: 150344
Score: 795.00 Matches: 156
Percent Similarity: 90.16% Conservative: 9
Best Local Similarity: 85.25% Mismatches: 18
Query Match: 83.92% Indels: 0
DB: 14 Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x AC152027 (1-150344)

QY 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 53438 ATGAAAGAGCGCAGAACTCTACTTTGAGCGCGTGGAGGAGCGCCCGGAGAGC 53379
QY 21 ArgProGluThrIleSerGluProLysThrValAspLeuThrAsnGluGluThr 40
Db 53378 CGGCCTCGGACCCCTGCCAGCCCGGCGCTGTGTGACCTTAAGCAACGAAGATACGACT 53319
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 53318 GATTCGAATGTTCTTAATAATCACCTCATCTGAAAATATTCAGCAAGAGATGCGAGTATG 53259
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 53258 TTCTCTTAATTACCTGGAAATATTGATGGATTGGATCTAAACAACCTGCAAGAGAGGGCT 53199
QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 53198 CGAGGGGTGTGTTCTTACTTAACTTTGTACAGTCCAGATGTGATATTCTTACAGGAAGTT 53139
QY 101 IleProProTyrTyrSerTyrLeuLysLeuLysSerSerAsnTyrGluIleIleThrGly 120
Db 53138 ATTCTCTCCGTACACAGTTACCTTAAAGAGAGCAAGTAATTACGAGATTTATACAGGT 53079
QY 121 HisGluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSer 140
Db 53078 CGTGAAGAGAGATTTTACAGCTATTAATGTTGAAGAAATCAAGAGTGAATTTAAAGAGC 53019
QY 141 GlnGluIleIleProPheProSerThrLysMetMetArgAsnLeuLeuValHisVal 160
Db 53018 CAAGAGATTTATCTTTTCCAAAGTACCAGAAATGATGAGAAACCTATTGTGTGCATGTG 52959
QY 161 AsnValSerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHis 180
Db 52958 AGTGTGTGAGAAATGAACCTTACCTTATGACTTCCCTTTAGAGACCAAGAGGCAT 52899
QY 181 AlaAlaGlu 183
Db 52898 GCTAAGGAA 52890

RESULT 16
LOCUS HSA420495 2151 bp mRNA linear PRI 23-NOV-2001
DEFINITION Homo sapiens mRNA full length insert cDNA clone EUROIIMAGE 1761756.
ACCESSION AJ420495
VERSION AJ420495.1 GI:17066359
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 Auffray, C., Ansoorge, W., Ballabio, A., Estivill, X., Gibson, K.,
Lehrach, H., Pouetka, A. and Lundeberg, J.
The European IMAGE consortium for integrated Molecular analysis of
human gene transcripts
Unpublished
2 (bases 1 to 2151)
PERSON, A.
Direct Submission
Submitted (02-OCT-2001) Persson A., Center for Molecular
Biotechnology, KTH, SCFAB, Institute of Biotechnology, Roslagavagen
30B, 106 91 Stockholm, SWEDEN
```

```
COMMENT This clone is available royalty-free through IMAGE Consortium
Distributors. IMPORTANT: This sequence represents the full insert
of this IMAGE cDNA clone. No attempt has been made to verify
whether this corresponds to the full-length of the original mRNA
from which it was derived.
FEATURES
Location/Qualifiers
source
1..2151
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="6"
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/clone_lib="NCI_CGAP_Kid3"
2105..2110
polya_signal
ORIGIN
Alignment Scores:
Pred. No.: 1,41e-73 Length: 2151
Score: 785.50 Matches: 172
Percent Similarity: 55.48% Conservative: 0
Best Local Similarity: 55.48% Mismatches: 2
Query Match: 83.12% Indels: 137
DB: 8 Gaps: 1
US-10-757-745-2_COPY_54_236 (1-183) x HSA420495 (1-2151)
QY 10 GluProValGluSerAlaLeuGluArgProGluThrIleSerGluProLys 29
Db 6 GAGGCTCCGTTGGAGAGAGCGCTTTGGAACGCCGACCTGAAACCATCTCTGAGCCCAAG 65
QY 29 ----- 29
Db 66 ACCTAGTAAGTATGATGAGGGAGCGGAGCCAGCTCCCGAGGAGCAGTTTGTATACCAGGT 125
QY 29 ----- 29
Db 126 AGCCCTCGCGTCTCTGGAGCTGCCGTGGAGCTGGCGGAGCATGCTGAGGCGAGATCTCC 185
QY 29 ----- 29
Db 186 AAGCTCGTAGCCAGAGAGAGGGCTTGGTGTGCTGCTGCGGGAGTTTGGGCCCA 245
QY 29 ----- 29
Db 246 GCAGCGGATTAACACTGCACAGACTGTCGCTTCGNAACGTGATTTGGGGTCCAGGGAGG 305
QY 29 ----- 29
Db 306 AAAAGATGGAATGTAATGTTTAACCTCAATGAAAGGAAATAAGTAAGCGAGAGGTTTGA 365
QY 29 ----- 29
Db 366 AACAAATGAACGAGGCTAAACCTTCTATCGAAAAATGGCAACTTGGAAAGTCTCTTGTCT 425
QY 30 -----ThyTyrValAsp 33
Db 426 TCCTGTATTGTTTATTATTCTAGGCCCTAGGCTGACCGGCCAGCAATAACAGT-GTTGAC 484
QY 34 LeuThrAsnGluThrThrAspSerThrThrSerLysIleSerProSerGluAspThr 53
Db 485 CTAACCAATGAAGAAACAACTGATTCACCACTTCTAAAAATCAGCCCATCTGAAGATACT 544
QY 54 GlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeu 73
Db 545 CAGCAAGAAAATGGCAGCATGTTCTCTCATTTACCTGGGAATATTGATGATAGATCTA 604
QY 74 AsnAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSerProAsp 93
Db 605 AACAACTGTGACAGAGGGCTCGAGGGGTGTGTTCTTACTTAGCTTTGTACAGGCCAGAT 664
QY 94 ValIlePheLeuGlnGluValIleProProTyrTyrSerTyrLeuLysLysArgSer 113
Db 665 GTGATATTTCTACAGGAAGTTATTTCCTCCCATATTATAGCTACCTAAAGAGAGATCAAGT 724
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QY 114 AenTyrGluIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeuLysLys 133
Db 725 AATATGAGATTATTACAGGTCATGAAGAGGATATTTACAGCTATATATGTTGAAGAA 784
QY 134 SerArgValLysLeuLysSerGlnGluIleLeuProPheProSerThrLysMetMetArg 153
Db 785 TCAAGAGTGAAATTAAAGCCAGAGATTATCTTTTCCAAAGTACCAGATGATGAGA 844
QY 154 AenLeuLeuCysValHisValAenValSerGlyAenGluLeuLysMetThrSerHis 173
Db 845 AACCTTTATGTGTCATGTGAATGTGTGAGAAATGAGCTTTGCTTATGACATCCCAT 904
QY 174 LeuGluSerThrArgGlyHisAlaGlu 183
Db 905 TTGGAGAGACCAGAGGGCATGCTCGGAA 934

RESULT 17
LOCUS BD205491 1312 bp DNA linear PAT 17-JUL-2003
DEFINITION CD40-Interacting and TRAF-Interacting protein.
ACCESSION BD205491
VERSION BD205491.1 GI:33015261
KEYWORDS JP 2002512796-A/2.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
1 (bases 1 to 1312)
Pype,S.M.C., Ghislain,J.E.F.J., Remacle and Huylebroeck,D.F.E.
CD40-Interacting and TRAF-Interacting protein
Patent: JP 2002512796-A 2 08-MAY-2002;
VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE VZW
OS Mus musculus (mouse)
PN JP 2002512796-A/2
PD 08-MAY-2002
PF 28-APR-1999 JP 2000545003
PR 29-APR-1998 EP 98201392.2
PI STEFAN MARIA CHRISTIAAN PYPE,
PI JACQUES EMILE FERNAND JOSTANE GHISLAIN REMACLE, PI DANNY
FRANCOIS EVELINE HUYLEBROECK
PC C12N15/09,A61K38/00,A61P9/10,A61P19/02,A61P25/00,A61P35/00, PC
A61P37/02,
PC A61P37/06,A61P43/00,C07K14/47,C07K16/18,G01N33/15,G01N33/50,
PC G01N33/566,
PC C12N15/00,A61K37/02
CC CD40-Interacting and TRAF-Interacting protein. PH Key
Location/Qualifiers
FT CDS (122)..(1234).

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Pred. No.: 1,44e-56 Length: 1312
Score: 623.50 Matches: 122
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Best Local Similarity: 67.03% Mismatches: 35
Query Match: 65.98% Indels: 1
DB: Gaps: 1

US-10-757-745-2_COPY_54_236 (1-183) x BD205491 (1-1312)

QY 2 GluArgAlaLeuAenSerTyrPheGluProProValGluGluSerAlaLeuGluArg 21
Db 317 CAGAAGCCCTGAGCGCTACTTCGAGTCCAGAGAACGACCAAGGGTGGCGGCCAG 376
QY 22 ProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrAsp 41

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Db 377 CCTCCAGCTCCTTCAAGTCGAGGCTATGTTGATCTTAACCAACGAGGATGCAATGAT 436
QY 42 SerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAenGlySerMetPhe 61
Db 437 ACAACCACTTTAGAAAGCCAGCTCATCT--GGAACCTCCTCTAGAGATAGCAGCACTATT 493
QY 62 SerLeuIleThrTyrPheAsnIleAspGlyLeuAspLeuAenLeuSerGluArgAlaArg 81
Db 494 TCTTTCTATTACTGGAATATTGATGGATTAGATGCAATCTGCCGAGAGGGCTCGA 553
QY 82 GlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIle 101
Db 554 GGGGTGIGTCTCGCTAGCTTTGTATAGTCCAGATGTGGTATTCTTACAGGAAGTTATC 613
QY 102 ProProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGlyHis 121
Db 614 CCCCCTACTGTGCTTACCTAAAGAGAGAGAGCCAGTCAGTTACACAAATTTATTACAGGTAAT 673
QY 122 GluGluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGln 141
Db 674 GAAGAGAGATATTTCACAGCTATATCTATTGAAGAAAGGAGAGTGAAATTTAAAGCTCAG 733
QY 142 GluIleIleProPheProSerThrLysMetMetArgAenLeuLeuLysValHisValAen 161
Db 734 GAGATTATTCTTTTCCAATACCAAAATGATGAGAAACCTGCTATGCTGTAATGTGAGT 793
QY 162 ValSerGlyAenGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAla 181
Db 794 TTGGGTGGAATGAATTTTGGCTTTATGACATCCCATTTGGAGAGACCAGAGAACATTTCT 853
QY 182 AlaGlu 183
Db 854 GCGGAA 859

RESULT 18
LOCUS AR594295 1312 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 3 from patent US 6812203.
ACCESSION AR594295
VERSION AR594295.1 GI:56643901
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1312)
AUTHORS Pype,S.M.C., Remacle,J.E.F. and Huylebroeck,D.F.E.
TITLE CD40-Interacting and TRAF-Interacting proteins
JOURNAL Patent: US 6812203-A 3 02-NOV-2004;
Vlaams Interuniversitair Instituut voor Biotechnologie VZW;
Zwijnaarde;
WOX;
Location/Qualifiers
1..1312
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1,44e-56 Length: 1312
Score: 623.50 Matches: 122
Percent Similarity: 80.22% Conservative: 24
Best Local Similarity: 67.03% Mismatches: 35
Query Match: 65.98% Indels: 1
DB: Gaps: 1

US-10-757-745-2_COPY_54_236 (1-183) x AR594295 (1-1312)

QY 2 GluArgAlaLeuAenSerTyrPheGluProProValGluGluSerAlaLeuGluArg 21
Db 317 CAGAAGCCCTGAGCGCTACTTCGAGTCCAGAGAACGACCAAGGGTGGCGGCCAG 376
QY 22 ProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrAsp 41

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QY 66 TrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArgGlyValCysSer 85
Db 436 TGGAAATATAGATCGCTTGTATGATCAATGTCGGAAGGGCTGCTGGTGTGTCTTC 495
QY 86 TyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluValIleProTyrTyr 105
Db 496 TATTGGCCCTGTACAGTCCAGATGTAGTATTCTTACAGAGGGTTATTCCACCATACTAT 555
QY 106 SerTyrLeuIlylsyAspSerSerAsnTyrGluIleIleThrGlyHisGluGlyTyr 125
Db 556 GAGTACTCTGAAGAAGAGAGCTGCAGCTACACAAATATTATACAGGTAAATGAGGATGAATAC 615
QY 126 PheThrAlaIleMetLeuIlylsySerArgValIlylsySerGlnGluIleIlePro 145
Db 616 TTCACCTGCTATGATGCTGAAGAAGAGCAGGGTAAAGTTAATAAGCCAGAAATGTACCA 675
QY 146 PheProSerThrIlylsyMetMetArgAsnLeuLeuCysValHisValAsnValSerGlyAsn 165
Db 676 TACCCATCCACGGTGTATGATGAGAAATTTGCTGTAGCAAAATGTGAATATCTCTGGCAAC 735
QY 166 GluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaGlu 183
Db 736 AGTATATGCTTAATGACTTCTCATCTAGAGACACAAAGATCATTTCAAAGGAG 789

RESULT 22
BD076937 483 bp DNA linear PAT 27-AUG-2002
LOCUS 5' EST of secretory protein expressed in prostate.
DEFINITION BD076937
ACCESSION BD076937.1 GI:22622540
VERSION JP 2001512013-A/184.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 483)
AUTHORS Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
TITLE 5' EST of secretory protein expressed in prostate
JOURNAL Patent: JP 2001512013-A 184 21-AUG-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001512013-A/184
PD 21-AUG-2001
PF 31-JUL-1998 JP 2000505291
PR 01-AUG-1997 US 08/905144
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO PI
LACROIX
PC C12N15/09,C07K14/47,C12P21/02,C12Q1/02,C12Q1/68,C12N15/00 CC
blastn
CC identity 99
CC region 1. .310
CC id T26956
CC est
CC blastn
CC identity 98
CC region 1. .315
CC id T31666
CC est
CC blastn
CC identity 100
CC region 137. .267
CC id R14990
CC est
CC blastn
CC identity 100
CC region 63. .137
CC id R14990
CC est
CC blastn
CC identity 100
CC region 1. .50
CC id R14990
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CC Von Heijne matrix
CC score 5.2
CC seq LCVEFASVASCDA/AV
FH Key Location/Qualifiers
FT misc feature 105..414
FT misc feature 45..359
FT misc feature 202..332
FT misc feature 127..201
FT misc feature 65..114
FT sig_peptide 1..120.
FEATURES
source
1..483
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 3.4e-50 Length: 483
Score: 559.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 59.15% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_54_236 (1-183) x BD076937 (1-483)
QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluSerAlaLeuGluArg 20
Db 160 ATGGAAGGGCTCTGAACCTCTACTTCGAGCCCTCCGGTGGAGAGAGCGCTTGGAAACGC 219
QY 21 ArgProGluThrIleSerGluProIlylsyThrTyrValAspLeuThrAsnGluThrThr 40
Db 220 CGACCTCGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAGAAACAACT 279
QY 41 AspSerThrThrSerIlylsySerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 280 GATTCCACCACCTCTAAATATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGAGCATG 339
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 340 TTCTCTCTCATCTACCTGGAATATTGATGGATTAGATCTAAACAATCTGTCCAGAGAGGCT 399
QY 81 ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
Db 400 CGAGGGGTGTGTCTTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTT 459
QY 101 IleProTyrTyrTyrSerTyrLeu 108
Db 460 ATTCCCCCATATTATAGTACCTA 483

RESULT 23
BD139846/c
LOCUS BD139846
DEFINITION Compounds for immunotherapy and diagnosis of breast cancer and methods for their use.
ACCESSION BD139846
VERSION BD139846.1 GI:23234791
KEYWORDS JP 2002507387-A/63.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1079)
AUTHORS Reed,S.G. and Xu,J.
TITLE Compounds for immunotherapy and diagnosis of breast cancer and methods for their use
JOURNAL Patent: JP 2002507387-A 63 12-MAR-2002;
COMMENT CORIXA CORP
OS Homo sapiens (human)
PN JP 2002507387-A/63
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PD 12-MAR-2002
PF 22-DEC-1998 JP 2000526543
PR 24-DEC-1997 US 08/998253,24-DEC-1997 US 08/998255 PR
17-JUL-1998 US 09/118627,17-JUL-1998 US 09/118554 PI STEVEN
G REED,JIANGCHUN XU
PC C12N15/09,A61K38/00,A61K39/00,A61K39/39,A61K39/395,A61P35/00,
PC C07K14/47,
PC C07K16/18,C12N1/19,C12N1/21,C12N5/10,C12P21/08,C12Q1/68,G01N33/ PC
53,
PC G01N33/577,C12N15/00,A61K37/02,C12N5/00
CC Compounds for immunotherapy and diagnosis
of breast cancer and
CC methods for
CC their use
FH Key Location/Qualifiers
FT source 1..1079
/organism="Homo sapiens (human)"
/ft_key Location/Qualifiers
FT source 1..1079
/organism="Homo sapiens"
/ft_key Location/Qualifiers
FEATURES
source
ORIGIN
Alignment Scores:
Pred. No.: 3.59e-46 Length: 1079
Score: 525.00 Matches: 101
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 55.56% Indels: 0
DB: 6 Gaps: 0
US-10-757-745-2_COPY_54_236 (1-183) x BD139846 (1-1079)
Qy 83 ValCysSerTyrLeuAlaLeuTyrSerProaspValIlePheLeuGlnGluValIlePro 102
Db 1077 GTGTGTTCTTACTTAGCTTTGTACAGCCAGATGATATTCTACAGGAAGTTATTCC 1018
Qy 103 ProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGlyHisGlu 122
Db 1017 CCATATTATAGCTACCTAAAGAGAGATCAAGTAAATTATGAGATTATTACAGGTCATGAA 958
Qy 123 GluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGlnGlu 142
Db 957 GAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAAGCCAGAG 898
Qy 143 IleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsnVal 162
Db 897 ATTATTCCTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTGAATGTG 838
Qy 163 SerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAla 182
Db 837 TCAGGAATGAGCTTTGCTTATGACATCCCATTTGGAGAGACCAGAGGCGATGCTCG 778
Qy 183 Glu 183
Db 777 GAA 775
RESULT 24
AR202950/c
LOCUS AR208051 1079 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 63 from patent US 6379951.
ACCESSION AR208051
VERSION AR208051.1 GI:21507966
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN
Alignment Scores:
Pred. No.: 3.59e-46 Length: 1079
Score: 525.00 Matches: 101
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 55.56% Indels: 0
DB: 6 Gaps: 0
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Qy 103 ProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluIleIleThrGlyHisGlu 122
Db 1017 CCATATTATAGCTACCTAAAGAGAGATCAAGTAAATTATGAGATTATTACAGGTCATGAA 958
Qy 123 GluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGlnGlu 142
Db 957 GAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAAGCCAGAG 898
Qy 143 IleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsnVal 162
Db 897 ATTATTCCTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTGAATGTG 838
Qy 163 SerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAla 182
Db 837 TCAGGAATGAGCTTTGCTTATGACATCCCATTTGGAGAGACCAGAGGCGATGCTCG 778
Qy 183 Glu 183
Db 777 GAA 775
RESULT 24
AR202950/c
LOCUS AR202950 1079 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 63 from patent US 6365348.
ACCESSION AR202950
VERSION AR202950.1 GI:21499210
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN
Alignment Scores:
Pred. No.: 3.59e-46 Length: 1079
Score: 525.00 Matches: 101
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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US-10-757-745-2_COPY_54_236 (1-183) x AR208051 (1-1079)
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Db      1077 GTGTGTTCTTACTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTCC 1018
Qy      103  ProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluLeuLeuThrGlyHisGlu 122
Db      1017 CCATATTATAGCTACCTTAAGAAGAGATCAAGTAATTATGAGATTATTACAGGTCATGAA 958
Qy      123  GluGlyTyrPheThrAlaIleMetLeuLysLysSerArgValLysLeuLysSerGlnGlu 142
Db      957 GAAGGATATTTACAGCTATATGTTGAAGAATCAAGAGTGAAATTAAGAAAGCCAAAGAG 898
Qy      143  IleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsnVal 162
Db      897 ATTATTCCTTTTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAATGTG 838
Qy      163  SerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAla 182
Db      837 TCAGGAATAGCTTTGGCTTTATGACATCCCTTTGGAGAGCACCAGAGGGCATGCTGCG 778
Qy      183  Glu 183
Db      777 GAA 775

RESULT 26
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LOCUS      AX429924      1079 bp      DNA      linear      PAT 21-JUN-2002
DEFINITION Sequence 63 from Patent WO0198339.
ACCESSION  AX429924
VERSION     AX429924.1  GI:21541088
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.

REFERENCE
1
AUTHORS    Reed,S.G., Xu,J., Dillon,D.C., Retter,M.W. and Harlocker,S.L.
TITLE      Compositions and methods for the therapy and diagnosis of breast
            cancer
JOURNAL    Patent: WO 0198339-A 63 27-DEC-2001;
            CORIXA CORPORATION (US)
FEATURES   .
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ORIGIN

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DB:             6      Gaps:      0

US-10-757-745-2_COPY_54_236 (1-183) x AX429924 (1-1079)

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Qy      103  ProTyrTyrSerTyrLeuLysLysArgSerSerAsnTyrGluLeuLeuThrGlyHisGlu 122
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Qy      143  IleIleProPheProSerThrLysMetMetArgAsnLeuLeuCysValHisValAsnVal 162
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Qy      163  SerGlyAsnGluLeuCysLeuMetThrSerHisLeuGluSerThrArgGlyHisAlaAla 182
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Qy      183  Glu 183
Db      777 GAA 775

RESULT 27
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LOCUS      CQ726600      858 bp      DNA      linear      PAT 03-FEB-2004
DEFINITION Sequence 12534 from Patent WO02068579.
ACCESSION  CQ726600
VERSION     CQ726600.1  GI:42290170
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.

REFERENCE
1
AUTHORS    Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE      Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
JOURNAL    Patent: WO 02068579-A 12534 06-SEP-2002;
            PE Corporation (NY) (US)
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DB:             6      Gaps:      1

US-10-757-745-2_COPY_54_236 (1-183) x CQ726600 (1-858)

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Qy      41  AspSerThrThrSerLysLysSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
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Qy      61  PheSerIleuLeuThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db      340 TTCTCTCTCATTAACCTGGAATATTGATGGATTAGATCTAAACAATCTGTGAGAGAGGGCT 399
Qy      81  ArgGlyValCysSerTyrLeuAlaLeuTyrSerProAspValIlePheLeuGlnGluVal 100
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Qy 181 AlaAlaGlu 183
Db 469 GCTGCGGAA 477

RESULT 28
LOCUS BC083404
DEFINITION Danio rerio TTRAP protein, mRNA (cdna clone IMAGE:7238334), partial
cds.
ACCESSION BC083404
VERSION BC083404.1 GI:53734140
KEYWORDS Danio rerio (zebrafish)
SOURCE Danio rerio
ORGANISM Danio rerio
REFERENCE 1 (bases 1 to 1451)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Haieh,F.,
Ditzchenko,L., Marusik,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Faney,J., Helton,E., Kettner,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1451)
NIH MGC Project
Direct Submission
Submitted (01-OCT-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: John Postlethwait, University of Oregon
cDNA Library Preparation: Dr. Sumio Sugano
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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Best Local Similarity: 48.11% Mismatches: 51
Query Match: 48.99% Indels: 32
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Qy 11 ---ProProValGluGluSerAlaLeuGluArgProGluThrIleSerGluProLys 29
Db 200 GCAGAGAAAACCTGAAGTCACTGGGAATAAGAGAAAAGATGACACTGCTGAAGCTTCAGGG 259
Qy 30 Thr-----TyrValAspLeuThrAsnGluGluThr 39
Db 260 ACGAAGAAGAAATTTGAAGACGACACATCGCGATTTCATTCGACACAGAGAGAGCC 319
Qy 40 ThrAspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGlnGlnGly--- 58
Db 320 ACCTGCTCTATTACTGTAAAC-----TCTAAGAAAATCAGGCTGAANAATGGCACA 370
Qy 59 -----SerMetPheSerLeuIleThrTrpAsnIleAspGlyLeu 71
Db 371 GCCAAATCTGAAGTGGAGGACAGCAGCTCTCCATCATCATCATGGAATGTCGCGTTTG 430
Qy 72 AspLeuAsnAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSer 91
Db 431 GACACATTAATCTTGCAGATCGTCCAGGGGCTTGTGCTCATATCTAGCTCTATACACA 490
Qy 92 ProAspValIlePheLeuGlnGluValIleProProTyrTyrSerTyrLeuLysLysArg 111
Db 491 CCAGATGGTGTTCCTTCAAGAGCTCAATCCAGCTTAATGTTAGTATCTTAAAGAAAGCT 550
Qy 112 SerSerAsnTyrGluIleIleThrGlyHisGluGlyTyrPheThrAlaIleMetLeu 131
Db 551 GCGCTCAGTACTGTTTGTGAAGGAAGCATGATGATGATGATGATGATGATGATGATGATG 610
Qy 132 LysLysSerArgValLysLeuLysSerGlnGluIleIleProPheProSerThrLysMet 151
Db 611 AGGAAATCAAGAGTCAAAATTTTGGAAAAGTGAAGATCATCTGCTTTCCCAACACACAAATG 670
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Db 731 TCCCATTTAGAAAGCTGTAAACCAACCAATCCCGAG 766

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LOCUS
DEFINITION
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BC097117.1 GI:66910444
Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE
AUTHORS
1 (bases 1 to 1455)
Srausberg,R.L., Feigold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schaefer,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

CONSTRM
TITLE
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1455)

REFERENCE
JOURNAL
PUBMED
AUTHORS
CONSTRM
TITLE
JOURNAL
REMARK
COMMENT
NIH MGC Project
Direct Submission
Submitted (01-JUN-2005) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Will Talbot
cDNA Library Preparation: Dr. Yutaka Suzuki and Dr. Sumio Sugano
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ULNL at: <http://image.llnl.gov>
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Query Match: 46.88% Indels: 33
DB: 5 Gaps: 4
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Qy 30 Thr-----TyrValAspLeuThrAsnGluThr 39
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Db 319 ACCTGCTCTATTACTGT-AAATCTC-----TAAGAAATCAGGCTGAAATGGCACA 368
Qy 59 -----SerMetPheSerLeuIleThrTrpAsnIleAspGlyLeu 71
Db 369 GCCAAATCTGAAGTGGAGGACAGCAAGCTCTCCATCATCAGCTGGAATGTGGACGGTTG 428
Qy 72 AspLeuAsnAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeuAlaLeuTyrSer 91
Db 429 GACACATTAAATCTTTGACATGTCGACGGGCTTGTGCTCATATCTAGCTCTATACACA 488
Qy 92 ProAspValIlePheLeuGlnGluValIleProProTyrTyrSerTyrLeuLysLysArg 111
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Qy 112 SerSerAsnTyrGluIleIleThrGlyHisGluGluGlyTyrPheThrAlaIleMetLeu 131
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Qy 172 SerHisLeuGluSerThrArgGlyHisAlaGlu 183

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 15:32:30 ; Search time 85.402 Seconds
(without alignments)
317.043 Million cell updates/sec

Title: US-10-757-745-2_COPY_54_140

Perfect score: 448

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Total number of hits satisfying chosen parameters: 6579870

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

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-TRANS=human40.cdi -LIST=500 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=30 -MODES=LOCAL -OUTFMt=pt0 -NOR=ext -HEARSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10757745 @CGN 1 343 @runat_01122005_091752_10210
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA.New.*

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- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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- 4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2.*
- 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3.*
- 10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	17.4	3672	US-10-821-234-301	Sequence 301, App
2	67.5	15.1	2361	US-10-485-517-118	Sequence 118, App
3	67	15.0	4265	US-11-044-051-74	Sequence 74, Appl
4	64.5	14.4	1914	US-10-750-185-42446	Sequence 42446, A
5	63.5	14.2	1673	US-10-750-185-41248	Sequence 41248, A
6	62	13.8	2031	US-11-135-855-5	Sequence 5, Appli
7	62	13.8	2048	US-10-750-185-54989	Sequence 54989, A
8	62	13.8	2154	US-11-135-855-6	Sequence 6, Appli

6	US-10-750-185-34532	2523	13.7	61.5	13.7	Sequence 34532, A
7	US-11-055-822-537	693	13.5	60.5	13.5	Sequence 537, App
7	US-10-750-185-50641	1611	13.5	60.5	13.5	Sequence 50641, A
6	US-10-821-234-462	2052	13.5	60.5	13.5	Sequence 462, App
6	US-10-821-234-373	442	13.4	60	13.4	Sequence 373, App
6	US-10-821-234-430	1146	13.4	60	13.4	Sequence 430, App
6	US-10-750-185-53598	1882	13.4	60	13.4	Sequence 53598, A
6	US-10-750-185-340	600	13.3	59.5	13.3	Sequence 340, App
9	US-11-082-389-435	1856	13.3	59.5	13.3	Sequence 435, App
6	US-10-750-185-59627	1907	13.3	59.5	13.3	Sequence 59627, A
6	US-10-750-185-35764	1331	13.2	59	13.2	Sequence 35764, A
6	US-10-750-185-62657	1482	13.1	58.5	13.1	Sequence 62657, A
7	US-11-081-566-1	2691	13.1	58.5	13.1	Sequence 1, Appli
7	US-11-060-005-1	5134	13.1	58.5	13.1	Sequence 1, Appli
6	US-10-750-185-34792	5306	13.1	58.5	13.1	Sequence 34792, A
7	US-11-060-008-3	6160	13.1	58.5	13.1	Sequence 3, Appli
6	US-10-750-185-24745	3045	12.9	58	12.9	Sequence 24745, A
6	US-10-750-185-57061	857	12.8	57.5	12.8	Sequence 57061, A
6	US-10-750-185-50453	1659	12.8	57.5	12.8	Sequence 50453, A
6	US-10-750-185-34783	1826	12.8	57.5	12.8	Sequence 34783, A
6	US-10-750-185-47296	1859	12.8	57.5	12.8	Sequence 47296, A
6	US-10-793-626-3606	3073	12.8	57.5	12.8	Sequence 3606, Ap
6	US-10-793-626-3455	3132	12.8	57.5	12.8	Sequence 3455, Ap
6	US-10-793-626-1779	3465	12.8	57.5	12.8	Sequence 1779, Ap
6	US-10-750-185-36325	1133	12.7	57	12.7	Sequence 36325, A
6	US-10-750-185-49833	1289	12.7	57	12.7	Sequence 49833, A
6	US-10-750-185-37878	1608	12.7	57	12.7	Sequence 37878, A
6	US-10-510-386-71	1621	12.7	57	12.7	Sequence 71, Appl
6	US-10-821-234-505	1218	12.6	56.5	12.6	Sequence 505, App
6	US-10-750-185-61772	1539	12.6	56.5	12.6	Sequence 61772, A
6	US-10-750-185-38884	1983	12.6	56.5	12.6	Sequence 38884, A
6	US-10-750-185-41925	2151	12.6	56.5	12.6	Sequence 41925, A
6	US-10-821-234-106	2213	12.6	56.5	12.6	Sequence 106, App
6	US-10-750-185-31054	3251	12.6	56.5	12.6	Sequence 31054, A
6	US-10-750-185-62663	372	12.6	56.5	12.6	Sequence 62663, A
6	US-10-750-185-50423	4508	12.6	56.5	12.6	Sequence 50423, A
6	US-10-750-185-31052	6816	12.6	56.5	12.6	Sequence 31052, A
6	US-10-750-185-59484	675	12.5	56	12.5	Sequence 59484, A
6	US-10-750-185-55038	877	12.5	56	12.5	Sequence 55038, A
6	US-10-750-185-60421	947	12.5	56	12.5	Sequence 60421, A
6	US-10-750-185-4678	1140	12.5	56	12.5	Sequence 4678, A
6	US-10-750-185-50291	1155	12.5	56	12.5	Sequence 50291, A
6	US-10-750-185-41396	1305	12.5	56	12.5	Sequence 41396, A
6	US-10-750-185-59960	1898	12.5	56	12.5	Sequence 59960, A
6	US-10-485-517-65	2422	12.5	56	12.5	Sequence 65, Appl
6	US-10-485-517-74	3052	12.5	56	12.5	Sequence 74, Appl
6	US-10-750-185-29284	352	12.5	56	12.5	Sequence 29284, A
6	US-10-821-234-431	4468	12.5	56	12.5	Sequence 431, App
6	US-10-750-185-60663	4884	12.5	56	12.5	Sequence 60663, A
6	US-10-750-185-56602	1252	12.4	55.5	12.4	Sequence 56602, A
6	US-10-821-234-101	1705	12.4	55.5	12.4	Sequence 101, App
6	US-10-750-185-26906	2647	12.4	55.5	12.4	Sequence 26906, A
7	US-11-108-172-1097	3424	12.4	55.5	12.4	Sequence 1097, Ap
6	US-10-750-185-60777	3459	12.4	55.5	12.4	Sequence 60777, A
6	US-10-750-185-34805	3515	12.4	55.5	12.4	Sequence 34805, A
6	US-10-793-626-107	3899	12.4	55.5	12.4	Sequence 107, App
6	US-10-793-626-2525	657	12.3	55	12.3	Sequence 2525, App
6	US-10-750-185-35895	660	12.3	55	12.3	Sequence 35895, A
6	US-10-750-185-48563	970	12.3	55	12.3	Sequence 48563, A
7	US-11-074-176-323	1015	12.3	55	12.3	Sequence 323, App
6	US-10-750-185-35382	1167	12.3	55	12.3	Sequence 35382, A
6	US-10-514-761-33	1188	12.3	55	12.3	Sequence 33, Appl
7	US-11-074-176-91	1200	12.3	55	12.3	Sequence 91, Appl
6	US-10-750-185-52244	1218	12.3	55	12.3	Sequence 52244, A
6	US-10-750-185-29477	1454	12.3	55	12.3	Sequence 29477, A
6	US-10-510-386-149	1650	12.3	55	12.3	Sequence 149, App
6	US-10-750-185-57545	2200	12.3	55	12.3	Sequence 57545, A
6	US-10-793-626-3473	2581	12.3	55	12.3	Sequence 3473, Ap
6	US-10-750-185-28948	3197	12.3	55	12.3	Sequence 28948, A
6		3326	12.3	55	12.3	

C 82	55	12.3	3504	6	US-10-793-626-3859	Sequence 3859, Ap	155	53	11.8	11115	6	US-10-513-786-8	Sequence 8, Appli
C 83	54.5	12.2	600	6	US-10-750-185-21840	Sequence 21840, A	C 156	52.5	11.7	413	7	US-11-108-172-506	Sequence 606, App
C 84	54.5	12.2	956	7	US-11-055-822-799	Sequence 799, App	C 157	52.5	11.7	942	6	US-10-750-185-37702	Sequence 37702, A
C 85	54.5	12.2	956	7	US-11-055-822-845	Sequence 845, App	C 158	52.5	11.7	952	6	US-10-750-185-55027	Sequence 55027, A
C 86	54.5	12.2	958	7	US-11-055-822-843	Sequence 843, App	C 159	52.5	11.7	1172	6	US-10-750-185-40064	Sequence 40064, A
C 87	54.5	12.2	1058	6	US-10-750-185-57478	Sequence 57478, A	C 160	52.5	11.7	1422	6	US-10-750-185-47601	Sequence 47601, A
C 88	54.5	12.2	1327	6	US-10-750-185-53596	Sequence 53596, A	C 161	52.5	11.7	1610	6	US-10-750-185-48234	Sequence 48234, A
C 89	54.5	12.2	1419	6	US-10-131-826A-517	Sequence 517, App	C 162	52.5	11.7	1642	6	US-10-750-185-40484	Sequence 40484, A
C 90	54.5	12.2	1563	6	US-10-750-185-54318	Sequence 54318, A	C 163	52.5	11.7	1766	6	US-10-967-648A-3	Sequence 3, Appli
C 91	54.5	12.2	1661	6	US-10-750-185-30971	Sequence 30971, A	C 164	52.5	11.7	1897	6	US-10-750-185-40175	Sequence 40175, A
C 92	54.5	12.2	2197	6	US-10-750-185-63583	Sequence 63583, A	C 165	52.5	11.7	1935	6	US-10-750-185-50882	Sequence 50882, A
C 93	54.5	12.2	2961	6	US-10-750-185-37281	Sequence 37281, A	C 166	52.5	11.7	1948	6	US-10-750-185-53525	Sequence 53525, A
C 94	54.5	12.2	6210	7	US-11-056-470-1	Sequence 1, Appli	C 167	52.5	11.7	2055	6	US-10-793-626-2097	Sequence 2097, Ap
C 95	54.5	12.2	17281	7	US-11-112-908-25	Sequence 25, Appli	C 168	52.5	11.7	2348	6	US-10-750-185-60768	Sequence 60768, A
C 96	54	12.1	708	7	US-11-008-727-3	Sequence 3, Appli	C 169	52.5	11.7	2431	6	US-10-510-386-11	Sequence 11, Appli
C 97	54	12.1	1413	7	US-11-008-727-19	Sequence 19, Appli	C 170	52.5	11.7	2534	6	US-10-750-185-33021	Sequence 33021, A
C 98	54	12.1	1426	6	US-10-750-185-40264	Sequence 40264, A	C 171	52.5	11.7	2999	6	US-10-793-626-3580	Sequence 3580, Ap
C 99	54	12.1	1431	7	US-11-008-727-21	Sequence 21, Appli	C 172	52.5	11.7	3040	6	US-10-793-626-3789	Sequence 3789, Ap
C 100	54	12.1	1503	6	US-10-821-234-606	Sequence 606, App	C 173	52.5	11.7	3204	6	US-10-793-626-4294	Sequence 4294, Ap
C 101	54	12.1	1530	7	US-11-008-727-15	Sequence 15, Appli	C 174	52.5	11.7	3386	6	US-10-750-185-37282	Sequence 37282, A
C 102	54	12.1	1534	6	US-10-750-185-37338	Sequence 37338, A	C 175	52.5	11.7	3994	6	US-10-793-626-3496	Sequence 3496, Ap
C 103	54	12.1	1668	6	US-10-750-185-30490	Sequence 30490, A	C 176	52.5	11.7	4015	6	US-10-793-626-3619	Sequence 3619, Ap
C 104	54	12.1	1892	6	US-10-750-185-35181	Sequence 35181, A	C 177	52.5	11.7	4207	6	US-10-793-626-3631	Sequence 3631, Ap
C 105	54	12.1	1941	6	US-10-750-185-44600	Sequence 44600, A	C 178	52.5	11.7	6497	6	US-10-821-234-839	Sequence 839, App
C 106	54	12.1	2073	6	US-10-750-185-53186	Sequence 53186, A	C 179	52.5	11.7	131855	7	US-11-112-908-29	Sequence 29, Appli
C 107	54	12.1	2445	6	US-10-750-185-43005	Sequence 43005, A	C 180	52.5	11.7	143389	7	US-11-112-908-30	Sequence 30, Appli
C 108	54	12.1	3692	6	US-10-485-517-1	Sequence 1, Appli	C 181	52.5	11.7	150173	7	US-11-112-908-26	Sequence 26, Appli
C 109	54	12.1	3822	6	US-10-485-517-77	Sequence 77, Appli	C 182	52.5	11.7	166020	7	US-11-112-908-28	Sequence 28, Appli
C 110	54	12.1	3915	6	US-10-750-185-50975	Sequence 50975, A	C 183	52.5	11.7	171247	7	US-11-112-908-27	Sequence 27, Appli
C 111	54	12.1	11667	6	US-10-508-263-122	Sequence 122, App	C 184	52	11.6	522	6	US-10-821-234-439	Sequence 439, App
C 112	54	12.1	11667	6	US-10-508-263-122	Sequence 122, App	C 185	52	11.6	730	6	US-10-750-185-61019	Sequence 61019, A
C 113	53.5	11.9	303	6	US-10-655-855-2	Sequence 2, Appli	C 186	52	11.6	921	6	US-10-467-657-7005	Sequence 7005, Ap
C 114	53.5	11.9	600	6	US-10-750-185-278	Sequence 278, App	C 187	52	11.6	1136	6	US-10-750-185-39134	Sequence 39134, A
C 115	53.5	11.9	600	6	US-10-750-185-1267	Sequence 1267, App	C 188	52	11.6	1331	6	US-10-750-185-46539	Sequence 46539, A
C 116	53.5	11.9	600	6	US-10-750-185-1804	Sequence 1804, Ap	C 189	52	11.6	1699	6	US-10-750-185-62714	Sequence 62714, A
C 117	53.5	11.9	600	6	US-10-750-185-21256	Sequence 21256, A	C 190	52	11.6	1800	6	US-10-750-185-43252	Sequence 43252, A
C 118	53.5	11.9	695	6	US-10-750-185-62194	Sequence 62194, A	C 191	52	11.6	1839	6	US-10-750-185-42616	Sequence 42616, A
C 119	53.5	11.9	696	9	US-11-082-389-25	Sequence 25, Appli	C 192	52	11.6	1851	6	US-10-750-185-55335	Sequence 55335, A
C 120	53.5	11.9	907	6	US-10-750-185-56125	Sequence 56125, A	C 193	52	11.6	1878	6	US-10-750-185-29847	Sequence 29847, A
C 121	53.5	11.9	915	6	US-10-750-185-46586	Sequence 46586, A	C 194	52	11.6	1978	6	US-10-750-185-42602	Sequence 42602, A
C 122	53.5	11.9	956	6	US-10-750-185-56717	Sequence 56717, A	C 195	52	11.6	3285	6	US-10-750-185-30271	Sequence 30271, A
C 123	53.5	11.9	1115	6	US-10-750-185-61687	Sequence 61687, A	C 196	52	11.6	3435	6	US-10-467-962B-88	Sequence 88, Appli
C 124	53.5	11.9	1141	6	US-10-750-185-40232	Sequence 40232, A	C 197	52	11.6	3772	6	US-10-131-826A-391	Sequence 391, App
C 125	53.5	11.9	1232	6	US-10-750-185-34314	Sequence 34314, A	C 198	52	11.6	4139	6	US-10-821-234-140	Sequence 140, App
C 126	53.5	11.9	1236	6	US-10-793-626-3155	Sequence 3155, Ap	C 199	52	11.6	5527	7	US-11-192-967-3	Sequence 3, Appli
C 127	53.5	11.9	1474	6	US-10-750-185-45637	Sequence 45637, A	C 200	52	11.6	5527	7	US-11-193-715-3	Sequence 3, Appli
C 128	53.5	11.9	1546	8	US-11-113-944-14	Sequence 14, Appli	C 201	51.5	11.5	369	6	US-10-467-657-1527	Sequence 1527, Ap
C 129	53.5	11.9	1946	6	US-10-750-185-36372	Sequence 36372, A	C 202	51.5	11.5	405	7	US-11-108-172-194	Sequence 194, App
C 130	53.5	11.9	2361	6	US-10-467-962B-102	Sequence 102, App	C 203	51.5	11.5	421	7	US-11-108-172-824	Sequence 824, App
C 131	53.5	11.9	3001	7	US-11-145-703-203	Sequence 203, App	C 204	51.5	11.5	636	6	US-10-131-826A-507	Sequence 507, App
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C 133	53.5	11.9	3413	6	US-10-793-626-4429	Sequence 4429, Ap	C 206	51.5	11.5	762	6	US-10-467-657-1533	Sequence 1533, Ap
C 134	53.5	11.9	4677	6	US-10-821-234-114	Sequence 114, App	C 207	51.5	11.5	778	6	US-10-750-185-56452	Sequence 56452, A
C 135	53	11.8	600	6	US-10-750-185-20772	Sequence 20772, A	C 208	51.5	11.5	787	6	US-10-750-185-64692	Sequence 64692, A
C 136	53	11.8	654	6	US-10-793-626-501	Sequence 501, App	C 209	51.5	11.5	841	6	US-10-528-031-18	Sequence 18, Appli
C 137	53	11.8	720	6	US-10-750-185-3009	Sequence 3009, Ap	C 210	51.5	11.5	941	6	US-10-750-185-61368	Sequence 61368, A
C 138	53	11.8	878	6	US-10-750-185-39079	Sequence 39079, A	C 211	51.5	11.5	955	6	US-10-750-185-38765	Sequence 38765, A
C 139	53	11.8	1071	9	US-11-082-389-61	Sequence 61, Appli	C 212	51.5	11.5	1002	6	US-10-821-234-471	Sequence 471, App
C 140	53	11.8	1166	6	US-10-750-185-56309	Sequence 56309, A	C 213	51.5	11.5	1132	6	US-10-750-185-50488	Sequence 50488, A
C 141	53	11.8	1419	7	US-11-074-176-337	Sequence 337, App	C 214	51.5	11.5	1228	6	US-10-750-185-31859	Sequence 31859, A
C 142	53	11.8	1461	7	US-11-074-176-337	Sequence 337, App	C 215	51.5	11.5	1388	6	US-10-750-185-53893	Sequence 53893, A
C 143	53	11.8	1883	6	US-10-750-185-54329	Sequence 54329, A	C 216	51.5	11.5	1408	6	US-10-750-185-38443	Sequence 38443, A
C 144	53	11.8	2029	6	US-10-750-185-50005	Sequence 50005, A	C 217	51.5	11.5	1412	6	US-10-821-234-266	Sequence 266, App
C 145	53	11.8	2076	6	US-10-750-185-39934	Sequence 39934, A	C 218	51.5	11.5	1520	6	US-10-750-185-45451	Sequence 45451, A
C 146	53	11.8	3363	6	US-10-750-185-55351	Sequence 55351, A	C 219	51.5	11.5	1756	6	US-10-750-185-42854	Sequence 42854, A
C 147	53	11.8	3569	6	US-10-415-198A-3	Sequence 3, Appli	C 220	51.5	11.5	1887	6	US-10-793-626-2843	Sequence 2843, Ap
C 148	53	11.8	3572	6	US-10-793-626-3527	Sequence 3527, Ap	C 221	51.5	11.5	1997	6	US-10-750-185-29682	Sequence 29682, A
C 149	53	11.8	3668	6	US-10-793-626-4046	Sequence 4046, Ap	C 222	51.5	11.5	2045	6	US-10-750-185-41561	Sequence 41561, A
C 150	53	11.8	3853	6	US-10-793-626-4331	Sequence 4331, Ap	C 223	51.5	11.5	2109	6	US-10-750-185-45958	Sequence 45958, A
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C 152	53	11.8	5700	6	US-10-513-786-7	Sequence 7, Appli	C 225	51.5	11.5	2443	6	US-10-131-826A-57	Sequence 57, Appli
C 153	53	11.8	5700	6	US-10-513-786-9	Sequence 9, Appli	C 226	51.5	11.5	2573	6	US-10-750-185-40185	Sequence 40185, A
C 154	53	11.8	11115	6	US-10-513-786-6	Sequence 6, Appli	C 227	51.5	11.5	2762	6	US-10-750-185-30392	Sequence 30392, A

228	51.5	11.5	3130	6	US-10-793-626-3630	Sequence 3630, Ap	301	50.5	11.3	1554	7	US-11-055-822-337	Sequence 337, App
c 229	51.5	3155	6	US-10-793-626-3424	Sequence 3424, Ap	c 302	50.5	11.3	1637	6	US-10-750-185-41849	Sequence 41849, A	
230	51.5	3231	6	US-10-821-234-21	Sequence 21, Appl	303	50.5	11.3	1637	6	US-10-858-730-161	Sequence 161, App	
231	51.5	3231	6	US-10-793-626-3996	Sequence 3996, Ap	c 304	50.5	11.3	1658	6	US-10-750-185-63553	Sequence 63553, A	
c 232	51.5	3555	6	US-10-750-185-60207	Sequence 60207, A	c 305	50.5	11.3	1660	6	US-10-750-185-61680	Sequence 61680, A	
c 233	51.5	3683	6	US-10-750-185-60207	Sequence 351, App	c 306	50.5	11.3	1709	6	US-10-750-185-42390	Sequence 42390, A	
c 234	51.5	4053	6	US-10-131-826A-351	Sequence 351, Ap	c 307	50.5	11.3	1709	6	US-10-750-185-61369	Sequence 61369, A	
c 235	51.5	4055	6	US-10-793-626-3357	Sequence 3357, Ap	c 308	50.5	11.3	1761	6	US-10-750-185-28284	Sequence 28284, A	
c 236	51.5	4965	6	US-10-485-517-43	Sequence 43, Appl	c 309	50.5	11.3	1772	6	US-10-750-185-59377	Sequence 59377, A	
c 237	51.5	5066	6	US-10-909-125-833	Sequence 833, App	c 310	50.5	11.3	1593	6	US-10-750-185-43425	Sequence 43425, A	
238	51.5	5246	6	US-10-909-125-804	Sequence 804, App	c 311	50.5	11.3	2008	6	US-10-909-125-1735	Sequence 1735, Ap	
239	51.5	8651	6	US-10-432-483-48	Sequence 48, Appl	c 312	50.5	11.3	2017	6	US-10-750-185-21716	Sequence 21716, A	
240	51.5	179892	7	US-11-112-908-39	Sequence 39, Appl	c 313	50.5	11.3	2035	6	US-10-750-185-42470	Sequence 42470, A	
c 241	51.5	191343	7	US-11-112-908-53	Sequence 53, Appl	c 314	50.5	11.3	2230	6	US-10-750-185-36519	Sequence 36519, A	
c 242	51.5	340000	7	US-11-102-978-3	Sequence 3, Appl1	c 315	50.5	11.3	2230	6	US-10-750-185-30632	Sequence 30632, A	
243	51.4	327	6	US-10-467-657-3701	Sequence 3701, Ap	c 316	50.5	11.3	2684	9	US-11-090-878-9	Sequence 9, Appl1	
c 244	51.4	991	6	US-10-750-185-63870	Sequence 63870, Ap	c 317	50.5	11.3	2762	9	US-11-090-878-3	Sequence 3, Appl1	
c 245	51.4	1014	6	US-10-793-626-1875	Sequence 1875, Ap	c 318	50.5	11.3	3356	6	US-10-750-185-31132	Sequence 31132, A	
c 246	51.4	1026	6	US-10-793-626-1277	Sequence 1277, Ap	c 319	50.5	11.3	3703	6	US-10-750-185-27363	Sequence 27363, A	
c 247	51.4	1058	6	US-10-750-185-33064	Sequence 33064, A	c 320	50.5	11.3	4243	6	US-10-821-234-59	Sequence 59, Appl	
c 248	51.4	1115	6	US-10-750-185-64842	Sequence 64842, A	c 321	50.5	11.3	4248	6	US-10-793-626-3885	Sequence 4, Appl1	
c 249	51.4	1179	6	US-10-793-626-193	Sequence 193, App	c 322	50.5	11.3	5690	6	US-10-485-517-4	Sequence 1, Appl1	
c 250	51.4	1303	6	US-10-750-185-28469	Sequence 28469, A	c 323	50.5	11.3	33014	7	US-11-077-716-1	Sequence 479, App	
251	51.4	1330	6	US-10-750-185-64434	Sequence 64434, A	c 324	50.5	11.3	34555	6	US-10-623-153-479	Sequence 23, Appl	
252	51.4	1387	6	US-10-750-185-34240	Sequence 34240, A	c 325	50.5	11.2	396	6	US-10-469-561-23	Sequence 643, App	
253	51.4	1406	6	US-10-750-185-64372	Sequence 64372, A	c 326	50.5	11.2	537	6	US-10-821-234-643	Sequence 770, App	
c 254	51.4	1564	6	US-10-750-185-61182	Sequence 61182, A	c 327	50.5	11.2	598	6	US-10-750-185-770	Sequence 4136, A	
c 255	51.4	1620	6	US-10-793-626-887	Sequence 887, App	c 328	50.5	11.2	642	6	US-10-750-185-44136	Sequence 61741, A	
c 256	51.4	1730	6	US-10-750-185-49223	Sequence 49223, A	c 329	50.5	11.2	709	6	US-10-750-185-61741	Sequence 49711, A	
257	51.4	1773	6	US-10-750-185-30343	Sequence 30343, A	c 330	50.5	11.2	795	6	US-10-750-185-49711	Sequence 33174, A	
258	51.4	1794	6	US-10-750-185-60035	Sequence 60035, A	c 331	50.5	11.2	824	6	US-10-750-185-33174	Sequence 52681, A	
259	51.4	1894	6	US-10-750-185-32092	Sequence 32092, A	c 332	50.5	11.2	860	6	US-10-750-185-52681	Sequence 39657, A	
260	51.4	1955	6	US-10-750-185-29205	Sequence 29205, A	c 333	50.5	11.2	906	6	US-10-750-185-39657	Sequence 26543, A	
c 261	51.4	1974	6	US-10-750-185-27854	Sequence 27854, A	c 334	50.5	11.2	986	6	US-10-750-185-26543	Sequence 63452, A	
c 262	51.4	2064	6	US-10-750-185-39327	Sequence 39327, A	c 335	50.5	11.2	991	6	US-10-750-185-63452	Sequence 2349, Ap	
c 263	51.4	2292	6	US-10-750-185-54648	Sequence 54648, A	c 336	50.5	11.2	999	6	US-10-793-626-2349	Sequence 58843, A	
c 264	51.4	2507	6	US-10-750-185-59638	Sequence 59638, A	c 337	50.5	11.2	1116	6	US-10-467-962B-40	Sequence 40, Appl	
c 265	51.4	2588	6	US-10-467-962B-32	Sequence 32, Appl	c 338	50.5	11.2	1124	6	US-10-750-185-50589	Sequence 50589, A	
c 266	51.4	2792	6	US-10-485-517-92	Sequence 92, Appl	c 339	50.5	11.2	1129	6	US-10-750-185-38446	Sequence 38446, A	
c 267	51.4	3112	6	US-10-750-185-25300	Sequence 25300, A	c 340	50.5	11.2	1183	6	US-10-821-234-356	Sequence 356, App	
c 268	51.4	3114	6	US-10-750-185-32681	Sequence 32681, A	c 341	50.5	11.2	1218	6	US-10-467-657-7419	Sequence 7419, App	
c 269	51.4	3133	6	US-10-750-185-51444	Sequence 51444, A	c 342	50.5	11.2	1219	6	US-10-750-185-56941	Sequence 56941, A	
c 270	51.4	3427	6	US-10-793-626-4289	Sequence 4289, Ap	c 343	50.5	11.2	1297	6	US-10-750-185-32030	Sequence 32030, A	
c 271	51.4	3488	6	US-10-793-626-3972	Sequence 3972, Ap	c 344	50.5	11.2	1302	6	US-10-793-626-1331	Sequence 1331, Ap	
c 272	51.4	3519	6	US-10-793-626-3836	Sequence 3836, Ap	c 345	50.5	11.2	1305	6	US-10-750-185-62879	Sequence 62879, A	
c 273	51.4	3561	6	US-10-793-626-4008	Sequence 4008, Ap	c 346	50.5	11.2	1323	6	US-10-467-657-3437	Sequence 3437, Ap	
c 274	51.4	3958	6	US-10-793-626-4279	Sequence 4279, Ap	c 347	50.5	11.2	1335	6	US-10-467-657-1583	Sequence 1583, Ap	
c 275	51.4	4434	6	US-10-793-626-3737	Sequence 3737, Ap	c 348	50.5	11.2	1388	6	US-10-750-185-28714	Sequence 28714, A	
c 276	51.4	4603	6	US-10-750-185-29449	Sequence 29449, A	c 349	50.5	11.2	1388	6	US-10-750-185-60725	Sequence 60725, A	
c 277	51.4	4765	6	US-10-821-234-110	Sequence 110, App	c 350	50.5	11.2	1463	6	US-10-750-185-38356	Sequence 38356, A	
c 278	51.4	6659	6	US-10-750-185-26060	Sequence 26060, A	c 351	50.5	11.2	1546	6	US-10-750-185-44276	Sequence 44276, A	
c 279	51.4	170508	7	US-11-112-908-62	Sequence 62, Appl	c 352	50.5	11.2	1561	6	US-10-750-185-44507	Sequence 44507, A	
c 280	51.4	173115	7	US-11-112-908-65	Sequence 65, Appl	c 353	50.5	11.2	1573	6	US-10-750-185-44052	Sequence 44052, A	
c 281	50.5	11.3	366	7	US-11-08-172-717	Sequence 17, App	c 354	50.5	11.2	1575	6	US-10-131-826A-431	Sequence 431, App
c 282	50.5	11.3	570	7	US-11-055-822-659	Sequence 659, App	c 355	50.5	11.2	1587	6	US-10-858-730-159	Sequence 159, App
c 283	50.5	11.3	694	6	US-10-750-185-64824	Sequence 64824, A	c 356	50.5	11.2	1620	6	US-10-750-185-31421	Sequence 31421, A
c 284	50.5	11.3	759	6	US-10-467-657-5683	Sequence 5683, Ap	c 357	50.5	11.2	1629	6	US-10-909-125-1747	Sequence 1747, Ap
c 285	50.5	11.3	883	6	US-10-750-185-52062	Sequence 52062, A	c 358	50.5	11.2	1685	6	US-10-750-185-53000	Sequence 53000, A
c 286	50.5	1026	6	US-10-793-626-1187	Sequence 1187, Ap	c 359	50.5	11.2	1719	6	US-10-750-185-33874	Sequence 33874, A	
c 287	50.5	1031	6	US-10-750-185-34569	Sequence 34569, A	c 360	50.5	11.2	1915	6	US-10-750-185-44158	Sequence 44158, A	
c 288	50.5	1038	6	US-10-467-657-2675	Sequence 2675, Ap	c 361	50.5	11.2	1933	6	US-10-750-185-50447	Sequence 50447, A	
c 289	50.5	1212	6	US-10-750-185-29015	Sequence 29015, A	c 362	50.5	11.2	1933	6	US-10-502-972-3	Sequence 3, Appl1	
c 290	50.5	1233	6	US-10-750-185-55375	Sequence 55375, A	c 363	50.5	11.2	2021	6	US-10-750-185-52859	Sequence 52859, A	
c 291	50.5	1281	7	US-11-055-822-585	Sequence 585, App	c 364	50.5	11.2	2114	6	US-10-909-125-1747	Sequence 1747, Ap	
c 292	50.5	1296	7	US-11-055-822-59	Sequence 59, Appl	c 365	50.5	11.2	2123	6	US-10-750-185-29713	Sequence 29713, A	
c 293	50.5	1296	7	US-11-055-822-299	Sequence 299, App	c 366	50.5	11.2	2216	6	US-10-750-185-41112	Sequence 41112, A	
c 294	50.5	1296	7	US-11-055-822-327	Sequence 327, App	c 367	50.5	11.2	2444	6	US-10-750-185-63110	Sequence 63110, A	
c 295	50.5	1338	6	US-10-750-185-56080	Sequence 56080, A	c 368	50.5	11.2	2459	6	US-10-750-185-37110	Sequence 37110, A	
c 296	50.5	1352	6	US-10-750-185-51740	Sequence 51740, A	c 369	50.5	11.2	2591	6	US-10-750-185-37110	Sequence 297, App	
c 297	50.5	1408	6	US-10-750-185-47977	Sequence 47977, A	c 370	50.5	11.2	2623	6	US-10-131-826A-297	Sequence 163, App	
c 298	50.5	1494	6	US-10-750-185-37627	Sequence 37627, A	c 371	50.5	11.2	2639	6	US-10-821-234-163		
c 299	50.5	1522	6	US-10-750-185-32175	Sequence 32175, A	c 372	50.5	11.2	2639	6			
c 300	50.5	1549	6	US-10-750-185-45801	Sequence 45801, A	c 373	50.5	11.2	2639	6			

C 374	50	11.2	2839	6	US-10-750-185-45644	Sequence 45644, A	C 447	49.5	11.0	22165	6	US-10-972-764-1	Sequence 1, Appli
C 375	50	11.2	3058	6	US-10-750-185-48442	Sequence 48442, A	C 448	49.5	11.0	165883	7	US-11-112-908-18	Sequence 18, Appli
C 376	50	11.2	3088	7	US-11-069-185-6	Sequence 6, Appli	C 449	49.5	11.0	171162	7	US-11-112-908-38	Sequence 38, Appli
C 377	50	11.2	3094	6	US-10-821-234-421	Sequence 421, App	C 450	49.5	10.9	477	6	US-10-793-626-2649	Sequence 2649, Ap
C 378	50	11.2	3119	6	US-10-750-185-34459	Sequence 34459, A	C 451	49	10.9	543	6	US-10-793-626-1587	Sequence 1587, Ap
C 379	50	11.2	3133	6	US-10-793-626-3663	Sequence 3663, Ap	C 452	49	10.9	561	7	US-11-080-248-1	Sequence 1, Appli
C 380	50	11.2	3135	6	US-10-793-626-3558	Sequence 3558, Ap	C 453	49	10.9	598	6	US-10-750-185-4803	Sequence 4803, Ap
C 381	50	11.2	3354	6	US-10-793-626-3763	Sequence 3763, Ap	C 454	49	10.9	674	7	US-10-467-657-1919	Sequence 1919, Ap
C 382	50	11.2	3388	6	US-10-750-185-33357	Sequence 33357, A	C 455	49	10.9	674	7	US-11-050-440-3	Sequence 3, Appli
C 383	50	11.2	3396	6	US-10-750-185-63174	Sequence 63174, A	C 456	49	10.9	748	6	US-10-750-185-56315	Sequence 56315, A
C 384	50	11.2	3407	6	US-10-750-185-44023	Sequence 44023, A	C 457	49	10.9	755	6	US-10-750-185-30479	Sequence 30479, A
C 385	50	11.2	3501	6	US-10-793-626-3346	Sequence 3346, Ap	C 458	49	10.9	825	6	US-10-750-185-43045	Sequence 43045, A
C 386	50	11.2	3592	6	US-10-793-626-4456	Sequence 4456, Ap	C 459	49	10.9	847	6	US-10-750-185-47730	Sequence 47730, A
C 387	50	11.2	3612	6	US-10-750-185-60333	Sequence 60333, A	C 460	49	10.9	855	6	US-10-467-657-221	Sequence 221, App
C 388	50	11.2	3772	6	US-10-750-185-36189	Sequence 36189, A	C 461	49	10.9	855	6	US-10-467-657-7371	Sequence 7371, Ap
C 389	50	11.2	4187	6	US-10-793-626-4354	Sequence 4354, Ap	C 462	49	10.9	855	6	US-10-467-657-8229	Sequence 8229, Ap
C 390	50	11.2	150481	7	US-11-112-908-37	Sequence 37, Appli	C 463	49	10.9	882	6	US-10-750-185-49695	Sequence 49695, A
C 391	50	11.2	171162	7	US-11-112-908-38	Sequence 38, Appli	C 464	49	10.9	900	6	US-10-750-185-31477	Sequence 31477, A
C 392	49.5	11.0	456	6	US-10-821-234-526	Sequence 526, App	C 465	49	10.9	902	6	US-10-750-185-61935	Sequence 61935, A
C 393	49.5	11.0	477	6	US-10-802-786-182	Sequence 182, App	C 466	49	10.9	905	6	US-10-750-185-27748	Sequence 27748, A
C 394	49.5	11.0	565	7	US-11-113-581-1	Sequence 1, Appli	C 467	49	10.9	922	6	US-10-750-185-24519	Sequence 24519, A
C 395	49.5	11.0	600	6	US-10-750-185-568	Sequence 568, App	C 468	49	10.9	927	6	US-10-793-626-577	Sequence 577, App
C 396	49.5	11.0	600	6	US-10-750-185-2549	Sequence 2549, Ap	C 469	49	10.9	940	6	US-10-750-185-39488	Sequence 39488, A
C 397	49.5	11.0	601	6	US-10-750-185-19702	Sequence 19702, A	C 470	49	10.9	1005	6	US-10-750-185-34831	Sequence 34831, A
C 398	49.5	11.0	669	6	US-10-821-234-699	Sequence 699, App	C 471	49	10.9	1061	6	US-10-750-185-48695	Sequence 48695, A
C 399	49.5	11.0	806	6	US-10-750-185-48285	Sequence 48285, A	C 472	49	10.9	1078	6	US-10-750-185-42453	Sequence 42453, A
C 400	49.5	11.0	888	7	US-11-091-100-1	Sequence 100-1, A	C 473	49	10.9	1151	6	US-10-750-185-31311	Sequence 31311, A
C 401	49.5	11.0	921	6	US-10-401-386B-30	Sequence 30, Appli	C 474	49	10.9	1152	6	US-10-793-626-385	Sequence 385, App
C 402	49.5	11.0	1175	6	US-10-750-185-57029	Sequence 57029, A	C 475	49	10.9	1188	6	US-10-750-185-32383	Sequence 32383, A
C 403	49.5	11.0	1170	6	US-10-510-386-151	Sequence 151, App	C 476	49	10.9	1203	6	US-10-793-626-1055	Sequence 1055, Ap
C 404	49.5	11.0	1296	7	US-11-092-140-5	Sequence 5, Appli	C 477	49	10.9	1205	6	US-10-750-185-27110	Sequence 27110, A
C 405	49.5	11.0	1315	6	US-10-750-185-34568	Sequence 34568, A	C 478	49	10.9	1210	6	US-10-793-626-397	Sequence 397, App
C 406	49.5	11.0	1326	7	US-11-055-822-335	Sequence 335, App	C 479	49	10.9	1254	6	US-10-750-185-64465	Sequence 64465, A
C 407	49.5	11.0	1414	6	US-10-750-185-60677	Sequence 60677, A	C 480	49	10.9	1311	6	US-10-750-185-41992	Sequence 41992, A
C 408	49.5	11.0	1476	6	US-10-467-657-7713	Sequence 7713, Ap	C 481	49	10.9	1359	6	US-10-821-234-305	Sequence 305, App
C 409	49.5	11.0	1518	9	US-11-082-389-283	Sequence 283, App	C 482	49	10.9	1383	6	US-10-990-276-2	Sequence 2, Appli
C 410	49.5	11.0	1553	6	US-10-750-185-48057	Sequence 48057, A	C 483	49	10.9	1419	6	US-10-821-234-73	Sequence 73, Appli
C 411	49.5	11.0	1573	6	US-10-750-185-46474	Sequence 46474, A	C 484	49	10.9	1436	6	US-10-750-185-26726	Sequence 26726, A
C 412	49.5	11.0	1643	6	US-10-750-185-63649	Sequence 63649, A	C 485	49	10.9	1442	6	US-10-750-185-64043	Sequence 64043, A
C 413	49.5	11.0	1722	6	US-10-986-501-87	Sequence 87, Appli	C 486	49	10.9	1449	6	US-10-750-185-38756	Sequence 38756, A
C 414	49.5	11.0	1804	6	US-10-750-185-39756	Sequence 39756, A	C 487	49	10.9	1473	6	US-10-750-185-47523	Sequence 47523, A
C 415	49.5	11.0	1824	6	US-10-750-185-37366	Sequence 37366, A	C 488	49	10.9	1538	6	US-10-750-185-43822	Sequence 43822, A
C 416	49.5	11.0	1837	6	US-10-750-185-59123	Sequence 59123, A	C 489	49	10.9	1589	6	US-10-750-185-36365	Sequence 36365, A
C 417	49.5	11.0	1965	9	US-11-046-668-3	Sequence 3, Appli	C 490	49	10.9	1601	6	US-10-750-185-50348	Sequence 50348, A
C 418	49.5	11.0	1978	9	US-11-090-878-17	Sequence 17, Appli	C 491	49	10.9	1616	6	US-10-750-185-64447	Sequence 64447, A
C 419	49.5	11.0	2038	9	US-11-090-878-15	Sequence 15, Appli	C 492	49	10.9	1621	6	US-10-750-185-64860	Sequence 64860, A
C 420	49.5	11.0	2038	9	US-11-090-878-23	Sequence 23, Appli	C 493	49	10.9	1692	6	US-10-750-185-56918	Sequence 56918, A
C 421	49.5	11.0	2052	9	US-11-046-668-1	Sequence 1, Appli	C 494	49	10.9	1715	6	US-10-750-185-39268	Sequence 39268, A
C 422	49.5	11.0	2070	6	US-10-750-185-35624	Sequence 35624, A	C 495	49	10.9	1716	6	US-10-750-185-58310	Sequence 58310, A
C 423	49.5	11.0	2154	7	US-11-074-176-305	Sequence 305, App	C 496	49	10.9	1779	6	US-10-750-185-44072	Sequence 44072, A
C 424	49.5	11.0	2169	7	US-11-074-176-17	Sequence 17, Appli	C 497	49	10.9	1786	6	US-10-750-185-41582	Sequence 41582, A
C 425	49.5	11.0	2187	9	US-11-090-878-7	Sequence 7, Appli	C 498	49	10.9	1831	6	US-10-750-185-44124	Sequence 44124, A
C 426	49.5	11.0	2240	9	US-11-046-668-5	Sequence 5, Appli	C 499	49	10.9	1841	6	US-10-750-185-50721	Sequence 50721, A
C 427	49.5	11.0	2283	9	US-11-090-878-11	Sequence 11, Appli	C 500	49	10.9	1851	6	US-10-750-185-55335	Sequence 55335, A
C 428	49.5	11.0	2361	9	US-11-090-878-5	Sequence 5, Appli							
C 429	49.5	11.0	2389	9	US-11-090-878-1	Sequence 1, Appli							
C 430	49.5	11.0	2415	6	US-10-750-185-24861	Sequence 24861, A							
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C 433	49.5	11.0	2725	6	US-10-131-826A-479	Sequence 479, App							
C 434	49.5	11.0	2726	6	US-10-750-185-48776	Sequence 48776, A							
C 435	49.5	11.0	2808	6	US-10-750-185-35178	Sequence 35178, A							
C 436	49.5	11.0	2869	6	US-10-750-185-49648	Sequence 49648, A							
C 437	49.5	11.0	2941	6	US-10-750-185-33540	Sequence 33540, A							
C 438	49.5	11.0	3020	6	US-10-750-185-42430	Sequence 42430, A							
C 439	49.5	11.0	3145	6	US-10-750-185-43218	Sequence 43218, A							
C 440	49.5	11.0	3343	6	US-10-401-386B-32	Sequence 32, Appli							
C 441	49.5	11.0	3422	6	US-10-750-185-27251	Sequence 27251, A							
C 442	49.5	11.0	3456	6	US-10-793-626-4026	Sequence 4026, Ap							
C 443	49.5	11.0	3842	6	US-10-793-626-3715	Sequence 3715, Ap							
C 444	49.5	11.0	4128	6	US-10-750-185-27864	Sequence 27864, A							
C 445	49.5	11.0	6159	7	US-11-013-759-8	Sequence 8, Appli							
C 446	49.5	11.0	6245	6	US-10-401-386B-61	Sequence 61, Appli							

ALIGNMENTS

RESULT 1

US-10-821-234-301

; Sequence 301, Application US/10821234

; Publication No. US20050255114A1

; GENERAL INFORMATION:

; APPLICANT: Labat, Ivan

; APPLICANT: Stache-Crain, Birgit

; APPLICANT: Andarmani, Susan

; APPLICANT: Tang, Y. Tom

; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

; FILE REFERENCE: 821A

; CURRENT APPLICATION NUMBER: US/10/821,234

; CURRENT FILING DATE: 2004-04-07

; PRIOR APPLICATION NUMBER: US 60/462,047

; PRIOR FILING DATE: 2003-04-07

```
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 301
; LENGTH: 3672
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-301

Alignment Scores:
Pred. No.: 6.22 Length: 3672
Score: 78.00 Matches: 26
Percent Similarity: 48.53% Conservative: 7
Best Local Similarity: 38.24% Mismatches: 32
Query Match: 17.41% Indels: 3
DB: 6 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x US-10-821-234-301 (1-3672)
QY 7 SerTyrPheGluProValGluGluSerAlaLeuGluArg-ArgProGluThrIleSe 26
Db 1760 TCACGTCTTTCCACCCCACTTCCTTTGCACTCTTGAGCAGTATCCAACTAGGATCTG 1819

QY 26 rGluProLysThrTyrValAspLeuThrAsnGluGluThrAspSerThrSerLys 46
Db 1820 CCAGTGGTACTGGGGTCCCACTCCCTGAGAAAGACTGAGCCAGGAACACAGGCTC 1879

QY 46 s-----lleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeu 64
Db 1880 CCCCACATTCCTCCAGCCTGGACCTAATTCCTTGAGAGGGGCTCTCTCTCAGCGACTG 1939

QY 64 eThrTrpAsnIleAspGlyLeu 71
Db 1940 TGTCTGGACTTTTGAGCAGGCTT 1961

RESULT 2
US-10-485-517-118
; Sequence 118, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynex Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629W0
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 118
; LENGTH: 2361
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-485-517-118

Alignment Scores:
Pred. No.: 93.7 Length: 2361
Score: 67.50 Matches: 19
Percent Similarity: 47.46% Conservative: 9
Best Local Similarity: 32.20% Mismatches: 22
Query Match: 15.07% Indels: 9
DB: 6 Gaps: 2

US-10-757-745-2_COPY_54_140 (1-87) x US-10-485-517-118 (1-2361)
QY 24 ThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrAspSerThr 43
Db 200 ACITTAGTTTCACCTACCGCTTATGCTGATACACCTCAAAAGATACACTACAGCTAAGACA 259

; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 301
; LENGTH: 3672
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-301

Alignment Scores:
Pred. No.: 6.22 Length: 3672
Score: 78.00 Matches: 26
Percent Similarity: 48.53% Conservative: 7
Best Local Similarity: 38.24% Mismatches: 32
Query Match: 17.41% Indels: 3
DB: 6 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x US-11-044-051-74 (1-4265)
QY 2 GluArgAlaLeuAsnSerTyrPheGluProValGluSerAlaLeuGluArg 21
Db 2123 GAGAAAGTAGAGAGACATGGACTCTCCCTCGAGGAGGCTCTGAGGAAAGTAGT 2064

QY 22 ProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 39
Db 2063 GAGGAGACAGGAGTCTCTCCCTGAGGGCTCTGAGGAAAGTAGTGTAGGAGAGACAGGAGT 2004

QY 40 -----ThrAspSerThrThrSerLysIle---SerPro----- 49
Db 2003 CCTCCCTCGAGGAGGCTCTGAGGAAAGTAGTGTAGGAGATAGGGAGTCTTCCCTCTGAG 1944

QY 50 -----SerGluAspThrGlnGluAsnGlySer-MetPheSerLeuIleThrTrpAs 67
Db 1943 GAGGGCTCTGAGGAAAGTAGTGTAGGAGACAGGAGGCTCTCCCTCAGGAAAGACTTGG-- 1886

QY 67 nIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArgGlyValCysSerTyr 86
Db 1885 -----AACAACTCTG---GAGAGGAGAAATGGGTATTCTTCCCTTTC 1850

RESULT 4
US-10-750-185-42446
; Sequence 42446, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
```

```
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42446
; LENGTH: 1914
; TYPE: DNA
; ORGANISM: Bovine 19866881384575
US-10-750-185-42446

Alignment Scores:
Pred. No.: 182 Length: 1914
Score: 64.50 Matches: 17
Percent Similarity: 47.06% Conservative: 7
Best Local Similarity: 33.33% Mismatches: 16
Query Match: 14.40% Indels: 11
DB: 6 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x US-10-750-185-42446 (1-1914)

Qy 48 SerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSer----- 62
Db 949 TCTCCAGGCAAAATACCTAGTGGTCCGCACTTCTTCCAGGGTATCTTCCCCCTC 1008
Qy 63 -----LeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeu 76
Db 1009 CAGAAATTGAACCTCTTCTCTGTATTGGCAGGCAGATCTTTACCACTGAACACCTT 1068
Qy 77 SerGluArgAlaArgGlyValCysSerTyrLeu 87
Db 1069 TGGCTCAGCTCAAGGGAGTCTGTTCTGACCTC 1101
```

RESULT 5

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US-10-750-185-41248
; Sequence 41248, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41248
; LENGTH: 1673
; TYPE: DNA
; ORGANISM: Bovine 19866881067831
US-10-750-185-41248
```

```
Alignment Scores:
Pred. No.: 207 Length: 1673
Score: 63.50 Matches: 15
Percent Similarity: 48.15% Conservative: 11
Best Local Similarity: 27.78% Mismatches: 27
Query Match: 14.17% Indels: 1
DB: 6 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x US-10-750-185-41248 (1-1673)
```

```
Qy 6 AsnSerTyrPheGluProValGluSerAlaLeuGluArgArgProGluThrIle 25
Db 1117 TCCTCCCTCCTCCTCCATACCCGAGAGAGTCCCAACAGGATAAGCCCAAGCG--- 1173
Qy 26 SerGluProLysThrTyrValAspLeuThrAsnGluGluThrThrAspSerThrSer 45
Db 1174 AACACACCCCAAGACACATATTAAATCAAAATTAAACAAGATCAACACAAAGAACAATATT 1233
Qy 46 LysIleSerProSerGluAspThrGlnGlnGluAsnGlySer 59
Db 1234 AAAAGCAGCAAGGAGGAAAAACAATAATACCAACAAGGGAAT 1275

RESULT 6
US-11-135-855-5
; Sequence 5, Application US/11135855
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GF50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2031
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-135-855-5

Alignment Scores:
Pred. No.: 433 Length: 2031
Score: 62.00 Matches: 25
Percent Similarity: 41.18% Conservative: 10
Best Local Similarity: 29.41% Mismatches: 34
Query Match: 13.84% Indels: 16
DB: 7 Gaps: 2

US-10-757-745-2_COPY_54_140 (1-87) x US-11-135-855-5 (1-2031)

Qy 14 GluGluSerAlaLeuGluArgArgProGluThrIleSerGluProLysThrTyrValAsp 33
Db 1747 GAGGAGCTGGCCGGGAGGAGGCCCCCGAGAGAGGAGGAGCAACGCCAGCACCCGAT 1806
Qy 34 LeuThrAsnGluGluThrThrAspSerThrSerLysIleSerProSerGluAspThr 53
Db 1807 CTCTCAGCCCCAGTGAATGGCGAGGCCACATCAGAGAAGGGGGGAGAGCGAGACCAAG 1866
Qy 54 GlnGlnGluAsn-----GlySerMetPheSerLeu 63
Db 1867 GAGCAGCAGGAGGGTTCGGGACTCGGAGGAGGGGCCAAGGTGTGGTCTCTCTGAAGACCTG 1926
Qy 64 IleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSer----- 77
Db 1927 CACGACAGCGTACGGGAGGGTCCCGACCTGGACACAGCGCTGGAGCGCACCGAGAGCGC 1986
Qy 78 GluArgAlaArgGly 82
Db 1987 GAGAGGGCACGGGGG 2001

RESULT 7
US-10-750-185-54989/c
; Sequence 54989, Application US/10750185
; Publication No. US20050260603A1
```

```
/
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FANTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ PRIOR FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 54989
/ LENGTH: 2048
/ TYPE: DNA
/ ORGANISM: Bovine 19866880791080
/
US-10-750-185-54989

Alignment Scores:
Pred. No.: 438 Length: 2048
Score: 62.00 Matches: 19
Percent Similarity: 46.38% Conservative: 13
Best Local Similarity: 27.54% Mismatches: 17
Query Match: 13.84% Indels: 20
DB: 6 Gaps: 4

US-10-757-745-2_COPY_54_140 (1-87) x US-10-750-185-54989 (1-2048)

QY 12 ProValGluSerAlaLeuGluArgProGluThrIleSerGluProLysThrTyr 31
Db 1125 CCATTCATCCAGCGCCCTGGAGAAAGGCGCGAGG---GTGACCGAGGCCCTCAAGTTTC 1069
QY 32 ValAspLeuThrAsnGluGluThrThrAspSerThrSerLysIleSerProSerGlu 51
Db 1068 -----AGCCCCAAGCTCTGCGCCAGACAGT 1045
QY 52 AspThr-----GlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsn 67
Db 1044 GAAACCCATGTCCTCCAGCAGCAGCAGAGTAAGGGGTTTGCTCTATCCCGGTGAGTGGAAAT 985
QY 68 -----IleAspGlyLeuAspLeu 73
Db 984 GAAAGGAAATGATGCTCTTGAGGTG 958

RESULT 8
US-11-135-855-6
/ Sequence 6, Application US/11135855
/ Publication No. US20050255557A1
/ GENERAL INFORMATION:
/ APPLICANT: SMITHKLINE BEECHAM CORPORATION
/ APPLICANT: SMITHKLINE BEECHAM P.L.C.
/ TITLE OF INVENTION: NOVEL COMPOUNDS
/ FILE REFERENCE: GP50013
/ CURRENT APPLICATION NUMBER: US/11/135,855
/ CURRENT FILING DATE: 2005-05-24
/ PRIOR APPLICATION NUMBER: US/10/203,708
/ PRIOR FILING DATE: 2002-08-13
/ PRIOR APPLICATION NUMBER: PCT/US01/04703
/ PRIOR FILING DATE: 2001-02-14
/ PRIOR APPLICATION NUMBER: 60/182,172
/ PRIOR FILING DATE: 2000-02-14
/ PRIOR APPLICATION NUMBER: 60/186,084
/ PRIOR FILING DATE: 2000-02-29
/ NUMBER OF SEQ ID NOS: 46
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 6
/ LENGTH: 2154
/ TYPE: DNA
/ ORGANISM: Homo sapiens

US-11-135-855-6
Alignment Scores:
Pred. No.: 470 Length: 2154
Score: 62.00 Matches: 25
Percent Similarity: 41.18% Conservative: 10
Best Local Similarity: 29.41% Mismatches: 34
Query Match: 13.84% Indels: 16
DB: 7 Gaps: 2

US-10-757-745-2_COPY_54_140 (1-87) x US-11-135-855-6 (1-2154)

QY 14 GluGluSerAlaLeuGluArgProGluThrIleSerGluProLysThrTyrValAsp 33
Db 1870 GAGGAGTGGCGGGGAGGAGGCCGCCAGAGAGAGAGGCGGAGGAGCAAGCCAGCACCAGAT 1929
QY 34 LeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSerProSerGluAspThr 53
Db 1930 CTTCTAGCCCCCAGTGAATGCGAGGCCACATCACAGAGGGGGGAGAGCGCAGAGGACAAG 1989
QY 54 GlnGlnGluAsn-----GlySerMetPheSerLeu 63
Db 1990 GAGCAGCAGGAGGTCGCGGACTCGGAGGAGGGCCAGGTGGCTCTCTTGAGACCTG 2049
QY 64 IleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSer----- 77
Db 2050 CACGACAGCGTACGGGAGGGTCCCGACCTGGACAGCGCTGGGAGCGACCGCAGGAGCGC 2109
QY 78 GluArgAlaArgGly 82
Db 2110 GAGAGGGCACGGGGG 2124

RESULT 9
US-10-750-185-34532
/ Sequence 34532, Application US/10750185
/ Publication No. US20050260603A1
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FANTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 34532
/ LENGTH: 2523
/ TYPE: DNA
/ ORGANISM: Bovine 19866881171401
/
US-10-750-185-34532

Alignment Scores:
Pred. No.: 682 Length: 2523
Score: 61.50 Matches: 19
Percent Similarity: 46.97% Conservative: 12
Best Local Similarity: 28.79% Mismatches: 24
Query Match: 13.73% Indels: 11
DB: 6 Gaps: 3

US-10-757-745-2_COPY_54_140 (1-87) x US-10-750-185-34532 (1-2523)

QY 6 AsnSerTyrPheGluProProValGluGluSerAla-----Leu 18
Db 64 AATTCTTGG-----CCACAGACAATCTCAGAACTCACTACTCACTCACTCC 114
QY 19 GluArgArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGlu 38
```

Db	115	AAAAGTGATGAAATAAGCAAGCCAGTTGTTTCTGACTATGACGGAAGAAAC	174
Qy	39	ThrThrAspSerThr-Thr-SerLysIleSerProSerGluAspThrGlnGlnGluAsnGly	58
Db	175	ACCTCTGATTCAGATGAGTCATGCGCTTCT---CGAGAAAGCAACCATGAGGAARAATTCA	231
Qy	59	SerMetPheSerLeuIle	64
Db	232	AATTTTCTATCTAAAAATC	249

```

RESULT 10
US-11-055-822-537
; Sequence 537, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 537
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(670)
; OTHER INFORMATION: RXA02400
US-11-055-822-537

```

Db	206	ACCATGAGATCTTGACTACTTCTCAGAACCCAACTTCTGGAGCAGCACCTCAACCTCT					
Qy	41	AspSerThrTrpSerLysIleSerProSerGluAspThrGlnGluAunGlySerMet	::: :::	::: :::	::: :::	::: :::	::: :::
Db	266	TCCGCACGACTACTTCCTCAGCTCCTGTGTGAAGAGGACGTAGAGATCGTTGTTTCACCA					
Qy	61	PheSerLeu-----IlleThrTrpAsnIleAspGlyLeuAsp					
Db	326	GCAGCGTTGTGGACGTGAGCAGGTTACCTTCGAAATCTCTGCACCTGAT					
RESULT 11							
US-10-750-185-50641/c							
; Sequence 50641, Application US/10750185							
; Publication NO. US20050260603A1							
; GENERAL INFORMATION:							
; APPLICANT: MMI GENOMICS, INC.							
; APPLICANT: DENISE, Sue K.							
; APPLICANT: KERR, Richard							
; APPLICANT: ROSENFELD, David							
; APPLICANT: HOLM, Tom							
; APPLICANT: BATES, Stephen							
; APPLICANT: FANTIN, Dennis							
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS							
; FILE REFERENCE: MM1100-2							
; CURRENT APPLICATION NUMBER: US/10/750,185							
; CURRENT FILING DATE: 2003-12-31							
; PRIOR APPLICATION NUMBER: US 60/437,482							
; PRIOR FILING DATE: 2002-12-31							
; NUMBER OF SEQ ID NOS: 64922							
; SOFTWARE: PatentIn version 3.1							
; SEQ ID NO 50641							
; LENGTH: 1611							
; TYPE: DNA							
; ORGANISM: Bovine 19866880585640							
US-10-750-185-50641							
Alignment Scores:							
Pred No.: 508 Length: 1611							
Score: 60.50 Matches: 25							
Percent Similarity: 38.71% Conservative: 11							
Best Local Similarity: 26.88% Mismatches: 22							
Query Match: 13.50% Indels: 35							
DB: 6 Gaps: 4							
US-10-757-745-2_COPY_54_140 (1-87) x US-10-750-185-50641 (1-1611)							
Qy	1	MetGluArgAlaLeuAunSerTyrrPheGluProValGluGluSer-					
Db	703	CTTCAGAGGGCTTTAAATAGTATTACTTGGAAAAAGAGCTGAAGAGTCTAAAAGAGTGCA					
Qy	17	-----AlaLeuGluArgPro---GluThrIleSerGluProLysThrTyrrVal					
Db	643	TTCTGTTTCTCGCTTCTGTGCCCCCACTCCCAAGGGGTCACTGGGCCCAAGAACAATAT---					
Qy	33	AspLeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSerProSerGluAsp					
Db	587	-----					
Qy	53	ThrGlnGlnGluAunGlySerMetPheSerLeulleThrTrpAsnIleAspGlyLeuAsp					
Db	586	-----AATTCAACTCAAGTGGTGTTTTAATAACCCGAGGGNAITCTGAAGCCCTTAGGC					
Qy	73	LeuAunAenLeuSerGluArgAlaAargGlyValCysSer					
Db	532	TGGAC-----					
Db	533	-----					


```
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 462
; LENGTH: 2052
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-462

Alignment Scores:
Pred. No.: 706 Length: 2052
Score: 60.50 Matches: 14
Percent Similarity: 50.00% Conservative: 6
Best Local Similarity: 35.00% Mismatches: 9
Query Match: 13.50% Indels: 11
DB: 6 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x US-10-821-234-462 (1-2052)
QY 20 ArgAtgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 39
DB 1583 CGGAGACCTCA-----ACCGGAAGGAGTCT 1609
QY 40 ThrAspSerThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySer 59
DB 1610 ACACAGCTTCGTCCTCCCAAAATGAAGCCTTCGAGCCCTGCCACCAAGAGAACGGAGCA 1669

RESULT 13
US-10-821-234-373
; Sequence 373, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 373
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-373

Alignment Scores:
Pred. No.: 102 Length: 442
Score: 60.00 Matches: 14
Percent Similarity: 55.81% Conservative: 10
Best Local Similarity: 32.56% Mismatches: 13
Query Match: 13.39% Indels: 6
DB: 6 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x US-10-821-234-373 (1-442)
QY 3 ArgAlaLeuAsnSerTyrPheGluProProValGluSerAlaLeuGluArgPro 22
DB 138 AAATCTTAACCTCCAGGTCACCAACACAGTTCAG-----AAACCT 179
QY 23 GluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrAspSer 42
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DB 180 ACCACAGTAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAACACCAACAAAA 239
QY 43 ThrThrSer 45
DB 240 ACCACCACA 248

RESULT 14
US-10-821-234-490
; Sequence 490, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 490
; LENGTH: 1146
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-490

Alignment Scores:
Pred. No.: 374 Length: 1146
Score: 60.00 Matches: 14
Percent Similarity: 55.81% Conservative: 10
Best Local Similarity: 32.56% Mismatches: 13
Query Match: 13.39% Indels: 6
DB: 6 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x US-10-821-234-490 (1-1146)
QY 3 ArgAlaLeuAsnSerTyrPheGluProProValGluSerAlaLeuGluArgPro 22
DB 856 AAATCTTAACCTCCAGGTCACCAACACAGTTCAG-----AAACCT 897
QY 23 GluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrAspSer 42
DB 898 ACCACAGTAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAACACCAACAAAA 957
QY 43 ThrThrSer 45
DB 958 ACCACCACA 966

RESULT 15
US-10-750-185-53598
; Sequence 53598, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53598
```

```
; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Bovine 19866881072357
US-10-750-185-53598

Alignment Scores:
Pred. No.: 735 Length: 1882
Score: 60.00 Matches: 22
Percent Similarity: 41.84% Conservative: 19
Best Local Similarity: 22.45% Mismatches: 33
Query Match: 13.39% Indels: 24
DB: 6 Gaps: 4

US-10-757-745-2_COPY_54_140 (1-87) x US-10-750-185-53598 (1-1882)
Qy 6 AsnSerTyrPheGluProValGluGluSerAlaLeuGluArgProGluThrIle 25
Db 286 AATAGTCACTTACCTTACTACGGAAGAGGCGCTCTTGAACATAAAA--AATTCACTA 342
Qy 26 SerGluProLysThrTyr----- 31
Db 343 AGTCTCCACAGATCCTTTCACTGCTGTGTGTTATTGCTGATTCAGGAAAAATAAGGTACTA 402
Qy 32 -----ValAspLeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSerPro 49
Db 403 CAAGAATCCCGCTCCAGTCGAGGATGCAAGATGAGGGGTTTATCCCTGGGTGGA 462
Qy 50 SerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIle--- 68
Db 463 GAAGATCCCTGGAGGAGAAATGCAACCTACTCCAGTATTCCTGCTGGAAATCTCTA 522
Qy 69 -----AspGlyLeuAspLeuAsnLeuSerGluArgAlaArg 81
Db 523 TGCACAGGAAGTCTGAGGGGCTGCAGTTCATGGGG---TCACAAAGAGCCAGA 573

RESULT 16
US-10-750-185-340/C
; Sequence 340, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 340
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine MMBT05061
US-10-750-185-340

Alignment Scores:
Pred. No.: 182 Length: 600
Score: 59.50 Matches: 21
Percent Similarity: 45.83% Conservative: 12
Best Local Similarity: 29.17% Mismatches: 27
Query Match: 13.28% Indels: 12
DB: 6 Gaps: 2

US-10-757-745-2_COPY_54_140 (1-87) x US-10-750-185-340 (1-600)
Qy 28 ProLysThrTyrValAspLeuThrAsnGluGluThrThrAspSerThr----- 43
Db 286 AATAGTCACTTACCTTACTACGGAAGAGGCGCTCTTGAACATAAAA--AATTCACTA 342

; LENGTH: 1882
; TYPE: DNA
; ORGANISM: Bovine 19866881072357
US-10-750-185-53598

Alignment Scores:
Pred. No.: 735 Length: 1882
Score: 60.00 Matches: 22
Percent Similarity: 41.84% Conservative: 19
Best Local Similarity: 22.45% Mismatches: 33
Query Match: 13.39% Indels: 24
DB: 6 Gaps: 4

US-10-757-745-2_COPY_54_140 (1-87) x US-10-750-185-53598 (1-1882)
Qy 6 AsnSerTyrPheGluProValGluGluSerAlaLeuGluArgProGluThrIle 25
Db 286 AATAGTCACTTACCTTACTACGGAAGAGGCGCTCTTGAACATAAAA--AATTCACTA 342
Qy 26 SerGluProLysThrTyr----- 31
Db 343 AGTCTCCACAGATCCTTTCACTGCTGTGTGTTATTGCTGATTCAGGAAAAATAAGGTACTA 402
Qy 32 -----ValAspLeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSerPro 49
Db 403 CAAGAATCCCGCTCCAGTCGAGGATGCAAGATGAGGGGTTTATCCCTGGGTGGA 462
Qy 50 SerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIle--- 68
Db 463 GAAGATCCCTGGAGGAGAAATGCAACCTACTCCAGTATTCCTGCTGGAAATCTCTA 522
Qy 69 -----AspGlyLeuAspLeuAsnLeuSerGluArgAlaArg 81
Db 523 TGCACAGGAAGTCTGAGGGGCTGCAGTTCATGGGG---TCACAAAGAGCCAGA 573

RESULT 17
US-10-750-185-26007
; Sequence 26007, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26007
; LENGTH: 1075
; TYPE: DNA
; ORGANISM: Bovine 19866880799801
US-10-750-185-26007

Alignment Scores:
Pred. No.: 401 Length: 1075
Score: 59.50 Matches: 19
Percent Similarity: 42.65% Conservative: 10
Best Local Similarity: 27.94% Mismatches: 30
Query Match: 13.28% Indels: 9
DB: 6 Gaps: 2

US-10-757-745-2_COPY_54_140 (1-87) x US-10-750-185-26007 (1-1075)
Qy 7 SerTyrPheGluProValGluGluSerAlaLeuGluArgArgProGluThrIleSer 26
Db 140 AGCCTTGCTAATCTCCAGTAGACAATGCTGTTTACATAGCGCGCTGCAGCGTGT 199
Qy 27 GluProLysThr-----TyrValAspLeuThrAsnGluGlu 38
Db 200 ACTCAAAAAGCGGCTCTGGTTCGAGATTCAGCCCTTCTGTTGTTGCTAAATGGGAG 259
Qy 39 ThrThrAspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGly 58
Db 260 GCCCTTCGCTCCAGGATCTGCCCTTTTCCCGAGGTAGA---GCCCGCTCTGCTCCGCGC 316
Qy 59 SerMetPheSerLeuIleThrTrp 66
Db 317 TCCAGGTTTCCTTGCTGTATCTTGG 340

RESULT 18
US-11-082-389-435
; Sequence 435, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
```

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; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2003-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 435
; LENGTH: 1856
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1833)
; OTHER INFORMATION: RXS01658
US-11-082-389-435

Alignment Scores:
Pred. No.: 844 Length: 1856
Score: 59.50 Matches: 15
Percent Similarity: 54.90% Conservative: 13
Best Local Similarity: 29.41% Mismatches: 22
Query Match: 13.28% Indels: 1
DB: Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x US-11-082-389-435 (1-1856)
Qy 6 AnSerTyrPheGluProValGluGluSerAlaLeuGluArgProGluThrIle 25
Db 1075 GATCGGTTCTGGTCTGTCCAGGTGACCACTGCAGCGAGGCGCCAGGAA---CTT 1131
Qy 26 SerGluProLysThrTyrValAspLeuThrAsnGluGluThrThrAspSerThrSer 45
Db 1132 AAGCAGCCTCTTACTACGTGTGTGGCAGCAGCCAGACCGGTGAGTCCAGCTCCAG 1191
Qy 46 LysIleSerProSerGluAspThrGlnGlnGlu 56
Db 1192 CTGATCACCCCGTTCCGTGGACTTCAGCGGAG 1224

RESULT 19
US-10-750-185-59627/c
; Sequence 59627, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 35764
; LENGTH: 1331
; TYPE: DNA
; ORGANISM: Bovine 19866880594163
US-10-750-185-59627

Alignment Scores:
Pred. No.: 629 Length: 1331
Score: 59.00 Matches: 13
Percent Similarity: 61.29% Conservative: 6
Best Local Similarity: 41.94% Mismatches: 11
DB: Gaps: 11

; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 59627
; LENGTH: 1907
; TYPE: DNA
; ORGANISM: Bovine 19866881071815
US-10-750-185-59627

Alignment Scores:
Pred. No.: 876 Length: 1907
Score: 59.50 Matches: 21
Percent Similarity: 45.83% Conservative: 12
Best Local Similarity: 29.17% Mismatches: 27
Query Match: 13.28% Indels: 12
DB: Gaps: 2

US-10-757-745-2_COPY_54_140 (1-87) x US-10-750-185-59627 (1-1907)
Qy 28 ProLysThrTyrValAspLeuThrAsnGluGlu-ThrThrAspSerThr----- 43
Db 670 CCAAGGACTAAGTGAATCTAGTCTCCAGTCTTACACTGGAGCAGTCAGATAATGGG 611
Qy 44 -----ThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPh 61
Db 610 CTGTTGGACCAAGGAGTAAAGCATGACTGCAGAGGGGCGACTGGCAGCAACAATTTGTT 551
Qy 61 eSerLeulleThrTrpAsn-----lleAspGlyLeuAspLeuAsnLe 76
Db 550 TAGTCTTTAAATTTGGCAGCAACAGTACTGATATAAATTCATCCAGAAATTCATC 491
Qy 76 uSerGluArgAlaArgGlyValCysSerTyrLeu 87
Db 490 TTCACTAGTGGCGAAGCATCTGCTCTACTTA 457

RESULT 20
US-10-750-185-35764/c
; Sequence 35764, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 35764
; LENGTH: 1331
; TYPE: DNA
; ORGANISM: Bovine 19866880594163
US-10-750-185-35764

Alignment Scores:
Pred. No.: 629 Length: 1331
Score: 59.00 Matches: 13
Percent Similarity: 61.29% Conservative: 6
Best Local Similarity: 41.94% Mismatches: 11
DB: Gaps: 11
```



```

; GENERAL INFORMATION:
; APPLICANT: ORNO, SHIGERU
; APPLICANT: TIANNE, KAZUO
; APPLICANT: DOI, TAKEYOSHI
; TITLE OF INVENTION: METHOD FOR PREVENTING MINERALIZATION IN THE PERIODONTAL LIGAMENT
; TITLE OF INVENTION: (PDL)
; FILE REFERENCE: 245819US0
; CURRENT APPLICATION NUMBER: US/11/081,566
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US/10/717,708
; PRIOR FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-081-566-1

Alignment Scores:
Pred. No.: 1.92e+03 Length: 2691
Score: 58.50 Matches: 14
Percent Similarity: 47.50% Conservative: 5
Best Local Similarity: 35.00% Mismatches: 10
Query Match: 13.06% Indels: 11
DB: 9 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x US-11-081-566-1 (1-2691)

QY 20 ArgArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 39
Db 1630 CGAGACCTCA-----ACCGGAAGAGTCT 1656

QY 40 ThrAspSerThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySer 59
Db 1657 ACACAGCTCTTGTCTCCCAAAATGAAGCCTTCGAGCCTGCGCACCACAGAGAACGAGCA 1716

RESULT 24
US-11-060-005-1
; Sequence 1, Application US/11060005
; Publication No. US20050260693A1
; GENERAL INFORMATION:
; APPLICANT: Irwin H. Gelman
; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
; FILE REFERENCE: A3058-A-FWC-A-A 070156.0597
; CURRENT APPLICATION NUMBER: US/11/060,005
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: 09/902,432
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 08/978,277
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: 08/665,401
; PRIOR FILING DATE: 1996-06-18
; PRIOR APPLICATION NUMBER: 08/635,121
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5134
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-060-005-1

Alignment Scores:
Pred. No.: 4.62e+03 Length: 5134
Score: 58.50 Matches: 23
Percent Similarity: 43.37% Conservative: 13
Best Local Similarity: 27.71% Mismatches: 26
Query Match: 13.06% Indels: 21
DB: 7 Gaps: 4

US-10-757-745-2_COPY_54_140 (1-87) x US-11-060-005-1 (1-5134)

; GENERAL INFORMATION:
; APPLICANT: ORNO, SHIGERU
; APPLICANT: TIANNE, KAZUO
; APPLICANT: DOI, TAKEYOSHI
; TITLE OF INVENTION: METHOD FOR PREVENTING MINERALIZATION IN THE PERIODONTAL LIGAMENT
; TITLE OF INVENTION: (PDL)
; FILE REFERENCE: 245819US0
; CURRENT APPLICATION NUMBER: US/11/081,566
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US/10/717,708
; PRIOR FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-081-566-1

QY 11 ProProValGluGluSerAla-----LeuGluArgArgPro----- 22
Db 1745 CCACCTGTTGAAGAGTCACTGAAAGAGACATATTGCAAGAAACCTCTGTGTCTCACC 1804

QY 23 GluThrIleSerGluProLys-----ThrTyrValAspLeu 34
Db 1805 CAGACGTTTACCAGAGGGTAAAGATGCCCATGACGACATGGTCACCAAGTGAAGTTC 1864

QY 35 ThrAsnGluGluThrThrAspSerThrSerLysIleSerProSerGluAspThrGln 54
Db 1865 ACCTCAGAAGCTGTGACAGACCCACAGAGCTCTCCGTACTGAAGAAGTATCC 1924

QY 55 GlnGluAsnGlySer-----MetPheSerLeuIleThrTrpAsnIleAsp 69
Db 1925 GAAGCATCGGGGCGGCGAAGAGACACAGACATGGTGTCCGACGTTTCCAGCTGACTGAC 1984

QY 70 GlyLeuAsp 72
Db 1985 TCCCCAGAC 1993

RESULT 25
US-10-750-185-34792/C
; Sequence 34792, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34792
; LENGTH: 5306
; TYPE: DNA
; ORGANISM: Bovine 19866880543010
US-10-750-185-34792

Alignment Scores:
Pred. No.: 4.83e+03 Length: 5306
Score: 58.50 Matches: 13
Percent Similarity: 66.67% Conservative: 11
Best Local Similarity: 36.11% Mismatches: 11
Query Match: 13.06% Indels: 1
DB: 6 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x US-10-750-185-34792 (1-5306)

QY 15 GluSerAlaLeuGluArgArgProGluThrIleSerGluProLysThrTyrValAspLeu 34
Db 2373 AAAGAGCAGAGAGAGAGGCGAGTCAGAA---ATTTCAGATCCAGAGAGTTCCTGTCAAAA 2317

QY 35 ThrAsnGluGluThrThrAspSerThrSerLysIleSerProSer 50
Db 2316 ACCATAATTGGTCACAAACAATTTGAAGAGCCACCTTTCCACCGGT 2269

RESULT 26
US-11-060-005-3
; Sequence 3, Application US/11060005
; Publication No. US20050260693A1
; GENERAL INFORMATION:
; APPLICANT: Irwin H. Gelman
; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
; FILE REFERENCE: A3058-A-FWC-A-A 070156.0597
; CURRENT APPLICATION NUMBER: US/11/060,005
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; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: 09/902,432
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 08/978,277
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: 08/665,401
; PRIOR FILING DATE: 1996-06-18
; PRIOR APPLICATION NUMBER: 08/635,121
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6160
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-060-005-3

Alignment Scores:
Pred. No.: 5.92e+03 Length: 6160
Score: 58.50 Matches: 23
Percent Similarity: 43.37% Conservative: 13
Best Local Similarity: 27.71% Mismatches: 26
Query Match: 13.06% Indels: 21
DB: 7 Gaps: 4

US-10-757-745-2_COPY_54_140 (1-87) x US-11-060-005-3 (1-6160)

Qy 11 ProProValGluGluSerAla-----LeuGluArgArgPro----- 22
Db 2763 CCACCTGTTGAAGAGGTCACTGAAAGAGACATCATTCGAGAAGAACTCCTGCTGCTCACC 2822
Qy 23 GluThrIleSerGluProLys-----ThrTyrValAspLeu 34
Db 2823 CAGACGTTACAGAGGGTAAAGATGCCCATGACGACATGTCACCACTGAAGTGGATTTC 2882
Qy 35 ThrAsnGluGluThrThrAspSerThrThrSerLysIleSerProSerGluAspThrGln 54
Db 2883 ACCTCAGAAAGCTGTGACAGCCACGACAGACCTCCCGTACTGAAAGAGTTACC 2942
Qy 55 GlnGluAsnGlySer-----MetPheSerLeuIleThrTrpAsnIleAsp 69
Db 2943 GAAGCATCGGGGGCCGAAGAGACACGACATGGTTCGGCAGTTTCCACGCTGACTGAC 3002
Qy 70 GlyLeuAsp 72
Db 3003 TCCCCAGAC 3011

RESULT 27
US-10-750-185-24745/c
; Sequence 24745, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24745
; LENGTH: 857
; TYPE: DNA
; ORGANISM: Bovine 19866880567012
US-10-750-185-57061

Alignment Scores:
Pred. No.: 554 Length: 857
Score: 57.50 Matches: 23
Percent Similarity: 45.00% Conservative: 13
Best Local Similarity: 28.75% Mismatches: 37
Query Match: 12.83% Indels: 7
DB: 6 Gaps: 3

US-10-757-745-2_COPY_54_140 (1-87) x US-10-750-185-57061 (1-857)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 230 ATGAGGTCCCAATAACACATATACACAG-----GAATTGTTATCTCCAAACCAA 180
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 179 TATGGAAGAAGACAGTTCGGAATGTAAGATTATGTTCCCTCAGCAACATGAATAAGCA 120
Qy 41 AspSerThrThrSerLysIleSerPro-----SerGluAspThrGlnGluAsn 57
Db 119 CCGAAGAAGAAACCTTCAAGGTGCACCATTCATAAAGTTATTCCTTCATCTCTAAACAT 60
Qy 58 GlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSer 77
Db 59 GCAGATCTCTTC---CTGCACACATTAGAGATTATCAGGACTACTTTTATATACACCAAGT 3
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RESULT 29

US-10-750-185-50453/c
; Sequence 50453, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50453
; LENGTH: 1659
; TYPE: DNA
; ORGANISM: Bovine 19866880997394
US-10-750-185-50453

Alignment Scores:
Pred. No.: 1.36e+03 Length: 1659
Score: 57.50 Matches: 17
Percent Similarity: 54.17% Conservative: 9
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Query Match: 12.83% Indels: 9
DB: Gaps: 2

US-10-757-745-2_COPY_54_140 (1-87) x US-10-750-185-50453 (1-1659)

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QY 35 ThrAsnGluThrThrAspSerThr-----ThrSerLysIleSerProSerGlu 51
Db 1435 GGCTGGGAACAGTCCACTGAGTCAGTCGACGCGGCGGATCATCTGAGTTTCATCAGCAGTGGT 1376
QY 52 AspThrGlnGlnGluAsnGlySer 59
Db 1375 GATACAGACCCAGCGCAATGGAAAT 1352

RESULT 30

US-10-750-185-34783/c
; Sequence 34783, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34783
; LENGTH: 1826
; TYPE: DNA
; ORGANISM: Bovine 19866881129491

US-10-750-185-34783

Alignment Scores:
Pred. No.: 1.55e+03 Length: 1826
Score: 57.50 Matches: 26
Percent Similarity: 44.16% Conservative: 8
Best Local Similarity: 33.77% Mismatches: 32
Query Match: 12.83% Indels: 11
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Db 614 ACATATATCCACCAGAAACTATGAGAAGTTTT-----CCGCATCAGAGTTGG 567
QY 27 GluProLysThr---TyrValAspLeuThrAsnGluGluThrThrAspSerThrThrSer 45
Db 566 GAATTCAAAATCTGGAGAGGTCTGGGCTACAGGGGAAACAAACAATAACACAAA 507
QY 46 LysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThr 65
Db 506 AAA-----ACTGAGACTGCCAGAGGATGGATGGC-----TACTTAAGACC 465
QY 66 TrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArgGly 82
Db 464 ACAGGAGTAGATGGAGTCACTTTGAATGAGAAGAGATAGAGAGAAAGAGGA 414

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DSEXT=7

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- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	448	100.0	1948	5	US-10-037-270-889
6	448	100.0	1948	6	US-10-117-722-889
7	448	100.0	1948	9	US-10-122-851-889
					Sequence 170, App
					Sequence 170, App
					Sequence 1, Appli
					Sequence 28, Appl
					Sequence 889, App
					Sequence 889, App
					Sequence 889, App

Sequence 88, Appli	3152	100.0	448	100.0	3	US-09-981-353-88
Sequence 826, App	391	92.4	414	92.4	5	US-10-066-543-826
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Sequence 783537, A	606	64.3	288	64.3	4	US-09-925-085A-783537
Sequence 783536, A	634	64.3	288	64.3	4	US-09-925-085A-783536
Sequence 3, Appli	1312	47.2	211.5	47.2	4	US-10-757-745-3
Sequence 21055, A	725	25.4	114	25.4	8	US-10-363-345A-21055
Sequence 21056, A	725	25.4	114	25.4	8	US-10-363-345A-21056
Sequence 21055, A	725	25.4	114	25.4	8	US-10-363-483A-21055
Sequence 21056, A	725	25.4	114	25.4	8	US-10-363-483A-21056
Sequence 14608, A	60	22.5	101	22.5	3	US-09-908-975-14608
Sequence 23304, A	1589	84.5	18.9	84.5	9	US-10-450-763-23304
Sequence 23303, A	2228	84.5	18.9	84.5	9	US-10-450-763-23303
Sequence 18712, A	217	18.9	84.5	18.9	9	US-10-450-763-18712
Sequence 11799, A	4002	18.9	84.5	18.9	9	US-10-450-763-11799
Sequence 23293, A	4890	18.9	84.5	18.9	9	US-10-450-763-23293
Sequence 18715, A	6448	18.9	84.5	18.9	9	US-10-450-763-18715
Sequence 23289, A	7197	18.9	84.5	18.9	9	US-10-450-763-23289
Sequence 18697, A	7556	18.9	84.5	18.9	9	US-10-450-763-18697
Sequence 23290, A	7731	18.9	84.5	18.9	9	US-10-450-763-23290
Sequence 23318, A	11742	18.9	84.5	18.9	9	US-10-450-763-23318
Sequence 11800, A	12036	18.9	84.5	18.9	9	US-10-450-763-11800
Sequence 11802, A	23157	18.9	84.5	18.9	9	US-10-450-763-11802
Sequence 18716, A	32313	18.9	84.5	18.9	9	US-10-450-763-18716
Sequence 4169, Ap	819	18.6	83.5	18.6	7	US-10-424-599-4169
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Sequence 4, Appli	1703	17.6	79	17.6	6	US-10-225-810-4
Sequence 1311, Ap	480	17.4	78	17.4	6	US-10-264-049-1311
Sequence 33, Appl	1142	17.4	78	17.4	5	US-10-208-408-33
Sequence 14, Appl	3672	17.4	78	17.4	6	US-10-133-937-64
Sequence 13, Appl	3672	17.4	78	17.4	6	US-10-465-572-13
Sequence 390, App	3672	17.4	78	17.4	6	US-10-172-118-390
Sequence 340, App	3672	17.4	78	17.4	6	US-10-159-563-64
Sequence 59, App	3672	17.4	78	17.4	7	US-10-342-887-390
Sequence 76, Appl	3672	17.4	78	17.4	9	US-10-848-755A-76
Sequence 9, Appli	4194	17.4	78	17.4	3	US-10-494-940-9
Sequence 13, Appl	5511	17.4	78	17.4	5	US-09-974-298-13
Sequence 285, App	5511	17.4	78	17.4	5	US-10-044-090-285
Sequence 238, App	5511	17.4	78	17.4	5	US-10-116-802-238
Sequence 152, App	5511	17.4	78	17.4	5	US-10-084-817-152
Sequence 112946, A	1620	17.3	77.5	17.3	7	US-10-424-599-112946
Sequence 21005, A	894	17.2	77	17.2	8	US-10-363-345A-21005
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Sequence 14, Appl	10617	16.9	75.5	16.9	8	US-10-743-975-14
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Sequence 20612, A	1339	16.1	72	16.1	8	US-10-363-345A-20612
Sequence 20611, A	1339	16.1	72	16.1	9	US-10-363-483A-20611
Sequence 20612, A	1339	16.1	72	16.1	9	US-10-363-483A-20612
Sequence 34261, A	2555	16.1	72	16.1	10	US-11-097-143-34261
Sequence 5051, Ap	2658	16.1	72	16.1	7	US-10-437-963-5051
Sequence 13687, A	3748	16.1	72	16.1	10	US-11-097-143-13687
Sequence 26910, A	4964	16.1	72	16.1	6	US-10-369-493-26910
Sequence 3, Appli	921	16.0	71	16.0	7	US-10-451-337-3
Sequence 7073, Ap	4320	16.0	71	16.0	10	US-11-097-143-7073
Sequence 90, Appl	139613	16.0	73	16.0	7	US-10-367-094-90
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Sequence 16071, A	6424	15.8	71	15.8	7	US-10-437-963-16071

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c 82	70.5	15.7	1772	8	US-10-739-930-4942	Sequence 4942, Ap	c 155	67	15.0	828	7	US-10-437-963-59504	Sequence 59504, A
83	70.5	15.7	6012	8	US-10-472-928-2305	Sequence 2305, Ap	156	67	15.0	1059	6	US-10-029-386-22670	Sequence 22670, A
c 84	70.5	15.7	15213	2	US-08-961-527-26	Sequence 26, Appl	157	67	15.0	1428	6	US-10-156-761-1143	Sequence 1143, Ap
c 85	70.5	15.7	15213	7	US-10-158-844-26	Sequence 26, Appl	158	67	15.0	1506	8	US-10-739-930-4777	Sequence 4777, Ap
c 86	70.5	15.7	2162598	8	US-10-472-928-4979	Sequence 4979, Ap	159	67	15.0	1518	3	US-09-976-165-20	Sequence 20, Appl
c 87	70	15.6	496	4	US-09-925-065A-747874	Sequence 747874, Ap	160	67	15.0	1518	6	US-10-342-276-20	Sequence 20, Appl
88	70	15.6	834	7	US-10-424-599-121845	Sequence 121845, Ap	161	67	15.0	1923	3	US-09-864-761-5159	Sequence 5159, Ap
c 89	70	15.6	835	7	US-09-765-272-93	Sequence 93, Appl	c 162	67	15.0	2229	7	US-10-437-963-45409	Sequence 45409, A
90	70	15.6	835	10	US-11-106-649-93	Sequence 93, Appl	163	67	15.0	2636	6	US-09-976-165-21	Sequence 21, Appl
91	70	15.6	1714	3	US-09-765-272-3	Sequence 3, Appl	164	67	15.0	2636	6	US-10-342-276-21	Sequence 21, Appl
92	70	15.6	2303	7	US-11-106-649-3	Sequence 3, Appl	c 165	67	15.0	4031	5	US-10-085-108-1	Sequence 1, Appl
93	70	15.6	2303	10	US-10-767-701-5132	Sequence 5132, Ap	c 166	67	15.0	4031	6	US-10-160-237-1	Sequence 1, Appl
94	70	15.6	2405	10	US-11-097-143-42206	Sequence 42206, A	c 167	67	15.0	4225	5	US-10-085-108-9	Sequence 9, Appl
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96	70	15.6	3875	6	US-10-172-118-39	Sequence 39, Appl	c 169	67	15.0	4225	6	US-10-160-237-9	Sequence 9, Appl
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98	70	15.6	4061	5	US-10-037-270-363	Sequence 363, App	c 171	67	15.0	4265	8	US-10-670-472A-74	Sequence 74, Appl
99	70	15.6	4061	6	US-10-117-722-363	Sequence 363, App	c 172	67	15.0	4265	9	US-10-450-763-24157	Sequence 24157, A
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c 104	69.5	15.5	871	8	US-10-363-345A-31900	Sequence 31900, A	177	67	15.0	12294	10	US-11-097-143-40240	Sequence 40240, A
c 105	69.5	15.5	871	9	US-10-363-483A-31899	Sequence 31899, A	178	67	15.0	21230	5	US-10-087-192-601	Sequence 601, App
c 106	69.5	15.5	871	9	US-10-363-483A-31900	Sequence 31900, A	178	67	15.0	21230	5	US-11-097-143-982	Sequence 982, App
c 107	69.5	15.5	2845	7	US-10-444-467-7	Sequence 7, Appl	c 179	67	15.0	1163020	7	US-10-398-221-10	Sequence 10, Appl
c 108	69.5	15.5	2887	7	US-10-437-963-65599	Sequence 65599, A	c 180	67	15.0	3011208	7	US-10-398-221-2058	Sequence 2058, Ap
c 109	69.5	15.5	25569	8	US-10-840-512-48	Sequence 48, Appl	c 181	67	15.0	9025608	6	US-10-156-761-1	Sequence 1, Appl
c 110	69	15.4	645	8	US-10-363-345A-31819	Sequence 31819, A	182	66.5	14.8	468	9	US-10-450-763-710	Sequence 710, App
c 111	69	15.4	645	8	US-10-363-345A-31820	Sequence 31820, A	183	66.5	14.8	550	8	US-10-363-345A-21433	Sequence 21433, A
c 112	69	15.4	645	9	US-10-363-483A-31819	Sequence 31819, A	184	66.5	14.8	550	8	US-10-363-483A-21434	Sequence 21434, A
c 113	69	15.4	645	9	US-10-363-483A-31820	Sequence 31820, A	185	66.5	14.8	550	9	US-10-363-483A-21433	Sequence 21433, A
c 114	69	15.4	1049	7	US-10-425-114-21196	Sequence 21196, A	186	66.5	14.8	550	9	US-10-363-483A-21434	Sequence 21434, A
c 115	69	15.4	1049	8	US-10-425-115-76948	Sequence 76948, A	c 187	66.5	14.8	664	4	US-09-925-065A-610817	Sequence 610817, A
c 116	68.5	15.3	438	3	US-09-770-444-959	Sequence 959, App	188	66.5	14.8	718	5	US-10-027-632-148691	Sequence 148691, A
c 117	68.5	15.3	503	8	US-10-425-115-67780	Sequence 67780, A	189	66.5	14.8	718	6	US-10-027-632-148691	Sequence 148691, A
c 118	68.5	15.3	599	9	US-10-972-079-16312	Sequence 16312, A	190	66.5	14.8	1950	9	US-10-450-763-16599	Sequence 16599, A
c 119	68.5	15.3	3587	8	US-10-739-930-69	Sequence 69, Appl	191	66.5	14.8	1950	9	US-10-450-763-17506	Sequence 17506, A
c 120	68.5	15.3	6698	6	US-10-311-455-829	Sequence 829, Appl	192	66.5	14.8	2667	8	US-10-425-115-113915	Sequence 113915, A
c 121	68	15.2	692	8	US-10-363-345A-39055	Sequence 39055, A	193	66.5	14.8	3099	7	US-10-437-963-38322	Sequence 38322, A
c 122	68	15.2	692	8	US-10-363-345A-39056	Sequence 39056, A	194	66.5	14.8	3119	5	US-10-116-048-1	Sequence 1, Appl
c 123	68	15.2	692	9	US-10-363-483A-39055	Sequence 39055, A	195	66.5	14.8	3800	10	US-11-056-106-2	Sequence 2, Appl
c 124	68	15.2	692	9	US-10-363-483A-39056	Sequence 39056, A	196	66.5	14.8	8561	5	US-10-116-048-3	Sequence 3, Appl
c 125	68	15.2	2229	10	US-11-097-143-7718	Sequence 7718, Ap	c 197	66	14.7	581	8	US-10-363-345A-26697	Sequence 26697, A
c 126	68	15.2	2796	3	US-09-815-242-4523	Sequence 4523, Ap	198	66	14.7	581	8	US-10-363-345A-26698	Sequence 26698, A
c 127	68	15.2	2799	3	US-09-815-242-8340	Sequence 8340, Ap	c 199	66	14.7	581	9	US-10-363-483A-26697	Sequence 26697, A
c 128	68	15.2	4291	10	US-11-097-143-7717	Sequence 7717, Ap	c 200	66	14.7	581	9	US-10-363-483A-26698	Sequence 26698, A
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c 132	67.5	15.1	699	5	US-10-128-714-1033	Sequence 1033, Ap	c 204	66	14.7	603	9	US-10-363-483A-286	Sequence 286, App
c 133	67.5	15.1	699	5	US-10-128-714-1033	Sequence 1033, Ap	c 205	66	14.7	609	8	US-10-363-345A-21947	Sequence 21947, A
c 134	67.5	15.1	1073	7	US-10-424-599-77774	Sequence 77774, A	c 206	66	14.7	609	8	US-10-363-345A-21947	Sequence 21947, A
c 135	67.5	15.1	1509	5	US-10-128-714-7033	Sequence 7033, Ap	c 207	66	14.7	609	9	US-10-363-483A-21948	Sequence 21948, A
c 136	67.5	15.1	1616	5	US-10-424-599-77771	Sequence 77771, A	c 208	66	14.7	609	9	US-10-363-483A-21948	Sequence 21948, A
c 137	67.5	15.1	1656	5	US-10-128-714-6033	Sequence 6033, Ap	c 209	66	14.7	674	7	US-10-425-114-1688	Sequence 1688, Ap
c 138	67.5	15.1	1857	6	US-10-470-048B-9	Sequence 9, Appl	c 210	66	14.7	762	3	US-09-975-719-153	Sequence 153, App
c 139	67.5	15.1	2019	6	US-10-369-493-29257	Sequence 29257, A	c 211	66	14.7	801	3	US-09-975-719-154	Sequence 154, App
c 140	67.5	15.1	2184	7	US-10-424-599-124040	Sequence 124040, A	c 212	66	14.7	870	3	US-09-888-615-11	Sequence 11, Appl
c 141	67.5	15.1	2319	10	US-11-097-143-31400	Sequence 31400, A	c 213	66	14.7	1119	7	US-10-767-701-11721	Sequence 11721, A
c 142	67.5	15.1	2343	7	US-10-437-963-75555	Sequence 75555, A	c 214	66	14.7	1139	8	US-10-467-622-10	Sequence 10, Appl
c 143	67.5	15.1	2699	5	US-10-128-714-33	Sequence 33, Appl	c 215	66	14.7	1139	8	US-10-467-622-11	Sequence 11, Appl
c 144	67.5	15.1	3522	9	US-10-831-070-21	Sequence 21, Appl	c 216	66	14.7	1314	3	US-09-808-568-3	Sequence 3, Appl
c 145	67.5	15.1	3570	9	US-10-956-157-4997	Sequence 4997, Ap	c 217	66	14.7	1314	5	US-10-156-239-50	Sequence 50, Appl
c 146	67.5	15.1	3656	5	US-10-128-714-5033	Sequence 5033, Ap	c 218	66	14.7	1386	6	US-10-168-425-19	Sequence 19, Appl
c 147	67.5	15.1	4422	9	US-10-956-157-1965	Sequence 1965, Ap	c 219	66	14.7	1632	7	US-10-302-172-297	Sequence 297, App
c 148	67.5	15.1	5340	10	US-11-097-143-31399	Sequence 31399, A	c 220	66	14.7	1685	7	US-10-425-114-29198	Sequence 29198, A
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c 152	67	15.0	693	8	US-10-767-795-3660	Sequence 3660, Ap	c 224	66	14.7	1929	8	US-10-425-115-100767	Sequence 100767, A
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232	66	14.7	2736	8	US-09-808-568-4	Sequence 4, Appli	305	65	14.5	1400	10	US-11-060-756-2664	Sequence 2664, Ap
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C 244	65.5	14.6	707	8	US-10-363-345A-307	Sequence 307, App	317	65	14.5	1730	10	US-11-019-829-25	Sequence 25, Appli
C 245	65.5	14.6	707	8	US-10-363-345A-308	Sequence 308, App	318	65	14.5	1742	6	US-10-159-563-167	Sequence 167, App
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C 247	65.5	14.6	707	9	US-10-363-483A-308	Sequence 308, App	320	65	14.5	1827	6	US-10-327-813-15	Sequence 15, Appli
C 248	65.5	14.6	740	8	US-10-363-345A-3655	Sequence 3655, Ap	321	65	14.5	1827	6	US-10-329-668-15	Sequence 15, Appli
C 249	65.5	14.6	740	8	US-10-363-345A-3656	Sequence 3656, Ap	322	65	14.5	1827	8	US-10-717-049-15	Sequence 15, Appli
C 250	65.5	14.6	740	9	US-10-363-483A-3655	Sequence 3655, Ap	323	65	14.5	1827	8	US-10-899-458-21	Sequence 21, Appli
C 251	65.5	14.6	740	9	US-10-363-483A-3656	Sequence 3656, Ap	324	65	14.5	1841	5	US-10-240-965-22	Sequence 22, Appli
C 252	65.5	14.6	741	8	US-10-363-345A-25765	Sequence 25765, A	325	65	14.5	1841	5	US-10-084-817-167	Sequence 167, App
C 253	65.5	14.6	741	9	US-10-363-345A-25766	Sequence 25766, A	326	65	14.5	1841	7	US-10-240-965-22	Sequence 22, Appli
C 254	65.5	14.6	741	9	US-10-363-483A-25765	Sequence 25765, A	327	65	14.5	1914	8	US-10-425-114-13973	Sequence 13973, A
C 255	65.5	14.6	741	9	US-10-363-483A-25766	Sequence 25766, A	328	65	14.5	2342	7	US-10-425-114-136077	Sequence 136077, A
C 256	65.5	14.6	779	7	US-10-437-963-5101	Sequence 5101, Ap	329	65	14.5	2439	5	US-10-100-957A-3	Sequence 3, Appli
C 257	65.5	14.6	791	7	US-10-398-221-1614	Sequence 1614, Ap	330	65	14.5	2439	5	US-10-100-957A-5	Sequence 5, Appli
C 258	65.5	14.6	1085	8	US-10-363-345A-1675	Sequence 1675, Ap	331	65	14.5	2834	10	US-11-097-143-37366	Sequence 37366, A
C 259	65.5	14.6	1085	8	US-10-363-345A-1676	Sequence 1675, Ap	332	65	14.5	3051	2	US-10-425-115-79631	Sequence 116, App
C 260	65.5	14.6	1085	9	US-10-363-483A-1675	Sequence 1675, Ap	333	65	14.5	3112	7	US-08-961-521-116	Sequence 116, App
C 261	65.5	14.6	1085	9	US-10-363-483A-1676	Sequence 1676, Ap	334	65	14.5	3112	7	US-10-158-844-116	Sequence 11, Appli
C 262	65.5	14.6	1235	7	US-10-398-221-3246	Sequence 3246, Ap	335	65	14.5	3171	5	US-10-100-957A-31	Sequence 31, Appli
C 263	65.5	14.6	1377	3	US-09-861-696-9	Sequence 9, Appli	336	65	14.5	3378	5	US-10-100-957A-151	Sequence 151, Appli
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C 265	65.5	14.6	1730	9	US-10-450-763-28120	Sequence 28120, A	338	65	14.5	4872	10	US-11-097-143-42278	Sequence 42278, A
C 266	65.5	14.6	1829	9	US-10-974-440-105	Sequence 105, App	339	65	14.5	7319	6	US-10-311-455-2017	Sequence 2017, Ap
C 267	65.5	14.6	2820	6	US-10-259-165-169	Sequence 169, App	340	65	14.5	123526	3	US-09-910-185-11	Sequence 11, Appli
C 268	65.5	14.6	3156	3	US-09-814-353-19673	Sequence 19673, A	341	65	14.5	1754382	9	US-10-501-282-6651	Sequence 4979, Ap
C 269	65.5	14.6	8160	3	US-09-070-927A-159	Sequence 159, App	342	65	14.5	2162598	8	US-10-472-928-4979	Sequence 1521, Ap
C 270	65.5	14.6	10846	6	US-09-923-109-5	Sequence 5, Appli	343	65	14.5	401	3	US-09-795-668-1521	Sequence 1521, Ap
C 271	65.5	14.6	10846	6	US-10-164-204-5	Sequence 5, Appli	344	64.5	14.4	401	3	US-09-795-668-1521	Sequence 1521, Ap
C 272	65.5	14.6	10846	7	US-10-705-430-5	Sequence 5, Appli	345	64.5	14.4	401	3	US-09-946-807-1521	Sequence 1521, Ap
C 273	65.5	14.6	10900	3	US-09-923-109-6	Sequence 6, Appli	346	64.5	14.4	401	3	US-09-946-807-1521	Sequence 1521, Ap
C 274	65.5	14.6	10900	6	US-10-164-204-6	Sequence 6, Appli	347	64.5	14.4	401	9	US-10-995-011-1521	Sequence 1521, Ap
C 275	65.5	14.6	10900	7	US-10-705-430-6	Sequence 6, Appli	348	64.5	14.4	467	7	US-10-779-543-9731	Sequence 9731, Ap
C 276	65.5	14.6	12860	3	US-09-070-927A-144	Sequence 144, App	349	64.5	14.4	567	7	US-10-021-323-3988	Sequence 3988, Ap
C 277	65	14.5	204	3	US-09-732-627A-3894	Sequence 3894, Ap	350	64.5	14.4	576	6	US-10-369-493-38616	Sequence 38616, A
C 278	65	14.5	387	8	US-10-472-928-2877	Sequence 2877, Ap	351	64.5	14.4	598	6	US-10-369-493-38616	Sequence 38616, A
C 279	65	14.5	390	3	US-09-769-787-198	Sequence 198, App	352	64.5	14.4	613	5	US-10-369-493-38616	Sequence 38616, A
C 280	65	14.5	455	3	US-09-918-995-12435	Sequence 12435, A	353	64.5	14.4	613	5	US-10-027-632-96634	Sequence 96634, A
C 281	65	14.5	472	7	US-10-767-701-928	Sequence 928, App	354	64.5	14.4	613	6	US-10-027-632-96634	Sequence 96634, A
C 282	65	14.5	528	8	US-10-425-115-114384	Sequence 114384, A	355	64.5	14.4	613	6	US-10-027-632-96634	Sequence 96634, A
C 283	65	14.5	585	4	US-09-925-065A-887050	Sequence 887050, A	356	64.5	14.4	634	9	US-10-756-149-3451	Sequence 3451, Ap
C 284	65	14.5	585	4	US-09-925-065A-887051	Sequence 887051, A	357	64.5	14.4	676	7	US-10-398-221-3966	Sequence 3966, Ap
C 285	65	14.5	827	8	US-10-425-115-92299	Sequence 92299, A	358	64.5	14.4	683	8	US-10-653-041-7228	Sequence 7228, Ap
C 286	65	14.5	834	10	US-11-097-143-37367	Sequence 37367, A	359	64.5	14.4	775	3	US-09-765-272-89	Sequence 89, Appli
C 287	65	14.5	1005	7	US-10-437-963-99892	Sequence 99892, A	360	64.5	14.4	775	10	US-11-106-649-89	Sequence 89, Appli
C 288	65	14.5	1024	5	US-10-100-957A-141	Sequence 141, App	361	64.5	14.4	898	7	US-10-739-930-3723	Sequence 3723, Ap
C 289	65	14.5	1102	8	US-10-363-345A-15871	Sequence 15871, A	362	64.5	14.4	939	7	US-10-437-963-87712	Sequence 87712, A
C 290	65	14.5	1102	8	US-10-363-345A-15872	Sequence 15872, A	363	64.5	14.4	946	8	US-10-363-345A-17921	Sequence 17921, A
C 291	65	14.5	1102	9	US-10-363-483A-15871	Sequence 15871, A	364	64.5	14.4	946	8	US-10-363-345A-17922	Sequence 17922, A
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C 293	65	14.5	1105	3	US-09-765-272-75	Sequence 75, Appli	366	64.5	14.4	946	9	US-10-363-483A-17922	Sequence 17922, A
C 294	65	14.5	1105	10	US-11-106-649-75	Sequence 75, Appli	367	64.5	14.4	1117	6	US-10-369-493-35439	Sequence 35439, A
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C 296	65	14.5	1139	8	US-10-467-622-7	Sequence 7, Appli	369	64.5	14.4	1696	10	US-09-765-272-217	Sequence 217, App
C 297	65	14.5	1139	8	US-10-467-622-8	Sequence 8, Appli	370	64.5	14.4	1696	10	US-11-106-649-217	Sequence 217, App
C 298	65	14.5	1139	8	US-10-467-622-9	Sequence 9, Appli	371	64.5	14.4	1848	7	US-10-450-763-25860	Sequence 25860, A
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375	64.5	14.4	2108	7	US-10-424-599-60959	Sequence 80959, A	448	64	14.3	4378	10	US-11-097-143-22217	Sequence 22217, A
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377	64.5	14.4	2918	7	US-10-437-963-8274	Sequence 8274, Ap	450	64	14.3	4611	8	US-10-357-930-23396	Sequence 23396, A
378	64.5	14.4	3159	10	US-11-097-143-36266	Sequence 36266, A	451	64	14.3	4611	8	US-10-357-930-23396	Sequence 23396, A
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380	64.5	14.4	3272	7	US-10-437-963-52977	Sequence 52977, A	453	64	14.3	5182	9	US-10-887-553A-341	Sequence 341, App
381	64.5	14.4	3930	6	US-10-363-493-25343	Sequence 25343, A	454	64	14.3	5727	10	US-11-097-143-37702	Sequence 37702, A
382	64.5	14.4	5430	9	US-10-713-978A-94	Sequence 94, Appl	455	64	14.3	5764	7	US-10-282-122A-35229	Sequence 35229, A
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385	64.5	14.4	6442	7	US-10-437-963-16526	Sequence 16526, A	458	64	14.3	5926	3	US-09-880-107-3371	Sequence 3371, Ap
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388	64.5	14.4	12319	10	US-11-097-143-23821	Sequence 23821, A	461	64	14.3	5926	7	US-10-240-425-1440	Sequence 1440, Ap
389	64.5	14.4	12319	10	US-11-097-143-23821	Sequence 23821, A	462	64	14.3	5926	9	US-10-843-641A-247	Sequence 247, App
390	64.5	14.4	13262	2	US-08-961-527-5	Sequence 5, Appl	463	64	14.3	5926	9	US-10-843-641A-787	Sequence 787, App
391	64.5	14.4	13926	7	US-10-158-844-5	Sequence 5, Appl	464	64	14.3	5926	9	US-10-843-641A-3549	Sequence 3549, Ap
392	64.5	14.4	15882	6	US-10-440-419-56	Sequence 56, Appl	465	64	14.3	5926	9	US-10-843-641A-7773	Sequence 7773, Ap
393	64.5	14.4	27845	10	US-11-097-143-28127	Sequence 28127, A	466	64	14.3	5926	9	US-10-756-149-2402	Sequence 2402, Ap
394	64.5	14.4	48718	10	US-11-097-143-28126	Sequence 28126, A	467	64	14.3	6161	10	US-11-097-143-11584	Sequence 11584, A
395	64.5	14.4	63284	10	US-11-097-143-28273	Sequence 28273, A	468	64	14.3	9775	10	US-11-097-143-37201	Sequence 37201, A
396	64.5	14.4	71962	10	US-11-097-143-26251	Sequence 26251, A	469	64	14.3	10592	5	US-10-156-275-51	Sequence 51, Appl
397	64.5	14.4	109906	7	US-10-235-192A-31	Sequence 31, Appl	470	64	14.3	10592	5	US-10-156-275-51	Sequence 51, Appl
398	64.5	14.4	123297	9	US-10-737-082-89	Sequence 89, Appl	471	64	14.3	52764	5	US-10-087-192-127	Sequence 127, App
399	64.5	14.4	129297	9	US-10-765-790-89	Sequence 89, Appl	472	64	14.3	119057	7	US-10-322-281-609	Sequence 609, App
400	64.5	14.4	149062	7	US-10-367-094-93	Sequence 93, Appl	473	64	14.3	121600	8	US-10-723-860-1125	Sequence 1125, Ap
401	64	14.3	274	7	US-10-242-535A-2682	Sequence 2682, Ap	474	64	14.3	121600	9	US-10-756-149-1098	Sequence 1098, Ap
402	64	14.3	274	7	US-10-085-783A-2682	Sequence 2682, Ap	475	64	14.3	3309400	3	US-09-738-626-1	Sequence 1, Appl
403	64	14.3	312	4	US-09-925-065A-203999	Sequence 203999, A	476	63.5	14.2	235	8	US-10-425-115-174463	Sequence 174463, A
404	64	14.3	343	7	US-10-242-535A-15708	Sequence 15708, A	477	63.5	14.2	314	8	US-10-425-115-15357	Sequence 15357, A
405	64	14.3	343	7	US-10-085-783A-15708	Sequence 15708, A	478	63.5	14.2	400	2	US-08-781-986A-4278	Sequence 4278, Ap
406	64	14.3	453	5	US-10-060-036-2073	Sequence 2073, Ap	479	63.5	14.2	400	7	US-10-329-624-4278	Sequence 4278, Ap
407	64	14.3	517	7	US-10-021-323-10211	Sequence 10211, A	480	63.5	14.2	436	7	US-10-242-535A-24861	Sequence 24861, A
408	64	14.3	548	8	US-10-357-930-60851	Sequence 60851, A	481	63.5	14.2	436	7	US-10-085-783A-24861	Sequence 24861, A
409	64	14.3	600	8	US-10-363-345A-10187	Sequence 10187, A	482	63.5	14.2	605	7	US-10-021-323-9275	Sequence 9275, Ap
410	64	14.3	600	8	US-10-363-345A-10188	Sequence 10188, A	483	63.5	14.2	648	4	US-09-925-065A-750498	Sequence 750498, A
411	64	14.3	600	9	US-10-363-483A-10188	Sequence 10188, A	484	63.5	14.2	705	8	US-10-653-047-7121	Sequence 7121, Ap
412	64	14.3	600	9	US-10-363-483A-10188	Sequence 10188, A	485	63.5	14.2	865	8	US-10-363-345A-33501	Sequence 33501, A
413	64	14.3	602	7	US-10-021-323-9082	Sequence 9082, Ap	486	63.5	14.2	865	8	US-10-363-345A-33502	Sequence 33502, A
414	64	14.3	610	7	US-10-021-323-17229	Sequence 17229, A	487	63.5	14.2	865	9	US-10-363-483A-33501	Sequence 33501, A
415	64	14.3	665	8	US-10-767-795-4024	Sequence 4024, Ap	488	63.5	14.2	865	9	US-10-363-483A-33502	Sequence 33502, A
416	64	14.3	693	7	US-10-424-599-140075	Sequence 140075, A	489	63.5	14.2	1072	7	US-10-424-599-53906	Sequence 53906, A
417	64	14.3	703	8	US-10-363-345A-20171	Sequence 20171, A	490	63.5	14.2	1089	7	US-10-282-122A-35824	Sequence 35824, A
418	64	14.3	703	8	US-10-363-345A-20172	Sequence 20172, A	491	63.5	14.2	1206	6	US-10-369-493-43552	Sequence 43552, A
419	64	14.3	703	9	US-10-363-483A-20171	Sequence 20171, A	492	63.5	14.2	1290	8	US-10-363-345A-28431	Sequence 28431, A
420	64	14.3	703	9	US-10-363-483A-20172	Sequence 20172, A	493	63.5	14.2	1290	8	US-10-363-345A-28432	Sequence 28432, A
421	64	14.3	975	3	US-09-738-626-3123	Sequence 3123, Ap	494	63.5	14.2	1290	9	US-10-363-483A-28431	Sequence 28431, A
422	64	14.3	1087	7	US-10-424-599-12441	Sequence 12441, A	495	63.5	14.2	1290	9	US-10-363-483A-28432	Sequence 28432, A
423	64	14.3	1118	8	US-10-363-345A-31751	Sequence 31751, A	496	63.5	14.2	1291	8	US-10-363-345A-28453	Sequence 28453, A
424	64	14.3	1118	8	US-10-363-345A-31752	Sequence 31752, A	497	63.5	14.2	1291	8	US-10-363-345A-28454	Sequence 28454, A
425	64	14.3	1118	9	US-10-363-483A-31751	Sequence 31751, A	498	63.5	14.2	1291	9	US-10-363-483A-28453	Sequence 28453, A
426	64	14.3	1118	9	US-10-363-483A-31752	Sequence 31752, A	499	63.5	14.2	1291	9	US-10-363-483A-28454	Sequence 28454, A
427	64	14.3	1299	8	US-10-363-345A-8451	Sequence 8451, Ap	500	63.5	14.2	1322	7	US-10-424-599-124764	Sequence 124764, A
428	64	14.3	1299	8	US-10-363-345A-8452	Sequence 8452, Ap							
429	64	14.3	1299	9	US-10-363-483A-8451	Sequence 8451, Ap							
430	64	14.3	1331	8	US-10-363-483A-8452	Sequence 8452, Ap							
431	64	14.3	1331	8	US-10-739-930-3251	Sequence 3251, Ap							
432	64	14.3	1371	8	US-10-767-795-4086	Sequence 4086, Ap							
433	64	14.3	1569	5	US-10-156-275-57	Sequence 57, Appl							
434	64	14.3	1629	8	US-10-425-115-35167	Sequence 35167, A							
435	64	14.3	1774	9	US-10-487-901-7469	Sequence 7469, Ap							
436	64	14.3	1774	9	US-09-925-065A-711158	Sequence 711158, A							
437	64	14.3	1779	9	US-10-450-763-16768	Sequence 16768, A							
438	64	14.3	1839	7	US-10-282-132A-25571	Sequence 25571, A							
439	64	14.3	2176	3	US-09-925-300-611	Sequence 611, App							
440	64	14.3	3164	9	US-10-210-120-25	Sequence 25, Appl							
441	64	14.3	3164	9	US-10-909-035-25	Sequence 25, Appl							
442	64	14.3	3192	3	US-09-925-300-502	Sequence 502, App							
443	64	14.3	3414	9	US-10-450-763-10009	Sequence 10009, A							
444	64	14.3	3593	10	US-11-097-143-11585	Sequence 11585, A							
445	64	14.3	3897	3	US-09-814-353-21410	Sequence 21410, A							

ALIGNMENTS

RESULT 1

US-09-925-299-170 ; Sequence 170, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P1102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12

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; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 170
; LENGTH: 1296
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1261)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1276)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-170

Alignment Scores:
Pred. No.: 6,54e-54 Length: 1296
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x US-09-925-299-170 (1-1296)
QY 1 MetGluArgAlaLeuAAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
DB 183 ATGGAAGGGCTCTGAACCTCTTACCTCGAGCCCTCGGTCGAGAGAGCGCTTGGAAACGC 242
QY 21 ArgProGluThrIleSerGluProValAspLeuThrValAspLeuThrAsnGluThrThr 40
DB 243 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACACT 302
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 303 GATTCACCACTCTTAAATCAGCCATCTGAAGATCTCAGCAAGAAATGCGCAGCATG 362
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 363 TTCTCTCTCATTTACCTGGAATATTGATGGATTAGATCTAAACAATCTGTCTCAGAGGGCT 422
QY 81 ArgGlyValCysSerTyrLeu 87
DB 423 CGAGGGGTGTGTCTTACTTAA 443

RESULT 3
US-10-757-745-1
; Sequence 1, Application US/10757745
; Publication No. US20050101769A1
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut Voor Biotechnologie VZW
; TITLE OF INVENTION: CD-40 INTERACTING AND TRAF-INTERACTING PROTEINS
; FILE REFERENCE: 2676-4555US
; CURRENT APPLICATION NUMBER: US/10/757,745
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: US/09/697,863A
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: PCT/EP99/03025
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EPO 98201392.2
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1627)..(1627)
; OTHER INFORMATION: N stands for any nucleotide.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1108)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1849)..(1849)
; OTHER INFORMATION: N stands for any nucleotide.
US-10-757-745-1

Alignment Scores:
Pred. No.: 1.13e-53 Length: 1920
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 170
; LENGTH: 1296
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1261)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1276)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-170

Alignment Scores:
Pred. No.: 6,54e-54 Length: 1296
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x US-09-925-299-170 (1-1296)
QY 1 MetGluArgAlaLeuAAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
DB 183 ATGGAAGGGCTCTGAACCTCTTACCTCGAGCCCTCGGTCGAGAGAGCGCTTGGAAACGC 242
QY 21 ArgProGluThrIleSerGluProValAspLeuThrValAspLeuThrAsnGluThrThr 40
DB 243 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACACT 302
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 303 GATTCACCACTCTTAAATCAGCCATCTGAAGATCTCAGCAAGAAATGCGCAGCATG 362
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 363 TTCTCTCTCATTTACCTGGAATATTGATGGATTAGATCTAAACAATCTGTCTCAGAGGGCT 422
QY 81 ArgGlyValCysSerTyrLeu 87
DB 423 CGAGGGGTGTGTCTTACTTAA 443

RESULT 2
US-09-925-299-170
; Sequence 170, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 170
; LENGTH: 1296
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1261)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1276)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-170
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Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
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Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 239 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAAC 298
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnAsnGlySerMet 60
Db 299 GATTCACCACTTCTTAAATCAGCCATCTGAAGATCTCAGCAAGAAAAATGGCAGCATG 358
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 359 TTCTCTCTCATACCTGGAATATTGATGATTAGATCTAAACAATCTGTCTCAGAGGGCT 418
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 419 CGAGGGGTGTGTTCTACTTA 439
RESULT 4
US-10-783-271-28
; Sequence 28, Application US/10783271
; Publication No. US20050186577A1
; GENERAL INFORMATION:
; APPLICANT: Veridex, LLC
; APPLICANT: Wang, Yixin
; TITLE OF INVENTION: BREAST CANCER PROGNOSTICS
; FILE REFERENCE: VDX-5003 USNP
; CURRENT APPLICATION NUMBER: US/10/783,271
; PRIOR FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 1940
; TYPE: DNA
; ORGANISM: human
US-10-783-271-28
Alignment Scores:
Pred. No.: 1.14e-53 Length: 1940
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x US-10-783-271-28 (1-1940)
Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 185 ATGGAAGGGCTCTGAATCTCTACTTCGAGCTCCGGTGGAGGAGCGCTTGGAAACGC 244
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 245 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAAC 304
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnAsnGlySerMet 60
Db 305 GATTCACCACTTCTTAAATCAGCCATCTGAAGATCTCAGCAAGAAAAATGGCAGCATG 364
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 365 TTCTCTCTCATACCTGGAATATTGATGATTAGATCTAAACAATCTGTCTCAGAGGGCT 424
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 425 CGAGGGGTGTGTTCTACTTA 445
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RESULT 5
US-10-037-270-889
; Sequence 889, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yuning
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghast, John
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pc_FL_genes Version 1.0
; SEQ ID NO 889
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(1127)
US-10-037-270-889
Alignment Scores:
Pred. No.: 1.15e-53 Length: 1948
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 198 ATGGAAGGGCTCTGAATCTCTACTTCGAGCTCCGGTGGAGGAGCGCTTGGAAACGC 257
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 258 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAAC 317
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnAsnGlySerMet 60
Db 318 GATTCACCACTTCTTAAATCAGCCATCTGAAGATCTCAGCAAGAAAAATGGCAGCATG 377
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 378 TTCTCTCTCATACCTGGAATATTGATGATTAGATCTAAACAATCTGTCTCAGAGGGCT 437
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 438 CGAGGGGTGTGTTCTACTTA 458
RESULT 6
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US-10-117-722-889
; Sequence 889, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 784CIP28CIP
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 889
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(1127)
US-10-117-722-889
Alignment Scores:
Pred. No.: 1,15e-53 Length: 1948
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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QY 1 MetGluArgAlaLeuAenSerTyrPheGluProProValGluSerAlaLeuGluArg 20
Db 198 ATGGAAGGGCTCTGAACCTCTTCTGAGCCTCCGGTGGAGAGAGCGCTTTGGAACGC 257
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
Db 258 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACA 317
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 318 GATTCACCACTCTTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGCAGCATG 377
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 378 TTCTCTCTCATACCTGGAATATTGATGATTAGATCTAAACAATCTCTCAGAGAGGGCT 437
QY 81 ArgGlyValCysSerTyrLeu 87
Db 438 CGAGGGGTGTGTTCTTACTTA 458
RESULT 7
US-10-122-851-889
; Sequence 889, Application US/10122851
; Publication No. US20050239060A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 784CIP28CIP
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 889
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(1127)
US-10-117-722-889
Alignment Scores:
Pred. No.: 1,15e-53 Length: 1948
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x US-10-117-722-889 (1-1948)
QY 1 MetGluArgAlaLeuAenSerTyrPheGluProProValGluSerAlaLeuGluArg 20
Db 198 ATGGAAGGGCTCTGAACCTCTTCTGAGCCTCCGGTGGAGAGAGCGCTTTGGAACGC 257
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
Db 258 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACA 317
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 318 GATTCACCACTCTTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGCAGCATG 377
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 378 TTCTCTCTCATACCTGGAATATTGATGATTAGATCTAAACAATCTCTCAGAGAGGGCT 437
QY 81 ArgGlyValCysSerTyrLeu 87
Db 438 CGAGGGGTGTGTTCTTACTTA 458
RESULT 8
US-09-981-353-88
; Sequence 88, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 88
; LENGTH: 3152
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 232992.1
; NAME/KEY: unsure
; LOCATION: 1171
; OTHER INFORMATION: a, t, c, g, or other
```

US-09-981-353-88

Alignment Scores:
Pred. No.: 2,23e-53 Length: 3152
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x US-09-981-353-88 (1-3152)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 1411 ATGGAAGGGCTCTGAACTCTTACCTCGAGCCTCGGTGGAGGAGCGCTTGGAAACGC 1470
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db 1471 CGACCTGAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACT 1530
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 1531 GATTCACCACTCTTAAATCAGCCCACTCGAGATCTCAGCAAGAAATGGCAGCATG 1590
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 1591 TTCTCTCATTAACCTGGAATATTGATGATTAGATCTTAAACAATCTGTCTCAGAGAGGGCT 1650
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 1651 CGAGGGGTGTGTCTCTACTTA 1671

RESULT 9

US-10-066-543-826/c

; Sequence 826, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indirias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 826
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 373
; OTHER INFORMATION: n = A,T,C or G

US-10-066-543-826

Alignment Scores:
Pred. No.: 1.01e-49 Length: 391
Score: 414.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 92.41% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x US-10-066-543-826 (1-391)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 286 ATGGAAGGGCTCTGAACTCTTACCTCGAGCCTCGGTGGAGGAGCGCTTGGAAACGC 227
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db 226 CGACCTGAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACT 167
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 166 GATTCACCACTCTTAAATCAGCCCACTCGAGATCTCAGCAAGAAATGGCAGCATG 107
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 106 TTCTCTCATTAACCTGGAATATTGATGATTAGATCTTAAACAATCTGTCTCAGAGAGGGCT 47
Qy 81 Arg 81
Db 46 CGA 44

RESULT 10

US-10-450-763-22059

; Sequence 22059, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22059
; LENGTH: 1227
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (84)..(203)
; OTHER INFORMATION: 85% homologous to Homo sapiens dj30M3.3 (novel protein
; OTHER INFORMATION: similar to C. elegans Y63D3A.4), accession number AL031775, Smith-
; OTHER INFORMATION: Waterman Score=164.

US-10-450-763-22059

Alignment Scores:
Pred. No.: 2.81e-37 Length: 1227
Score: 332.50 Matches: 84
Percent Similarity: 89.47% Conservative: 1
Best Local Similarity: 88.42% Mismatches: 2
Query Match: 74.22% Indels: 8
DB: 9 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x US-10-450-763-22059 (1-1227)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 235 ATGGAAGGGCTCTGAACTCTTACCTCGAGCCTCGGTGGAGGAGCGCTTGGAAACGC 294
Qy 20 gArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db 295 CCGACCTGAAACCACTCTTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACT 354
Qy 40 rAspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsn-GlySerM 60
Db 355 TGATTCACCACTCTTAAATCAGCCCACTCTGAGATCTCAGCAAGAAATGGCAGCA 414


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QY 60 etPheSerLeu-IleThrTrp-AsnIle-AspGlyLeuAsp---IleuAsnLeu-Ser 77
DB 415 TGTTCCTCTTCATTACCTGGGAATATTTGATGGGATTAGGATCTTAAACAATCTGTCCA 474
QY 78 Glu-ArgAlaArgGlyValCysSerTyrLeu 87
DB 475 GAGGAGGGCTCGAGGGGTGTGTCTCTACTTA 505

RESULT 11
US-09-925-065A-783537
; Sequence 783537, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 783537
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-783537

Alignment Scores:
Pred. No.: 2,98e-31 Length: 634
Score: 288.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 64.29% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x US-09-925-065A-783536 (1-634)
QY 32 ValAspLeuThrAsnGluThrThrAspSerThrSerLysIleSerProSerGlu 51
DB 265 GTTGACCTAACCAATGAAGAAACAACCTGATTCACCACTCTTAAATCAGCCCATCTGAA 324
QY 52 AspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeu 71
DB 325 GATACCTCAGCAAGAAATGCGAGCATGTTCTCTCTCATCTACCTGGATATTGATGATTA 384
QY 72 AspLeuAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeu 87
DB 385 GATCTAAACAATCTGTCTCAGAGAGGGCTCGAGGGGTGTGTCTCTACTTA 432

RESULT 13
US-10-757-745-3
; Sequence 3, Application US/10757745
; Publication No. US20050101769A1
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut Voor Biotechnologie VZW
; TITLE OF INVENTION: CD-40 INTERACTING AND TFAF-INTERACTING PROTEINS
; FILE REFERENCE: 2676-4555US
; CURRENT APPLICATION NUMBER: US/10/757,745
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: US/09/697,863A
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: PCT/EP99/03025
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EPO 98201392.2
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1312
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (122)..(1234)
; OTHER INFORMATION:
US-10-757-745-3

Alignment Scores:
Pred. No.: 8,88e-20 Length: 1312
Score: 211.50 Matches: 45
Percent Similarity: 66.28% Conservative: 12
Best Local Similarity: 52.33% Mismatches: 28
Query Match: 47.21% Indels: 1
DB: 9 Gaps: 1
```

```
US-10-757-745-2_COPY_54_140 (1-87) x US-10-757-745-3 (1-1312)
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 21056
; LENGTH: 725
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-21056
Alignment Scores:
Pred. No.: 4.59e-06 Length: 725
Score: 114.00 Matches: 19
Percent Similarity: 96.55% Conservative: 9
Best Local Similarity: 65.52% Mismatches: 1
Query Match: 25.45% Indels: 0
DB: 8 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x US-10-363-345A-21056 (1-725)
Qy 2 GluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 21
Db 571 CAAAAAACTCTAAACTCTCTACTTCGAACCTCCGATAAAAAAAGCGCTTAAACGCCGA 630
Qy 22 ProGluThrIleSerGluProLysThr 30
Db 631 CCTAAACCATCTCTTAAACCCAAAACC 657
RESULT 16
US-10-363-483A-21055/c
; Sequence 21055, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 21055
; LENGTH: 725
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-483A-21055
Alignment Scores:
Pred. No.: 4.59e-06 Length: 725
Score: 114.00 Matches: 19
Percent Similarity: 96.55% Conservative: 9
Best Local Similarity: 65.52% Mismatches: 1
Query Match: 25.45% Indels: 0
DB: 9 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x US-10-363-483A-21055 (1-725)
Qy 2 GluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 21
Db 155 CAAAAAACTCTAAACTCTCTACTTCGAACCTCCGATAAAAAAAGCGCTTAAACGCCGA 96
Qy 22 ProGluThrIleSerGluProLysThr 30
Db 95 CCTAAACCATCTCTTAAACCCAAAACC 69
RESULT 15
US-10-363-345A-21056
; Sequence 21056, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
```

```
US-10-757-745-2_COPY_54_140 (1-87) x US-10-757-745-3 (1-1312)
Qy 2 GluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 21
Db 317 CAGAAAGCCCTGAGCGCTACTTCGAGCTGCAGAACGACCAAGGCTGGCCGCCGAC 376
Qy 22 ProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrAsp 41
Db 377 CCTCCCGCTCTTCAAGCTCCGAGCCCTATGTTGATCTTAACACGAGGATGCAAAATGAT 436
Qy 42 SerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPhe 61
Db 437 ACAACCATTTTAGAGCCAGTCCATCT---CGAACTCTCTAGAGATAGCAGACATATT 493
Qy 62 SerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArg 81
Db 494 TCTTTCATTACCTGGAATATTGATGGATTAGATGATGATCAATCTGCCCGAGAGGGCTCGA 553
Qy 82 GlyValCysSerTyrLeu 87
Db 554 GGGGTGTGTTCTCGCTA 571
RESULT 14
US-10-363-345A-21055/c
; Sequence 21055, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 21055
; LENGTH: 725
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-21055
Alignment Scores:
Pred. No.: 4.59e-06 Length: 725
Score: 114.00 Matches: 19
Percent Similarity: 96.55% Conservative: 9
Best Local Similarity: 65.52% Mismatches: 1
Query Match: 25.45% Indels: 0
DB: 8 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x US-10-363-345A-21055 (1-725)
Qy 2 GluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 21
Db 155 CAAAAAACTCTAAACTCTCTACTTCGAACCTCCGATAAAAAAAGCGCTTAAACGCCGA 96
Qy 22 ProGluThrIleSerGluProLysThr 30
Db 95 CCTAAACCATCTCTTAAACCCAAAACC 69
RESULT 15
US-10-363-345A-21056
; Sequence 21056, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
```



```
Best Local Similarity: 29.21%
Query Match: 18.86%
DB: 9
Mismatches: 26
Indels: 21
Gaps: 5
```

US-10-757-745-2 COPY 54 140 (1-87) x US-10-450-763-11799 (1-4002)

Qy	10	GluProProValC	GluGluSerAlaLeu	GluArgProGluThrIleSerGluPro	28
Db	1435	GAACCTTACTATAAGAGCTCT	-----AGACCACAGCTATAAAGAACCTGTG	1482	

Qy	29	-----LysThrTyrValAspLeuThrAsnGluGluThrThrAspSerThrThr	44
Db	1483	AGCCAGTCTGAAAAACGGGATGTTAACTCTTAATGAGGACCATCAAGCAACCTACT	1542

Qy 45 SerLysIleSerProSerGluAspThrGlnGlnGluSerMetPheSerLeuIle 64
Db 1543 GAATCTGTTTAAAGAAATCTGAATCTTCGCAAAAGAA-----AGCACAGTT 1587

Qy 65 ThrTrpAsnIle---AspGlyLeuAsp-----LeuAsnAsnLeuSer 77
||| ::: ::: |||
Dh 1588 ACAGAAATTAAGAGAAGGTATCGACTGTTTACCCCTCATTTGTAGGTACTGCTGAT 1647

Qy 78 GluArgAlaArgGlyValCysSerTyr 86
 : : : : : : : : : :
Dh 1648 TCTTAAGCATGAGGGCTATTAAAGAAGACTAT 1674

RESULT 23

US-10-450-763-23293/c
; Sequence 23293, Application US/10450763
; Publication No. US20050196754A1

Alignment Scores:	1.16	Length:	4890
Pred. No.:	84.50	Matches:	26
Score:	47.1%	Conservative:	16
Percent Similarity:	29.21%	Mismatches:	26
Best Local Similarity:	18.8%	Indels:	21
Query Match:	9	Gaps:	5
DP:			

US-10-757-745-2 COPY 54 140 (1-87) X US-10-450-763-23293 (1-4890)

Qy	10	GluProProValGluGluSerAlaLeuGluArgProGluThrIleSerGluPro	28
pb	2181	GAACCTACTACTAAAGAGTCT-----AGACCACAGCGGTATAAAGAACCCTGTG	21334

Qy	29	-----LysThrTyrValAspLeuThrAsnGluGluThrThrAspSerThrThr	44
Dh	2133	AGCCAGCTCAAAACCGGATGTAAACCTTAAATGAGCAACCATCAAGCAACCTACT	2074

Qy	45	SerLysIleSerProSerGluAspThrGlnGlnGluasnGlySerMetPheSerLeulle	64
Db	2073	GAATCTGTTAAGAAACTTGAACAAAGAA-----AGCACAGTT	2099

QY 65 ThrTrpAsnIle--AspGlyLeuAsp-----LeuAsnAsnLeuSer 77
 ||| ::: ||| :::
 CCGCCTTTCACAGCGCCTGGTGTATCCCATTTCTGCTACTGTCAT 1969

Qy 78 GluArgAlaArgGlyValCysSerTyr 86
:::|::|::|::|::|::|
1029 TCGATCTCCCTATTATTCACACTAT 1043

RESIST 24

US-10-450-763-18715
; Sequence 18715, Application US/10450763
; Publication No. US20050196754A1

Alignment Scores:		
Pred. No.:	1.69	Length: 6448
Score:	84.50	Matches: 26
Percent Similarity:	47.13%	Conservative: 16
Best Local Similarity:	29.21%	Mismatches: 26
Query Match:	18.86%	Indels: 21
Da:	9	Gaps: 5

US-10-757-745-2 COPY 54 140 (1-87) x US-10-450-763-18715 (1-6448)

	Qy	10	GluProValGluGluSerAlaLeuGluArgProGluThrIleSerGluPro---	28
			:	
	Nb	102R	GAACCTACTAAAGAGTCT-----AGACCAcAGGTATATAAAGAACCCTGTG	1079S

Qy	29	-----LysThrTyrValAspIeuThrAsnGluGluThrThrAspSerThrThr	44
Dh	1076	AGCCAGTCTGAAAAACGGGATGTTAACTTAACTAATGAGCAACCATCAAGCAACCTACT	1139

Oy	45	SerLysIleSerProSerGluAspThrGlnGlnClnAsnGlySerMetPheSerLeuIle	64
Dh	1136	GAATCTGTAAAGAAAACCTGAAACTTCGC AAAAGAA-----AGCACAGTT	1180

Qy	65	ThrTrpAsnIle	---AspGlyLeuAsp	-----LeuAsnAsnLeuSer	77
			::: :::	::: :::	
Db	1181	ACAGAAGAAATTAAGAGAAAGGTATCGATGCTGTTTACCCCTCATTGGTAGTACTGCTGAT			1240

QY 78 GluArgAlaArgGlyValCysSerTyr 86
 1241 TCTAAGCAGAGGGTATTAGAACTAT 1267

RESULT 25

US-10-450-763-23289

```
; Sequence 23289, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 23289
; LENGTH: 7197
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (2650)..(3408)
; OTHER INFORMATION: 90% homologous to Bacteriophage N4 single-stranded DNA-
; OTHER INFORMATION: binding protein, accession number U29728, Smith-Waterman Score=1298
US-10-450-763-23289

Alignment Scores:
Pred. No.: 1.97 Length: 7197
Score: 84.50 Matches: 26
Percent Similarity: 47.19% Conservative: 16
Best Local Similarity: 29.21% Mismatches: 26
Query Match: 18.86% Indels: 21
DB: 9 Gaps: 5

US-10-757-745-2_COPY_54_140 (1-87) x US-10-450-763-23289 (1-7197)
Qy 10 GluProProValGluGluSerAlaLeuGluArgProGluThrIleSerGluPro--- 28
Db 5158 GAACCTACTACTAAAGAGTCT-----AGACCACAGGCTATATAAAGAACCTGTG 5205
Qy 29 -----LysThrTyrValAspLeuThrAsnGluThrAspSerThrThr 44
Db 5206 AGCCAGTCTGAAAAACGGGATGTTAACTTACTTAATGAGGACCATCAAGCAACCTACT 5265
Qy 45 SerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerIleuIle 64
Db 5266 GAATCTGTTAAGAACTGAACTTCTGCAAAAGAA-----AGCACAGTT 5310
Qy 65 ThrTrpAsnIle---AspGlyLeuAsp-----LeuAsnAsnLeuSer 77
Db 5311 ACAGAAGAATTAAGAGAAGGTATCGATCTGTTACCCCTCATTTGGTAGTACTGCTGAT 5370
Qy 78 GluArgAlaArgGlyValCysSerTyr 86
Db 5371 TCTAAGCAGAGGGGTATTAAAGAACTAT 5397

RESULT 26
US-10-450-763-18697/c
; Sequence 18697, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 23290
; LENGTH: 7731
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (792)..(4)
; OTHER INFORMATION: 90% homologous to Homo sapiens putative p150, accession number
; OTHER INFORMATION: U93569, Smith-Waterman Score=1271.
US-10-450-763-23290

Alignment Scores:
Pred. No.: 2.11 Length: 7556
Score: 84.50 Matches: 26
Percent Similarity: 47.19% Conservative: 16
Best Local Similarity: 29.21% Mismatches: 26
Query Match: 18.86% Indels: 21
DB: 9 Gaps: 5

US-10-757-745-2_COPY_54_140 (1-87) x US-10-450-763-18697 (1-7556)
Qy 10 GluProProValGluGluSerAlaLeuGluArgProGluThrIleSerGluPro--- 28
Db 4740 GAACCTACTACTAAAGAGTCT-----AGACCACAGGCTATATAAAGAACCTGTG 4693
Qy 29 -----LysThrTyrValAspLeuThrAsnGluThrAspSerThrThr 44
Db 4692 AGCCAGTCTGAAAAACGGGATGTTAACTTACTTAATGAGGACCATCAAGCAACCTACT 4633
Qy 45 SerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerIleuIle 64
Db 4632 GAATCTGTTAAGAACTGAACTTCTGCAAAAGAA-----AGCACAGTT 4588
Qy 65 ThrTrpAsnIle---AspGlyLeuAsp-----LeuAsnAsnLeuSer 77
Db 4587 ACAGAAGAATTAAGAGAAGGTATCGATCTGTTACCCCTCATTTGGTAGTACTGCTGAT 4528
Qy 78 GluArgAlaArgGlyValCysSerTyr 86
Db 4527 TCTAAGCAGAGGGGTATTAAAGAACTAT 4501

RESULT 27
US-10-763-23290/c
; Sequence 23290, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 23290
; LENGTH: 7731
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (792)..(4)
; OTHER INFORMATION: 90% homologous to Homo sapiens putative p150, accession number
; OTHER INFORMATION: U93569, Smith-Waterman Score=1271.
US-10-450-763-23290

Alignment Scores:
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Pred. No.: 2,17 Length: 7731
Score: 84.50 Matches: 26
Percent Similarity: 47.19% Conservative: 16
Best Local Similarity: 29.21% Mismatches: 26
Query Match: 18.86% Indels: 21
DB: 9 Gaps: 5

US-10-757-745-2_COPY_54_140 (1-87) x US-10-450-763-23290 (1-7731)
QY 10 GluProProValGluGluSerAlaLeuGluArgProGluThrIleSerGluPro--- 28
Db 3801 GAACCTACTACTAAAGAGTCT-----AGACCACAGGCTATATAAAGAACCTGTG 3754
QY 29 -----LysThrTyrValAspLeuThrAsnGluGluThrAspSerThrThr 44
Db 3753 AGCCAGTCTGAAACCGGATGTTAACTTACTTAATGAGACACCATCAAGCAACTACT 3694
QY 45 SerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIle 64
Db 3693 GAATCTGTTAAAGAACTGAACTTCTGCAAAAGAA-----AGCACAGTT 3649
QY 65 ThrTrpAsnIle---AspGlyLeuAsp-----LeuAsnAsnLeuSer 77
Db 3648 ACAGAAGATTAAAGAGAGGTATCGATGCTGTTTACCCTCATTTAGTAGTACTGCTGAT 3589
QY 78 GluArgAlaArgGlyValCysSerTyr 86
Db 3588 TCTAAAGCAGAGGGTATTAAAGAACTAT 3562

RESULT 28
US-10-450-763-23318
; Sequence 23318, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 23318
; LENGTH: 11742
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (5518)..(6258)
; OTHER INFORMATION: 27% homologous to Bacteriophage T4 DNA helicase, accession
; OTHER INFORMATION: number M93048, Smith-Waterman Score=171.
US-10-450-763-23318
Alignment Scores:
Pred. No.: 3,87 Length: 11742
Score: 84.50 Matches: 26
Percent Similarity: 47.19% Conservative: 16
Best Local Similarity: 29.21% Mismatches: 26
Query Match: 18.86% Indels: 21
DB: 9 Gaps: 5

US-10-757-745-2_COPY_54_140 (1-87) x US-10-450-763-23318 (1-11742)
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Db 10954 GAACCTACTACTAAAGAGTCT-----AGACCACAGGCTATATAAAGAACCTGTG 11001
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US-10-757-745-2_COPY_54_140 (1-87) x US-10-450-763-11800 (1-12036)
QY 10 GluProProValGluGluSerAlaLeuGluArgProGluThrIleSerGluPro--- 28
Db 4558 GAACCTACTACTAAAGAGTCT-----AGACCACAGGCTATATAAAGAACCTGTG 4605
QY 29 -----LysThrTyrValAspLeuThrAsnGluGluThrAspSerThrThr 44
Db 4606 AGCCAGTCTGAAACCGGATGTTAACTTACTTAATGAGACACCATCAAGCAACTACT 4665
QY 45 SerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIle 64
Db 4666 GAATCTGTTAAAGAACTGAACTTCTGCAAAAGAA-----AGCACAGTT 4710
QY 65 ThrTrpAsnIle---AspGlyLeuAsp-----LeuAsnAsnLeuSer 77
Db 4711 ACAGAAGATTAAAGAGAGGTATCGATGCTGTTTACCCTCATTTAGTAGTACTGCTGAT 4770
QY 78 GluArgAlaArgGlyValCysSerTyr 86
Db 4771 TCTAAAGCAGAGGGTATTAAAGAACTAT 4797
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RESULT 30

US-10-450-763-11802
; Sequence 11802, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790C1F3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 11802
; LENGTH: 23157
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (489)..(3767)
; OTHER INFORMATION: 100% homologous to Homo sapiens bcr,accession number
; OTHER INFORMATION: X02596,Smith-Waterman Score=5702.
US-10-450-763-11802

Alignment Scores:

Pred. No.:	9.89	Length:	23157
Score:	84.50	Matches:	26
Percent Similarity:	47.19%	Conservative:	16
Best Local Similarity:	29.21%	Mismatches:	26
Query Match:	18.86%	Indels:	21
DB:	9	Gaps:	5

US-10-757-745-2_COPY_54_140 (1-87) x US-10-450-763-11802 (1-23157)

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Qy	29	-----LysThrTyValAspLeuThrAsnGluThrAspSerThrThr	44
Db	15553	AGCCAGTCTGAAAACCGGATGTTAACCTTACTAATGAGGACCCATCAAGCAACCTACT	15612
Qy	45	SerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIle	64
Db	15613	GAATCTGTTAAGAAACCTGAACTTCTGCAAAAGAA-----AGCACAGTT	15657
Qy	65	ThrTrpAsnIle---AspGlyLeuAsp-----LeuAsnAsnLeuSer	77
Db	15658	ACAGAGAAATTAAAGAGAGGTATCGATGCTGTTTACCCTCATTTGGTAGGTACTGCTGAT	15717
Qy	78	GluArgAlaArgGlyValCysSerTyr	86
Db	15718	TCTAAGCAGAGGGTATTAAAGAACTAT	15744

Search completed: December 4, 2005, 20:42:37
Job time : 419.035 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: December 4, 2005, 00:49:56 ; Search time 80.9633 Seconds
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Perfect score: 448
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

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-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	448	100.0	1920	3	US-09-697-863A-1
2	448	100.0	1948	3	US-09-620-312D-889
3	211.5	47.2	1312	3	US-09-697-863A-3
4	145	32.4	379	3	US-09-621-976-8403
5	73.5	16.4	893	3	US-09-869-677B-1
6	72.5	16.2	573	3	US-09-248-796A-1008
7	71.5	16.0	999	3	US-09-248-796A-12164
8	71	15.8	24459	3	US-09-902-540-5004
9	71	15.8	32241	3	US-09-902-540-1247

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	11	70	15.6	835	3	US-08-961-083-93	Sequence 93, Appl
	12	70	15.6	835	3	US-09-536-784-93	Sequence 93, Appl
	13	70	15.6	835	3	US-09-765-271-93	Sequence 93, Appl
	14	70	15.6	835	3	US-09-765-272A-93	Sequence 93, Appl
	15	70	15.6	1714	3	US-08-961-083-3	Sequence 3, Appl
	16	70	15.6	1714	3	US-09-536-784-3	Sequence 3, Appl
	17	70	15.6	1714	3	US-09-765-272A-3	Sequence 3, Appl
	18	70	15.6	1714	3	US-09-765-594-888	Sequence 888, App
	19	70	15.6	3640	3	US-09-976-594-888	Sequence 888, App
	20	70	15.6	4061	3	US-09-620-312D-363	Sequence 363, App
	21	69.5	15.5	486	3	US-09-248-796A-13914	Sequence 13914, A
	22	69	15.4	231	3	US-09-543-681A-1380	Sequence 1380, Ap
	23	69	15.4	291	3	US-08-894-699-1	Sequence 1, Appli
	24	69	15.4	291	3	US-09-444-410-1	Sequence 1, Appli
	25	68	15.2	2817	6	PCT-US93-05944-1	Sequence 4, Appli
	26	68	15.2	3356	3	US-09-379-523-4	Sequence 1, Appli
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	28	67.5	15.1	3033	2	US-08-095-737-3	Sequence 3, Appli
	29	67.5	15.1	3033	2	US-08-480-145-3	Sequence 3, Appli
	30	67.5	15.1	3033	2	US-08-477-389-3	Sequence 3, Appli
	31	67.5	15.1	9623	3	US-08-956-171E-166	Sequence 166, App
	32	67.5	15.1	9623	3	US-08-781-986A-166	Sequence 166, App
	33	67	15.0	610	3	US-09-280-116-22	Sequence 22, Appl
	34	67	15.0	938	3	US-09-270-767-1642	Sequence 1642, Ap
	35	67	15.0	938	3	US-09-270-767-16924	Sequence 16924, A
	36	67	15.0	1230	3	US-09-248-796A-542	Sequence 542, App
	37	67	15.0	1488	3	US-08-216-592A-7	Sequence 7, Appli
	38	67	15.0	1518	2	US-08-820-170A-20	Sequence 20, Appl
	39	67	15.0	1518	3	US-09-055-699-20	Sequence 20, Appl
	40	67	15.0	1518	3	US-09-273-565-20	Sequence 20, Appl
	41	67	15.0	1518	3	US-09-565-538-20	Sequence 20, Appl
	42	67	15.0	1518	3	US-09-661-468-20	Sequence 20, Appl
	43	67	15.0	1518	3	US-09-976-165-20	Sequence 20, Appl
	44	67	15.0	1662	2	US-08-336-408B-5	Sequence 5, Appli
	45	67	15.0	1662	6	PCT-US91-00399-5	Sequence 5, Appli
	46	67	15.0	2636	2	US-08-820-170A-21	Sequence 21, Appl
	47	67	15.0	2636	3	US-09-055-699-21	Sequence 21, Appl
	48	67	15.0	2636	3	US-09-273-565-21	Sequence 21, Appl
	49	67	15.0	2636	3	US-09-565-538-21	Sequence 21, Appl
	50	67	15.0	2636	3	US-09-661-468-21	Sequence 21, Appl
	51	67	15.0	2636	3	US-09-976-165-21	Sequence 21, Appl
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	53	67	15.0	4031	3	US-08-845-528C-1	Sequence 1, Appli
	54	67	15.0	4031	3	US-09-066-281B-1	Sequence 1, Appli
	55	67	15.0	4031	3	US-09-468-433C-1	Sequence 9, Appli
	56	67	15.0	4225	2	US-08-993-118-9	Sequence 9, Appli
	57	67	15.0	4225	3	US-08-845-528C-9	Sequence 9, Appli
	58	67	15.0	4225	3	US-09-066-281B-9	Sequence 9, Appli
	59	67	15.0	4225	3	US-09-468-433C-9	Sequence 9, Appli
	60	67	15.0	4265	3	US-09-061-709-1	Sequence 1, Appli
	61	67	15.0	4265	3	US-09-899-651-1	Sequence 1, Appli
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	63	67	15.0	4265	3	US-09-270-437D-1	Sequence 1, Appli
	64	67	15.0	10160	3	US-09-949-016-13215	Sequence 13215, A
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	66	66.5	14.8	3003	3	US-09-248-796A-6805	Sequence 6805, Ap
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	69	66.5	14.8	3119	3	US-10-116-048-1	Sequence 1, Appli
	70	66.5	14.8	8561	3	US-09-112-450-3	Sequence 3, Appli
	71	66.5	14.8	8561	3	US-09-419-291A-3	Sequence 3, Appli
	72	66.5	14.8	8561	3	US-10-116-048-3	Sequence 3, Appli
	73	66	14.7	762	3	US-09-199-637A-153	Sequence 153, App
	74	66	14.7	801	3	US-09-199-637A-154	Sequence 154, App
	75	66	14.7	891	3	US-09-252-991A-13439	Sequence 13439, A
	76	66	14.7	1275	3	US-09-252-991A-13638	Sequence 13638, A
	77	66	14.7	1632	3	US-09-799-451-297	Sequence 297, App
	78	66	14.7	2032	3	US-09-241-581B-5	Sequence 5, Appli
	79	66	14.7	2032	3	US-08-265-428-5	Sequence 5, Appli
	80	66	14.7	2032	6	PCT-US95-07721-5	Sequence 5, Appli
	81	66	14.7	2048	3	US-09-199-637A-136	Sequence 136, App
	82	66	14.7	2442	3	US-10-098-108-8	Sequence 8, Appli

83	66	14.7	2736	3	US-10-098-108-6	Sequence 6, Appli	c 156	64.5	14.4	74545	3	US-09-949-002-606	Sequence 606, App
84	66	14.7	5329	3	US-09-562-702A-19	Sequence 19, Appli	c 157	64.5	14.4	131860	3	US-09-949-002-730	Sequence 730, App
85	66	14.7	5329	3	US-09-561-818A-19	Sequence 19, Appli	c 158	64	14.3	1098	3	US-09-602-777A-141	Sequence 141, App
86	66	14.7	5329	3	US-10-037-182-11	Sequence 11, Appli	c 159	64	14.3	1569	2	US-08-680-726A-57	Sequence 57, Appli
87	66	14.7	5689	3	US-09-562-702A-17	Sequence 17, Appli	c 160	64	14.3	1569	3	US-09-092-409-57	Sequence 57, Appli
88	66	14.7	5689	3	US-09-561-818A-17	Sequence 17, Appli	c 161	64	14.3	1847	3	US-09-949-016-5449	Sequence 5449, Ap
89	66	14.7	5689	3	US-10-037-182-9	Sequence 9, Appli	c 162	64	14.3	5926	3	US-09-917-254-41	Sequence 41, Appli
90	65.5	14.6	1317	2	US-09-134-000C-3152	Sequence 3152, Ap	c 163	64	14.3	10592	2	US-08-680-726A-51	Sequence 51, Appli
91	65.5	14.6	1377	2	US-07-809-457A-14	Sequence 14, Appli	c 164	64	14.3	10592	2	US-08-680-726A-52	Sequence 52, Appli
92	65.5	14.6	1377	2	US-08-476-008-9	Sequence 9, Appli	c 165	64	14.3	10592	3	US-09-092-409-51	Sequence 51, Appli
93	65.5	14.6	1377	2	US-08-306-063-9	Sequence 9, Appli	c 166	64	14.3	10592	3	US-09-092-409-52	Sequence 52, Appli
94	65.5	14.6	1377	2	US-08-553-943-14	Sequence 14, Appli	c 167	64	14.3	194714	3	US-09-949-016-11869	Sequence 11869, A
95	65.5	14.6	1377	2	US-08-833-485-9	Sequence 9, Appli	c 168	64	14.3	196714	3	US-09-949-016-15474	Sequence 15474, A
96	65.5	14.6	1377	2	US-09-137-440-9	Sequence 9, Appli	c 169	64	14.3	246230	3	US-09-949-016-17019	Sequence 17019, A
97	65.5	14.6	1377	6	PCT-US91-06148A-9	Sequence 9, Appli	c 170	64	14.3	246230	3	US-09-949-016-17020	Sequence 17020, A
98	65.5	14.6	1377	6	PCT-US91-09437-14	Sequence 14, Appli	c 171	64	14.3	246230	3	US-09-949-016-17021	Sequence 17021, A
99	65.5	14.6	2334	3	US-09-434-039A-32	Sequence 32, Appli	c 172	64	14.3	246230	3	US-09-949-016-17022	Sequence 17022, A
100	65.5	14.6	2352	3	US-09-434-039A-30	Sequence 30, Appli	c 173	63.5	14.2	400	3	US-08-956-171E-4278	Sequence 4278, Ap
101	65.5	14.6	7291	3	US-09-949-016-12425	Sequence 12425, A	c 174	63.5	14.2	400	3	US-08-781-986A-4278	Sequence 4278, Ap
102	65.5	14.6	7299	3	US-09-949-016-15948	Sequence 15948, A	c 175	63.5	14.2	705	3	US-09-533-559-7121	Sequence 7121, Ap
103	65.5	14.6	8012	3	US-09-182-117-1	Sequence 1, Appli	c 176	63.5	14.2	2397	3	US-09-221-017B-272	Sequence 272, App
104	65.5	14.6	8012	3	US-09-434-039A-1	Sequence 1, Appli	c 177	63.5	14.2	3081	3	US-09-248-796A-2025	Sequence 2025, Ap
105	65.5	14.6	8418	3	US-09-182-117-5	Sequence 5, Appli	c 178	63.5	14.2	3799	3	US-09-949-016-1653	Sequence 1653, Ap
106	65.5	14.6	8418	3	US-09-434-039A-5	Sequence 5, Appli	c 179	63.5	14.2	3804	3	US-09-949-016-739	Sequence 739, App
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111	65.5	14.6	10846	3	US-09-923-109-5	Sequence 5, Appli	c 184	63	14.1	601	3	US-09-949-016-49688	Sequence 49688, A
112	65.5	14.6	10900	3	US-09-098-219B-6	Sequence 6, Appli	c 185	63	14.1	1014	3	US-09-248-796A-635	Sequence 635, App
113	65.5	14.6	10900	3	US-10-164-204-6	Sequence 6, Appli	c 186	63	14.1	1059	3	US-09-248-796A-12476	Sequence 12476, A
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116	65	14.5	1024	3	US-09-513-783A-141	Sequence 141, App	c 189	63	14.1	72704	3	US-09-902-540-1273	Sequence 1273, Ap
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122	65	14.5	1105	3	US-09-765-272A-75	Sequence 75, Appli	c 195	62.5	14.0	1335	3	US-09-583-110-2490	Sequence 2490, Ap
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137	65	14.5	3378	3	US-09-430-656-151	Sequence 151, App	c 210	62	13.8	2272	3	US-10-006-768A-307	Sequence 307, App
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144	64.5	14.4	775	3	US-09-536-784-89	Sequence 89, Appli	c 217	62	13.8	2577	3	US-09-685-166A-552	Sequence 552, App
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147	64.5	14.4	1689	3	US-09-902-540-6020	Sequence 6020, Ap	c 220	62	13.8	2577	3	US-09-651-236-552	Sequence 552, App
148	64.5	14.4	1696	3	US-08-961-083-217	Sequence 217, App	c 221	62	13.8	2577	3	US-09-657-279-552	Sequence 552, App
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151	64.5	14.4	1696	3	US-09-765-272A-217	Sequence 217, App	c 224	62	13.8	2772	3	US-09-252-991A-12393	Sequence 12393, A
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155	64.5	14.4	50109	3	US-09-949-016-14112	Sequence 14112, A	c 228	62	13.8	5433	3	US-09-562-702A-15	Sequence 15, Appli

229	62	13.8	5433	3	US-09-561-818A-15	Sequence 15, Appl	302	61	13.6	2525	3	US-10-104-047-910	Sequence 910, App
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251	61.5	13.7	977	3	US-09-956-004-18	Sequence 18, Appl	324	60.5	13.5	1337	3	US-09-620-405B-467	Sequence 467, App
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255	61.5	13.7	1729	3	US-09-433-826B-466	Sequence 466, App	328	60.5	13.5	1337	3	US-09-590-751A-467	Sequence 467, App
256	61.5	13.7	1729	3	US-09-604-287A-466	Sequence 466, App	329	60.5	13.5	1337	3	US-09-551-621-467	Sequence 467, App
257	61.5	13.7	1729	3	US-09-834-759-466	Sequence 466, App	330	60.5	13.5	1337	3	US-09-551-621A-467	Sequence 467, App
258	61.5	13.7	1729	3	US-09-590-751A-466	Sequence 466, App	c 332	60.5	13.5	1344	3	US-09-252-991A-10181	Sequence 10181, A
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263	61.5	13.7	2232	3	US-09-620-405B-491	Sequence 491, App	337	60.5	13.5	1419	3	US-09-107-433-963	Sequence 963, App
264	61.5	13.7	2232	3	US-09-834-759-491	Sequence 491, App	338	60.5	13.5	1785	3	US-09-252-991A-9890	Sequence 9890, App
265	61.5	13.7	2232	3	US-10-076-622-491	Sequence 491, App	339	60.5	13.5	2029	2	US-08-933-750C-69	Sequence 69, Appl
266	61.5	13.7	2307	3	US-09-792-024-43	Sequence 43, Appl	340	60.5	13.5	2030	3	US-09-234-613-69	Sequence 15, Appl
267	61.5	13.7	3045	3	US-10-076-622-548	Sequence 548, App	341	60.5	13.5	2030	3	US-09-451-739H-15	Sequence 15, Appl
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274	61.5	13.7	3681	3	US-09-834-759-463	Sequence 463, App	348	60.5	13.5	2307	3	US-09-834-759-468	Sequence 468, App
275	61.5	13.7	3681	3	US-09-590-751A-463	Sequence 463, App	349	60.5	13.5	2307	3	US-09-590-751A-468	Sequence 468, App
276	61.5	13.7	3681	3	US-09-551-621-463	Sequence 463, App	350	60.5	13.5	2307	3	US-09-551-621-468	Sequence 468, App
277	61.5	13.7	3681	3	US-09-551-621A-463	Sequence 463, App	351	60.5	13.5	2307	3	US-09-551-621A-468	Sequence 468, App
278	61.5	13.7	3681	3	US-10-076-622-463	Sequence 463, App	352	60.5	13.5	2307	3	US-10-076-622-468	Sequence 468, App
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280	61.5	13.7	3865	3	US-09-604-287A-474	Sequence 474, App	355	60.5	13.5	3519	2	US-08-380-403A-1	Sequence 1, Appl
281	61.5	13.7	3865	3	US-09-834-759-474	Sequence 474, App	356	60.5	13.5	3519	2	US-08-895-810D-1	Sequence 1, Appl
282	61.5	13.7	3865	3	US-09-590-751A-474	Sequence 474, App	357	60.5	13.5	3537	3	US-09-543-681A-3647	Sequence 3647, App
283	61.5	13.7	3865	3	US-09-551-621-474	Sequence 474, App	358	60.5	13.5	3728	2	US-08-111-939-1	Sequence 1, Appl
284	61.5	13.7	3865	3	US-09-551-621A-474	Sequence 474, App	359	60.5	13.5	4047	3	US-10-076-622-566	Sequence 1, Appl
285	61.5	13.7	3865	3	US-10-076-622-474	Sequence 474, App	360	60.5	13.5	4165	2	US-08-095-737-1	Sequence 1, Appl
286	61.5	13.7	8959	2	US-08-920-812-1	Sequence 1, Appl	361	60.5	13.5	4165	2	US-08-480-145-1	Sequence 1, Appl
287	61.5	13.7	8959	2	US-08-920-827-1	Sequence 1, Appl	362	60.5	13.5	4165	2	US-08-477-389-1	Sequence 1, Appl
288	61.5	13.7	8959	2	US-08-921-177-1	Sequence 1, Appl	363	60.5	13.5	4256	3	US-09-949-016-4812	Sequence 4812, App
289	61.5	13.7	8959	2	US-08-362-577C-1	Sequence 1, Appl	364	60.5	13.5	4458	3	US-09-949-016-284	Sequence 54, App
290	61.5	13.7	8959	2	US-08-920-828-1	Sequence 1, Appl	365	60.5	13.5	4458	3	US-10-076-622-564	Sequence 1, Appl
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297	61	13.6	822	3	US-09-328-475C-245	Sequence 245, App	372	60.5	13.5	39299	3	US-09-949-016-16625	Sequence 1, Appl
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60 13.4 894 3 US-10-101-464A-276 Sequence 276, Ap
60 13.4 969 2 US-08-310-416A-12 Sequence 12, Appl
60 13.4 969 2 US-08-888-171-12 Sequence 12, Appl
60 13.4 1605 3 US-09-487-558B-123 Sequence 123, Ap
60 13.4 1848 3 US-09-475-460A-31 Sequence 31, Appl
60 13.4 1848 3 US-09-748-060A-31 Sequence 31, Appl
60 13.4 1878 2 US-08-435-149-17 Sequence 16, Appl
60 13.4 1930 3 US-08-126-505A-16 Sequence 10, Appl
60 13.4 1947 2 US-08-185-282-10 Sequence 10, Appl
60 13.4 1999 3 US-09-949-016-4523 Sequence 4523, Ap
60 13.4 2017 3 US-09-844-311-1 Sequence 1, Appl
60 13.4 2096 2 US-08-458-084-1 Sequence 1, Appl
60 13.4 2096 2 US-08-205-508-1 Sequence 1, Appl
60 13.4 2096 2 US-08-278-630A-10 Sequence 10, Appl
60 13.4 2096 6 PCT-US95-02965-1 Sequence 1, Appl
c 407 60 13.4 2097 3 US-09-270-767-11871 Sequence 11871, A
60 13.4 2115 2 US-09-014-240-1 Sequence 1, Appl
60 13.4 2116 2 US-07-811-048-9 Sequence 9, Appl
60 13.4 2139 3 US-09-248-796A-171 Sequence 171, Ap
60 13.4 2148 3 US-09-219-983A-19 Sequence 19, Appl
60 13.4 2148 3 US-10-114-774-19 Sequence 19, Appl
60 13.4 2220 3 US-09-023-655-1064 Sequence 1064, Ap
60 13.4 2220 3 US-09-844-311-3 Sequence 3, Appl
60 13.4 2233 3 US-09-014-240-3 Sequence 3, Appl
60 13.4 2234 2 US-07-811-048-10 Sequence 10, Appl
60 13.4 2373 2 US-08-264-101-1 Sequence 1, Appl
60 13.4 2373 2 US-08-765-243-1 Sequence 1, Appl
60 13.4 2373 6 PCT-US95-07295-1 Sequence 1, Appl
60 13.4 2492 3 US-09-219-983A-18 Sequence 18, Appl
60 13.4 2492 3 US-10-114-774-18 Sequence 18, Appl
60 13.4 2650 3 US-08-765-243-7 Sequence 7, Appl
60 13.4 2650 6 PCT-US95-07295-7 Sequence 7, Appl
60 13.4 2847 2 US-08-087-007-2 Sequence 2, Appl
60 13.4 2847 3 US-08-483-433-2 Sequence 2, Appl
60 13.4 2847 3 US-09-566-254A-2 Sequence 2, Appl
60 13.4 2847 6 PCT-US92-05920-2 Sequence 2, Appl
60 13.4 3367 3 US-10-101-464A-882 Sequence 882, Ap
60 13.4 3484 3 US-09-949-016-1893 Sequence 1893, Ap
60 13.4 3619 3 US-08-377-503-1 Sequence 1, Appl
60 13.4 3619 3 US-08-178-019-1 Sequence 1, Appl
60 13.4 4014 3 US-09-541-782-1 Sequence 1, Appl
60 13.4 4014 3 US-09-723-820-1 Sequence 1, Appl
60 13.4 4014 3 US-10-270-085-1 Sequence 1, Appl
60 13.4 4650 3 US-09-949-016-1452 Sequence 1452, Ap
60 13.4 4650 3 US-09-949-016-941 Sequence 941, Ap
60 13.4 1728 3 US-09-949-016-14245 Sequence 14245, A
60 13.4 30250 3 US-09-949-016-17528 Sequence 17528, A
60 13.4 94077 3 US-09-949-016-13635 Sequence 13635, A
60 13.4 134890 3 US-09-949-016-15602 Sequence 15602, A
59.5 13.3 705 3 US-09-248-796A-1143 Sequence 1143, Ap
59.5 13.3 773 3 US-09-533-559-6324 Sequence 6324, Ap
59.5 13.3 778 4 US-09-605-703B-1139 Sequence 1139, Ap
59.5 13.3 885 4 US-09-605-703B-1137 Sequence 1137, Ap
59.5 13.3 936 4 US-09-605-703B-2749 Sequence 2749, Ap
59.5 13.3 954 3 US-09-533-559-6076 Sequence 6076, Ap
59.5 13.3 1485 4 US-09-605-703B-711 Sequence 711, Ap

448 59.5 13.3 1856 4 US-09-605-703B-709 Sequence 709, Ap
449 59.5 13.3 1950 3 US-09-134-000C-1772 Sequence 1772, Ap
450 59.5 13.3 2255 3 US-10-104-047-981 Sequence 581, Ap
451 59.5 13.3 2460 3 US-09-614-221A-519 Sequence 519, Ap
452 59.5 13.3 3346 3 US-09-949-016-3747 Sequence 3747, Ap
453 59.5 13.3 3346 3 US-09-949-016-817 Sequence 817, Ap
454 59.5 13.3 3850 3 US-09-644-947A-1 Sequence 1, Appl
455 59.5 13.3 4521 3 US-09-902-540-3633 Sequence 3633, Ap
456 59.5 13.3 5183 2 US-08-459-568-3 Sequence 3, Appl
457 59.5 13.3 5183 2 US-08-399-411-3 Sequence 3, Appl
458 59.5 13.3 5643 3 US-09-079-415-5 Sequence 5, Appl
459 59.5 13.3 5643 3 US-08-750-458A-1 Sequence 1, Appl
460 59.5 13.3 5868 3 US-08-516-859A-3 Sequence 3, Appl
461 59.5 13.3 5868 3 US-09-586-472-3 Sequence 3, Appl
462 59.5 13.3 5868 3 US-09-588-706-3 Sequence 3, Appl
463 59.5 13.3 5868 3 US-10-024-450-3 Sequence 3, Appl
464 59.5 13.3 6127 3 US-09-799-451-797 Sequence 797, Ap
465 59.5 13.3 6173 3 US-09-949-016-5511 Sequence 5511, Ap
466 59.5 13.3 6173 3 US-09-949-016-5512 Sequence 5512, Ap
467 59.5 13.3 6178 3 US-09-799-451-798 Sequence 798, Ap
468 59.5 13.3 7393 3 US-09-620-312D-372 Sequence 372, Ap
469 59.5 13.3 12381 3 US-09-953-096-3 Sequence 3, Appl
c 470 59.5 13.3 16158 3 US-09-949-016-17568 Sequence 17568, A
471 59.5 13.3 16557 3 US-09-953-096-1 Sequence 1, Appl
472 59.5 13.3 19269 3 US-09-902-540-1175 Sequence 1175, Ap
473 59.5 13.3 34068 3 US-09-949-016-15489 Sequence 15489, A
474 59.5 13.3 42672 3 US-09-949-016-17254 Sequence 17254, A
475 59.5 13.3 42672 3 US-09-949-016-17254 Sequence 17254, A
476 59.5 13.3 51711 3 US-09-949-016-12559 Sequence 12559, A
477 59.5 13.3 63760 3 US-09-949-016-14087 Sequence 14087, A
478 59.5 13.3 63760 3 US-09-949-016-14088 Sequence 14088, A
479 59.5 13.3 96327 3 US-09-949-016-16541 Sequence 16541, A
c 480 59.5 13.3 176373 3 US-09-128-155-17 Sequence 17, Appl
59 13.2 381 3 US-09-188-930-3 Sequence 3, Appl
59 13.2 381 3 US-09-312-283C-3 Sequence 3, Appl
59 13.2 502 3 US-09-621-979C-1128 Sequence 1128, Ap
59 13.2 703 3 US-09-513-996C-1720 Sequence 1720, Ap
59 13.2 768 3 US-09-134-000C-1166 Sequence 1166, Ap
59 13.2 1042 3 US-09-533-559-5292 Sequence 5292, Ap
59 13.2 1114 3 US-09-799-451-642 Sequence 642, Ap
59 13.2 1186 3 US-09-533-559-5395 Sequence 5395, A
59 13.2 1227 3 US-09-248-796A-11083 Sequence 11083, A
59 13.2 1302 2 US-08-425-299A-1 Sequence 1, Appl
59 13.2 1374 3 US-09-568-470A-2 Sequence 2, Appl
59 13.2 1452 2 US-08-187-785-2 Sequence 2, Appl
59 13.2 1452 3 US-09-023-655-1048 Sequence 1048, Ap
59 13.2 1866 3 US-10-104-047-1398 Sequence 1398, Ap
59 13.2 2073 3 US-09-949-016-4551 Sequence 4551, Ap
59 13.2 2122 3 US-09-949-016-3401 Sequence 3401, Ap
59 13.2 2467 2 US-08-701-240-1 Sequence 1, Appl
59 13.2 2467 3 US-09-138-236-1 Sequence 1, Appl
59 13.2 3828 6 PCT-US93-10500-1 Sequence 1, Appl
59 13.2 4074 2 US-08-471-033-19 Sequence 19, Ap

ALIGNMENTS

RESULT 1

US-09-697-863A-1

; Sequence 1, Application US/09697863A

; Patent No. 6812203

; GENERAL INFORMATION:

; TITLE OF INVENTION: CD-40 INTERACTING AND TRAF-INTERACTING PROTEINS

; FILE REFERENCE: 2676-4555US

; CURRENT APPLICATION NUMBER: US/09/697.863A

; PRIOR FILING DATE: 2000-10-27

; PRIOR FILING DATE: 1999-04-28

; PRIOR FILING DATE: 1998-04-29

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

US-09-697-863A-1
; Sequence 1, Application US/09697863A
; Patent No. 6812203
; GENERAL INFORMATION:
; TITLE OF INVENTION: CD-40 INTERACTING AND TRAF-INTERACTING PROTEINS
; FILE REFERENCE: 2676-4555US
; CURRENT APPLICATION NUMBER: US/09/697.863A
; PRIOR FILING DATE: 2000-10-27
; PRIOR FILING DATE: 1999-04-28
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1

SEQ ID NO 1
LENGTH: 1920
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1627)..(1627)
OTHER INFORMATION: N stands for any nucleotide.
FEATURE:
NAME/KEY: CDS
LOCATION: (20)..(1108)
OTHER INFORMATION:
FEATURE:
NAME/KEY: misc feature
LOCATION: (1849)..(1849)
OTHER INFORMATION: N stands for any nucleotide.
US-09-697-863A-1

Alignment Scores:
Pred. No.: 4 52e-54 Length: 1920
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x US-09-697-863A-1 (1-1920)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 179 ATGGAAGGCTCTGAACCTCTACTTCGAGCCTCCGCTGGAGGAGAGCGCTTTGGAAACGC 238
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 239 CGACCTGAAACCACTCTCGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 298
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 299 GATTCACCACTCTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGACGATG 358
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 359 TTCTCTCTCATCTACCTGGATATTTGATGATTAGATCTAAACAATCTGTCTCAGAGAGGCT 418
QY 81 ArgGlyValCysSerTyrLeu 87
DB 419 CGAGGGGTGTCTCTACTTA 439

RESULT 2

US-09-620-312D-889
Sequence 889, Application US/09620312D
Patent No. 659662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunging
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 659662el Nucleic Acids and
OTHER INFORMATION: Polypeptides
FILE REFERENCE: 784CIP2B

CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PE FL-Seqes Version 1.0
SEQ ID NO 889
LENGTH: 1948
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (39)..(1127)
US-09-620-312D-889

Alignment Scores:
Pred. No.: 4 61e-54 Length: 1948
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x US-09-620-312D-889 (1-1948)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 198 ATGGAAGGCTCTGAACCTCTACTTCGAGCCTCCGCTGGAGGAGAGCGCTTTGGAAACGC 257
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 258 CGACCTGAAACCACTCTCGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 317
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 318 GATTCACCACTCTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGACGATG 377
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 378 TTCTCTCTCATCTACCTGGATATTTGATGATTAGATCTAAACAATCTGTCTCAGAGAGGCT 437
QY 81 ArgGlyValCysSerTyrLeu 87
DB 438 CGAGGGGTGTCTCTACTTA 458

RESULT 3

US-09-697-863A-3
Sequence 3, Application US/09697863A
Patent No. 6812203
GENERAL INFORMATION:
APPLICANT: Vlaams Interuniversitair Instituut Voor Biotechnologie VZW
TITLE OF INVENTION: CD-40 INTERACTING AND TRAF-INTERACTING PROTEINS
FILE REFERENCE: 2676-4555US
CURRENT APPLICATION NUMBER: US/09/697,863A
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: PCT/EP99/03025
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: EPO 98201392.2
PRIOR FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 1312
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (122)..(1234)
OTHER INFORMATION:
US-09-697-863A-3


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Query Match: 16.18% Indels: 19
DB: 3 Gaps: 5
US-10-757-745-2_COPY_54_140 (1-87) x US-09-248-796A-1008 (1-573)
QY 22 ProGluThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThrThrAsp 41
DB 262 CTTAAACAGCAAGTAACCA---ACAAGTAGTGCTGACGATGACCAACCAACGAGA 318
QY 42 SerThrThrSerIleSle-----SerProSerGlu 51
DB 319 ACTACTACTGATAAGTCAGACACTACCAACGAAGATATTGAACCAACAACCCCAAGAA 378
QY 52 AspThrGlnGlnAsnGlySerMet-----PheSerLeuIleThr--- 65
DB 379 AAAACGTGAGGAAGAAAGATGATTAATCAAGATATACCTTAATCCCAATTCCTCAATTACCACT 438
QY 66 ---TTPAsnIleAspGlyLeuAsp---LeuAsnAsnLeu 76
DB 439 TGGTGGAACTGGAAGGCTCTAATAAGTTAATTCACCT 477
RESULT 7
US-09-248-796A-12164
; Sequence 12164, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 12164
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-12164
Alignment Scores:
Pred. No.: 1.63 Length: 999
Score: 71.50 Matches: 20
Percent Similarity: 40.30% Conservatives: 7
Best Local Similarity: 29.85% Mismatches: 25
Query Match: 29.85% Indels: 15
DB: 3 Gaps: 1
US-10-757-745-2_COPY_54_140 (1-87) x US-09-248-796A-12164 (1-999)
QY 10 GluProValGluGluSerAlaLeuGluArgProGluThrIleSerGluProLys 29
DB 697 GAACCACTTAAAGGAAGAACTGCGAAGAAGACACACCCGAAACACTAATTTCAGTAA 756
QY 30 ThrTyVal-----AspLeu 34
DB 757 GAAATGTTTCCAACTCCCTCGTTCGTAACGAAAAAAGAAACATCAAGATGCC 816
QY 35 ThrAsnGluGluThrAspSerThrThrSerIleSleSerProSerGluAspThrGln 54
DB 817 GAAGAAGAAGAAGATGATAGCACTCTTGTGAAAAAGATTAAACCTTCTCAACGCTACTGCT 876
QY 55 GlnGluAsnGlySerMetPhe 61
DB 877 GAAGAAACACAGATCAATTATT 897
RESULT 8
US-09-902-540-5004/c
; Sequence 5004, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldmann, Barry S.
; APPLICANT: Hinkle, Steven C.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1247
; LENGTH: 32241
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(32241)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1247
```

```
; GENERAL INFORMATION:
; APPLICANT: Goldmann, Barry S.
; APPLICANT: Hinkle, Steven C.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5004
; LENGTH: 24459
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5004
Alignment Scores:
Pred. No.: 164 Length: 24459
Score: 71.00 Matches: 27
Percent Similarity: 40.00% Conservatives: 9
Best Local Similarity: 30.00% Mismatches: 36
Query Match: 15.85% Indels: 18
DB: 3 Gaps: 5
US-10-757-745-2_COPY_54_140 (1-87) x US-09-902-540-5004 (1-24459)
QY 5 LeuAsnSerTy-PheGluProValGluGluSerAlaLeuGluArgProGluThr 24
DB 15374 TTGAACCTCG-----AGGCTCCAGAAAGCCCTCATCGCTCTCACTCAAGCCGCGTC 15321
QY 25 IleSerGluProLysThrTyValAspLeuThrAsnGluGluThrThrAspSerThr 44
DB 15320 AAATCGAATTCGACGCTCTTCGAGAC-----GACTCCGCGGCC 15282
QY 45 SerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeu 64
DB 15281 TCCAGTTGACGCCCCCGGAGGCTCACCGCTCTCCCGCGCGGTTCTGCAGACCAACATC 15222
QY 65 ThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSer-----Glu 78
DB 15221 ACCTGGAAC---AGCGGACTCGGCTCAAGTCCCGCTCTGCTGTCAGCTCTCCACCAAC 15165
QY 79 ArgAlaArgGlyVal-----CysSerTy 86
DB 15164 CGCTGAAGGCACTTCCTGGTGGCGGTAC 15135
RESULT 9
US-09-902-540-1247
; Sequence 1247, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldmann, Barry S.
; APPLICANT: Hinkle, Steven C.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1247
; LENGTH: 32241
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(32241)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1247
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Alignment Scores:
Pred. No.: 241 Length: 32241
Score: 71.00 Matches: 27
Percent Similarity: 40.00% Conservative: 9
Best Local Similarity: 30.00% Mismatches: 36
Query Match: 15.85% Indels: 18
DB: 3 Gaps: 5

US-10-757-745-2_COPY_54_140 (1-87) x US-09-902-540-1247 (1-32241)

Qy 5 LeuSerGluProValGluGluSerAlaLeuGluArgProGluThr 24
Db 16968 TTGAACGCG-----AGCGCTCCAGAAAGCGCCCTCACTCAAGCGCGC 16921
Qy 25 IleSerGluProLysThrTyrValAspLeuThrAsnGluThrThrAspSerThrThr 44
Db 16922 AAATCGAACTTCGACGCTCTCGCAGAC-----GACTCGCGCGC 16960
Qy 45 SerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIle 64
Db 16961 TCCAGTTCAGCGCGCGGAGGCTCACCGCTCTCTCCCGCGCGGTCTGTCGAGCACCACATC 17020
Qy 65 ThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSer-----Glu 78
Db 17021 ACCTGGAAC--AGCGGACTCGGCTCAAGTCCCGCTCTGGCTGCAGCTCTCTCCACCAAC 17077
Qy 79 ArgAlaArgGlyVal-----CysSerTyr 86
Db 17078 CGCTCGAGGCGCACTCTCTGGTGGCGGTAC 17107

RESULT 10
US-08-961-527-26/c
; Sequence 26, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/961,527
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB34001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15213 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-26

Alignment Scores:
Pred. No.: 100 Length: 15213
Score: 70.50 Matches: 24
Percent Similarity: 44.09% Conservative: 17
Best Local Similarity: 25.81% Mismatches: 27
Query Match: 15.74% Indels: 25
DB: 3 Gaps: 2

US-10-757-745-2_COPY_54_140 (1-87) x US-08-961-527-26 (1-15213)

Qy 10 GluProValGluGluSerAlaLeuGluArgProGluThrIleSerGluProLys 29
Db 3350 AAACACACAGTTGAGAAATCAATCAACAGAAAAAAGCGAACTGCAACAAACAGAA 3491
Qy 30 ThrTyrValAspLeuThrAsnGlu----- 38
Db 3490 AATTGAGTAATACAAATCAGAGATGGAACAAACAGAACCAACCATCAACCGGAAAT 3431
Qy 39 -----ThrThrAspSerThrThrSerLysIleSerProSerGluAspThr 53
Db 3430 TCAACTGAGGATGTTTCAACCGAATCAACACATCCCAATTCAAATGGNAACGAAAGAAAT 3371
Qy 54 GlnGlnGluAsn-----GlySerMetPheSerLeuIle 64
Db 3370 AAACAGAAATGAACTAGACCTGATAAAAGGTAGAGAACCAAGAGAAACACTTGAA 3311
Qy 65 ThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSer 77
Db 3310 TTAAGAAATGTTCCGACCTAGAGTTATACAGTTTGTC 3272

RESULT 11
US-08-961-083-93
; Sequence 93, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/961,083
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 835 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-083-93
Alignment Scores:

Pred. No.: 2.08 Length: 835
Score: 70.00 Matches: 18
Percent Similarity: 48.44% Conservatives: 13
Best Local Similarity: 28.12% Mismatches: 17
Query Match: 15.62% Indels: 16
DB: 3 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x US-08-961-083-93 (1-835)

QY 10 GluProValGluGluSerAlaLeuArgArgProGluThrIleSerGluProLys 29
:::|||||:::|
Db 587 AAACACCAAGTTGAAGATCAATCAACACGAGAAACGGAACCTGCAACAAACAGAA 646
:::|||||:::|

QY 30 ThrTyrValAspLeuThrAsnGluGlu----- 38
:::|:::|
Db 647 AATTCAGGTAAATCAACATCAGAGATGGAACAAACAGAACCAACCATCAACCGAAT 706
:::|:::|

QY 39 -----ThrThrAspSerThrThrSerLysIleSerProSerGluAspThr 53
:::|||||:::|
Db 707 TCAACTGAGGATGTTTCAACCGAATCAACACATCAATCAATGGAACGAAAT 766
:::|||||:::|

QY 54 GlnGlnGluAsn 57
:::|||||
Db 767 AAACAAGAAAT 778
:::|||||

RESULT 12

US-09-536-784-93
; Sequence 93, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-09-536-784-93

Alignment Scores:

Pred. No.: 2.08 Length: 835
Score: 70.00 Matches: 18
Percent Similarity: 48.44% Conservatives: 13
Best Local Similarity: 28.12% Mismatches: 17

Query Match: 15.62% Indels: 16
DB: 3 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x US-09-536-784-93 (1-835)

QY 10 GluProValGluGluSerAlaLeuArgArgProGluThrIleSerGluProLys 29
:::|||||:::|
Db 587 AAACACCAAGTTGAAGATCAATCAACACGAGAAACGGAACCTGCAACAAACAGAA 646
:::|||||:::|

QY 30 ThrTyrValAspLeuThrAsnGluGlu----- 38
:::|:::|
Db 647 AATTCAGGTAAATCAACATCAGAGATGGAACAAACAGAACCAACCATCAACCGAAT 706
:::|:::|

QY 39 -----ThrThrAspSerThrThrSerLysIleSerProSerGluAspThr 53
:::|||||:::|
Db 707 TCAACTGAGGATGTTTCAACCGAATCAACACATCAATCAATGGAACGAAAT 766
:::|||||:::|

QY 54 GlnGlnGluAsn 57
:::|||||
Db 767 AAACAAGAAAT 778
:::|||||

RESULT 13
US-09-765-271-93
; Sequence 93, Application US/09765271
; Patent No. 6887663
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,271
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/536,784
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-09-765-271-93

Alignment Scores:
Pred. No.: 2.08 Length: 835
Score: 70.00 Matches: 18
Percent Similarity: 48.44% Conservatives: 13
Best Local Similarity: 28.12% Mismatches: 17
Query Match: 15.62% Indels: 16
DB: 3 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x US-09-765-271-93 (1-835)

```

QY 10 GluProValGluGluSerAlaLeuGluArgProGluThrIleSerGluProLys 29
   ::::::::::::::::::::::::::::
Db 587 AAACCCAGTTGAAGAAATCAATCAACGAGAAAAAAGCGAACTGCACAAACCGAGAA 646
   ::::::::::::::::::::::::::::
QY 30 ThrTyrValAspLeuThrAsnGluGlu----- 38
   ::::::::::::::::::::::::::::
Db 647 AATTCAAGTAATACATCAGAGATGGCAACAGACAGAACCATCAACCGGAAT 706
   ::::::::::::::::::::::::::::
QY 39 -----ThrThraspSerThrThrSerLysIleSerProSerGluAspThr 53
   ::::::::::::::::::::::::::::
Db 707 TCAACTGAGGATGTTTCAACCGAATCAACACATCCAAATTCAAATGGAAACGAGAAATT 766
   ::::::::::::::::::::::::::::
QY 54 GlnGlnGluAsn 57
   ::::::::::::::::::::::::::::
Db 767 AAACAAGAAAT 778

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RESULT 14

```

; Sequence 93, Application US/09765272A
; Patent No. 6929930
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and
; Vaccines
; NUMBER OF SEQUENCES: 454
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: Dell Latitude C610
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272A
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lin J. Hymel
; REGISTRATION NUMBER: 45,414
; REFERENCE/DOCKET NUMBER: PB340P2C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 610-5790
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 835 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 93:

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US-09-765-272A-93
Alignment Scores:
Pred. No.: 2.08 Length: 835
Score: 70.00 Matches: 18
Percent Similarity: 48.4% Conservative: 13
Best Local Similarity: 28.1% Mismatches: 17
Query Match: 15.6% Indels: 16
DB: 3 Gaps: 1

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US-10-757-745-2_COPY_54_140 (1-87) x US-09-765-272A-93 (1-835)

```

QY 10 GluProValGluGluSerAlaLeuGluArgProGluThrIleSerGluProLys 29
   ::::::::::::::::::::::::::::
Db 587 AAACCCAGTTGAAGAAATCAATCAACGAGAAAAAAGCGAACTGCACAAACCGAGAA 646
   ::::::::::::::::::::::::::::
QY 30 ThrTyrValAspLeuThrAsnGluGlu----- 38
   ::::::::::::::::::::::::::::
Db 647 AATTCAAGTAATACATCAGAGATGGCAACAGACAGAACCATCAACCGGAAT 706
   ::::::::::::::::::::::::::::
QY 39 -----ThrThraspSerThrThrSerLysIleSerProSerGluAspThr 53
   ::::::::::::::::::::::::::::
Db 707 TCAACTGAGGATGTTTCAACCGAATCAACACATCCAAATTCAAATGGAAACGAGAAATT 766
   ::::::::::::::::::::::::::::
QY 54 GlnGlnGluAsn 57
   ::::::::::::::::::::::::::::
Db 767 AAACAAGAAAT 778

```

RESULT 15

```

; Sequence 3, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1714 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-961-083-3

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Alignment Scores:
Pred. No.: 5.67 Length: 1714
Score: 70.00 Matches: 18
Percent Similarity: 48.4% Conservative: 13
Best Local Similarity: 28.1% Mismatches: 17
Query Match: 15.6% Indels: 16
DB: 3 Gaps: 1

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US-10-757-745-2_COPY_54_140 (1-87) x US-08-961-083-3 (1-1714)

```

QY 10 GluProValGluGluSerAlaLeuGluArgProGluThrIleSerGluProLys 29
   ::::::::::::::::::::::::::::
Db 1448 AAACCCAGTTGAAGAAATCAATCAACGAGAAAAAAGCGAACTGCACAAACCGAGAA 1507
   ::::::::::::::::::::::::::::
QY 30 ThrTyrValAspLeuThrAsnGluGlu----- 38

```

```
Db 1508 AATTGAGTAAATACATCAGAGTAATGCAAAACAGAACCATCAAAACGGAAAT 1567
QY 39 -----ThrThrAspSerThrThrSerLysIleSerProSerGluAspThr 53
Db 1568 TCAACTGAGGATGTTTCAACCGAATCAAAACACATCAATTCAAATCGNAACGAAATTT 1627
QY 54 GlnGlnGluAsn 57
Db 1628 AAACAAGAAAT 1639

RESULT 16
US-09-536-784-3
; Sequence 3, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1714 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-536-784-3

Alignment Scores:
Pred. No.: 5.67 Length: 1714
Score: 70.00 Matches: 18
Percent Similarity: 48.44% Conservative: 13
Best Local Similarity: 28.12% Mismatches: 17
Query Match: 15.62% Indels: 16
DB: 3 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x US-09-536-784-3 (1-1714)
QY 10 GluProValGluGluSerAlaLeuGluArgProGluThrIleSerGluProLys 29
Db 1448 AAACACCAAGTTGAGTAATCAATCAACAGAAAACGAACTGCAACAAACAGAA 1507
QY 30 ThrTyrValAspLeuThrAsnGluGlu----- 38
Db 1508 AATTGAGTAAATACATCAGAGTAATGCAAAACAGAACCATCAAAACGGAAAT 1567
QY 1508 AATTGAGTAAATACATCAGAGTAATGCAAAACAGAACCATCAAAACGGAAAT 1567
QY 39 -----ThrThrAspSerThrThrSerLysIleSerProSerGluAspThr 53
Db 1568 TCAACTGAGGATGTTTCAACCGAATCAAAACACATCAATTCAAATCGNAACGAAATTT 1627
QY 39 -----ThrThrAspSerThrThrSerLysIleSerProSerGluAspThr 53
```

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Db 1568 TCAACTGAGGATGTTTCAACCGAATCAAAACACATCAATTCAAATCGNAACGAAATTT 1627
QY 54 GlnGlnGluAsn 57
Db 1628 AAACAAGAAAT 1639

RESULT 17
US-09-765-271-3
; Sequence 3, Application US/09765271
; Patent No. 6887663
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,271
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/536,784
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1714 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-765-271-3

Alignment Scores:
Pred. No.: 5.67 Length: 1714
Score: 70.00 Matches: 18
Percent Similarity: 48.44% Conservative: 13
Best Local Similarity: 28.12% Mismatches: 17
Query Match: 15.62% Indels: 16
DB: 3 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x US-09-765-271-3 (1-1714)
QY 10 GluProValGluGluSerAlaLeuGluArgProGluThrIleSerGluProLys 29
Db 1448 AAACACCAAGTTGAGTAATCAATCAACAGAAAACGAACTGCAACAAACAGAA 1507
QY 30 ThrTyrValAspLeuThrAsnGluGlu----- 38
Db 1508 AATTGAGTAAATACATCAGAGTAATGCAAAACAGAACCATCAAAACGGAAAT 1567
QY 39 -----ThrThrAspSerThrThrSerLysIleSerProSerGluAspThr 53
Db 1568 TCAACTGAGGATGTTTCAACCGAATCAAAACACATCAATTCAAATCGNAACGAAATTT 1627
```

Qy 54 GlnGlnGluAen 57
:::|||||
Db 1628 AACACAGAAAT 1639

RESULT 18
US-09-765-272A-3
; Sequence 3, Application US/09765272A
; Patent No. 6929930
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigenes and
; ;
; NUMBER OF SEQUENCES: 454
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: Dell Latitude C610
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272A
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lin J. Hymel
; REGISTRATION NUMBER: 45,414
; REFERENCE/DOCKET NUMBER: PB340P2C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 610-5790
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1714 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-765-272A-3

Alignment Scores:
Pred. No.: 5.67 Length: 1714
Score: 70.00 Matches: 18
Percent Similarity: 48.44% Conservative: 13
Best Local Similarity: 28.12% Mismatches: 17
Query Match: 15.62% Indels: 16
DB: 3 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x US-09-765-272A-3 (1-1714)

Qy 10 GluProProValGluGluSerAlaLeuGluArgProGluThrIleSerGluProLys 29
:::|||||
Db 1448 AACACACAGTTGAAGATCAATCAACCAAGAAAAACCGAATCGCAACCAACAGNA 1507
:::|||||

Qy 30 ThrTyValAspLeuThrAsnGluGlu----- 38
:::|||||

Db 1508 AATTTCAGGTAATACACATCAGAGATGGACAAACAGACACAGACCAATCAACCGAAT 1567
:::|||||

Qy 39 -----ThrThrAspSerThrThrSerLysIleSerProSerGluAspThr 53
:::|||||

Db 1568 TCAACTGAGGATGTTTCAACCGAATCAATCAACCAATCCAAATTCAAATGGAACGAGAAATT 1627
:::|||||

Qy 54 GlnGlnGluAen 57
:::|||||

Db 1628 AACACAGAAAT 1639

RESULT 19
US-09-976-594-888
; Sequence 888, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 888
; LENGTH: 3640
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 5202390CB1
US-09-976-594-888

Alignment Scores:
Pred. No.: 16.2 Length: 3640
Score: 70.00 Matches: 33
Percent Similarity: 39.82% Conservative: 12
Best Local Similarity: 29.20% Mismatches: 32
Query Match: 15.62% Indels: 36
DB: 3 Gaps: 8

US-10-757-745-2_COPY_54_140 (1-87) x US-09-976-594-888 (1-3640)

Qy 6 AsnSerTyrrPheGluPro-----ProValGlu 14
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Db 827 AATCCTTTTATGAACCTTAATCAACTCTCTCCAATAATTTGGTAAATCCTGTTCAA 886
||| :::::|||||

Qy 15 GluSerAlaLeuGluArgArg-----ProGluThrIleSerGlu 27
||| |||||

Db 887 GAAC TAGAACTGAAAGCGAGTGAAAAGAGCCCGGCTCCACGAGTCTCTCA--- 943
||| |||||

Qy 28 ProLysThrTyrrValAspLeuThrAsnGluGluThrThrAsp-----Ser 42
||| |||||

Db 944 CCAAAAAACAGGAGTA-----TTAAATGAAAACACAGTTTCTGCAGGAAAAAGATCTCTCT 997
||| |||||

Qy 43 ThrThrSerLysIleSerProSerGluAspThr-----GlnGlnGluAsnGlySer 59
||| :::::|||||

Db 998 ACTTCTCTTAGCCAGCCCTATACCAAGTCTCTTTTGGGGGCGAAGCCAAATGCTAGT 1057
||| :::::|||||

Qy 60 MetPheSerLeuIleThrTrp-----AsnIleAspGlyLeuAspLeu 73
||| |||||

Db 1058 CAG---TCTTTGCTTGATGCTGTGTAAGAGATTACAAAGAACTACCGAGGAGTAAAAATC 1114
||| |||||

Qy 74 AsnAsnLeuSerGluArgAlaArgGlyValCysSerTyrr 86
||| :::::|||||

Db 1115 ACCAATTTTACTACATCGTGGAGAAATGGTTTATCTTTT 1153
||| :::::|||||

RESULT 20
US-09-620-312D-363
; Sequence 363, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom


```
Db 10 ATGATCTTACCATGAA-----CTTGACGCAAGGAGAGCGC 48
Qy 25 IleSerGluProLysThrTyValAspLeuThrAenGluGluThrThrAspSerThrThr 44
Db 49 AAACAAGAAGACATCATGCTGATGATGCAAAAGGATGCTGAGTTAAGCAATGTCGCATTT 108
Qy 45 SerLysIleSer-----ProSerGluAspThrGlnGlnGlnAenGlySerMetPheSer 62
Db 109 AATGGTGTGATGGATTACCAAGGATATTACCAAGTCAATGGAGTGACAGCGTTTTCGAT 168
Qy 63 LeuIleThrTpAenIleAspGlyLeu-----AspLeuAenAenLeuSerGluArgAla 80
Db 169 ATG-----ACAAATTGATGCTTTTACAAAGGAGTTAAAGAACTATCAGCAACGTTAGG 219
Qy 81 Arg 81
Db 220 AGG 222

RESULT 23
US-08-894-699-1
; Sequence 1, Application US/08894699
; Patent No. 6030769
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOAI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; TITLE OF INVENTION: VIRUSES, AND USES THEREOF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,699
; FILING DATE: 01-DEC-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/00294
; FILING DATE: 26-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 291 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-894-699-1
Alignment Scores:
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Pred. No.: 0.669 Length: 291
Score: 69.00 Matches: 26
Percent Similarity: 37.50% Conservative: 10
Best Local Similarity: 27.08% Mismatches: 31
Query Match: 15.40% Indels: 29
DB: 3 Gaps: 3

US-10-757-745-2_COPY_54_140 (1-87) x US-08-894-699-1 (1-291)
Qy 6 AsnSerTyrPheGluProValGluSerAlaLeuGluArgArg----- 21
Db 30 AACAGTAAGTACTCAGCTAATATTAAATGGAACACTCTCAGAAGGAAAGATAAGATCAT 89
Qy 22 -----ProGluThrIleSerGluProLysThrTyVal--- 32
Db 90 GGCACAAAATAATTTCGGATAGTGGCCAAATATCATAGTGACCCCTAAATACTACTATAAA 149
Qy 33 ---AspLeuThrAenGluGluThrThrAspSerThrThrSerLys-IleSerProSerGly 51
Db 150 CATGACTGCGCAGAGACGAGACATCAACAGTACAGAGATAGGTCCA----- 204
Qy 51 uAspThrGlnGlnGluAenGlySerMetPheSerLeuIleThrTrpAenIleAspGlyLe 71
Db 205 -----ATGGCTGGTACAGCATGGGCTT 227

RESULT 24
US-09-444-410-1
; Sequence 1, Application US/09444410
; Patent No. 6270975
; GENERAL INFORMATION:
; APPLICANT: SIMON, FRANCOIS
; APPLICANT: SARAGOSTI, SENTOB
; APPLICANT: LOUSSERT-AJAKA, IBITISSAM
; APPLICANT: LY, THOAI-DUONG
; APPLICANT: CHAIX-BAUDIER, MARIE-LAURE
; TITLE OF INVENTION: GROUP O HIV-1, FRAGMENTS OF SUCH
; TITLE OF INVENTION: VIRUSES, AND USES THEREOF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, FOURTH
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/444,410
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/894,699
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95/02236
; FILING DATE: 27-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,614
; REFERENCE/DOCKET NUMBER: 0354-0020-0PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
```

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 291 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
US-09-444-410-1

Alignment Scores:
Pred. No.: 0.669      Length: 291
Score: 69.00      Matches: 26
Percent Similarity: 37.50%      Conservative: 10
Best Local Similarity: 27.08%      Mismatches: 31
Query Match: 15.40%      Indels: 29
DB: 3      Gaps: 3

US-10-757-745-2_COPY_54_140 (1-87) x US-09-444-410-1 (1-291)
QY 6 AnnSerTyrPheGluProValGluSerAlaLeuGluArg----- 21
Db 30 AACAGTAAGTACTACGCTAATATAATGGAACACTCTCAGAGGAAAGATAAGATGAT 89
QY 22 -----ProGluThrIleSerGluProLysThrTyrVal--- 32
Db 90 GGCAGAAAATATTTCCGATAGTGGCCAAATATCATAGTGACCTTAATACTATAAA 149
QY 33 ---AspLeuThrAsnGluThrAspSerThrThrSerLys-IleSerProSerGlu 51
Db 150 CATGACCTGCCAGAGACCAGGACATCAACAGTACCAAGAGATAAGTAGTCCA----- 204
QY 51 uAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTyrAsnIleAspGly 71
Db 205 -----ATGGCTGGTACGACGATGGGCTT 227
QY 71 uAspLeuAsnAsnLeuSerGluArgAlaArgGlyValCysSerTyr 86
Db 228 AGCGGCAGGAAACCGATCTGAGTCAAGAGAGCTTATTGTGATAT 273

RESULT 25
PCT-US93-05944-1
; Sequence 1, Application PC/TUS9305944
; GENERAL INFORMATION:
;   APPLICANT: Lin et al., Hun-Chi
;   TITLE OF INVENTION: Molecular cloning of the genes
;   TITLE OF INVENTION: responsible for collagenase product
;   NUMBER OF SEQUENCES: 3
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Harris Brotman
;   STREET: 401 B. St Ste 1700
;   CITY: San Diego
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 92101-4297
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US93/05944
;   FILING DATE: 19930622
; CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Brotman, Harris P.
;   TELEPHONE: (619) 699-3630
;   TELEFAX: (619) 236-1046
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2817 base pairs
;   TYPE: NUCLEIC ACID
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
US-10-757-745-2_COPY_54_140 (1-87) x PCT-US93-05944-1 (1-2817)
QY 24 ThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThrAspSerThr 43
Db 2059 ACAGCTCAGAGAAAGCTTTACT---ATAGAAATAAAGACGAAGATACAAACACCTATA 2115
QY 44 ThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeu 63
Db 2116 ACTAAGAAATGGAACCTAATGATATATAAAGAGGCTAATGGTCCAATAGTTGAAGGT 2175
QY 64 IleThrTyrAsnIleAspGlyLeuAspLeuAsn 74
Db 2176 GTTACT-----GTAAAGGT---GATTTAAT 2199

RESULT 26
US-09-379-523-4
; Sequence 4, Application US/09379523
; Patent No. 6280993
; GENERAL INFORMATION:
;   APPLICANT: YAMATO, Ichiro
;   APPLICANT: HOSAKA, Toshiaki
;   TITLE OF INVENTION: GENE ENCODING CLASS I COLLAGENASE
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Burgess, Ryan and Wayne
;   STREET: 370 Lexington Avenue, Suite 2105
;   CITY: NEW YORK
;   STATE: NEW YORK
;   COUNTRY: UNITED STATES OF AMERICA
;   ZIP: 10017
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3 1/2 inch disk
;   COMPUTER: PC'S LIMITED SYSTEM 200
;   OPERATING SYSTEM: WINDOWS 98
;   SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/379,523
;   FILING DATE: August 24, 1999
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wayne, Milton J.
;   REGISTRATION NUMBER: 17,906
;   REFERENCE/DOCKET NUMBER: U-Wp-5462
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 212-683-8150
;   TELEFAX: 212-532-4285
;   TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 3356
;   TYPE: nucleotide
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: linear
US-09-379-523-4
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Alignment Scores:
Pred. No.: 27.9 Length: 3356
Score: 68.00 Matches: 17
Percent Similarity: 60.78% Conservative: 14
Best Local Similarity: 33.33% Mismatches: 16
Query Match: 15.18% Indels: 4
DB: 3 Gaps: 3

US-10-757-745-2_COPY_54_140 (1-87) x US-09-379-523-4 (1-3356)
Qy 24 ThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThrAspSerThr 43
Db 2605 ACAGCTACAGAAAGCTTTACT---ATAGAAATAAAGAACGAGATACACACACCTATA 2661
Qy 44 ThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeu 63
Db 2662 ACTAAGAATAAGGAACCTAATGATGATATATAAAGAGGCTAATGGTCCCAATAGTTGAAGGT 2721
Qy 64 IleThrTrpAsnIleAspGlyLeuAspLeuAsn 74
Db 2722 GTTACT-----GTAAGAGGT---GATTTAAAT 2745

RESULT 27
US-09-308-453-1
; Sequence 1, Application US/09308453
; Patent No. 6475764
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GMBH
; TITLE OF INVENTION: Recombinant collagenase type I from Clostridium histolyticum and
; FILE REFERENCE: BMID9924US
; CURRENT APPLICATION NUMBER: US/09/308,453
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4358
; TYPE: DNA
; ORGANISM: Clostridium histolyticum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1332)..(4358)
US-09-308-453-1

Alignment Scores:
Pred. No.: 40.1 Length: 4358
Score: 68.00 Matches: 17
Percent Similarity: 60.78% Conservative: 14
Best Local Similarity: 33.33% Mismatches: 16
Query Match: 15.18% Indels: 4
DB: 3 Gaps: 3

US-10-757-745-2_COPY_54_140 (1-87) x US-09-308-453-1 (1-4358)
Qy 24 ThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThrAspSerThr 43
Db 3606 ACAGCTACAGAAAGCTTTACT---ATAGAAATAAAGAACGAGATACACACACCTATA 3662
Qy 44 ThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeu 63
Db 3663 ACTAAGAATAAGGAACCTAATGATGATATATAAAGAGGCTAATGGTCCCAATAGTTGAAGGT 3722
Qy 64 IleThrTrpAsnIleAspGlyLeuAspLeuAsn 74
Db 3723 GTTACT-----GTAAGAGGT---GATTTAAAT 3746

RESULT 28
US-08-095-737-3
; Sequence 3, Application US/08095737
; Patent No. 5487979
; GENERAL INFORMATION:
; APPLICANT: DiFiore, Pier P
; APPLICANT: Fazioli, Francesca

; TITLE OF INVENTION: A Substrate for the Epidermal Growth
; TITLE OF INVENTION: Factor Receptor Kinase
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: United States of America
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/095,737
; FILING DATE: 19930722
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH060.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 111..2802
; US-08-095-737-3

Alignment Scores:
Pred. No.: 28.6 Length: 3033
Score: 67.50 Matches: 27
Percent Similarity: 37.50% Conservative: 12
Best Local Similarity: 25.96% Mismatches: 36
Query Match: 15.07% Indels: 29
DB: 2 Gaps: 4

US-10-757-745-2_COPY_54_140 (1-87) x US-08-095-737-3 (1-3033)
Qy 5 LeuAsnSerTyrPheGluPro---ProValGluGluSerAlaLeuGluArgArgProGlu 23
Db 2520 CTGAATGATCCATTTTCAGCCCTTTCCAGGCAATGATAGTCCCAAGAAAGAAAGATCCTGAT 2579
Qy 24 ThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThrAspSerThr 43
Db 2580 ATGTTTTGTGTATCCATTCATCTCTTCTACCACTACCAATAAAGAGGCTGACCCAGCAAT 2639
Qy 44 ThrSerIleSer-----ProSerGluAsp-----
Db 2640 TTTTGCTAACTTCAGTGTCTTATCCCTCTCTGAAGAAGATATGATTAATGGGCAAAAGGAA 2699
Qy 53 -----
Db 2700 AGTGAGCGGGGAAGAACACAGAGGCTTTCAGAGACTAAATCAGCAGGAGCAAGAGACTTG 2759
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAsnLeuSerGluArgAla 80
Db 2760 GAACCTGGCCATT-----GCACCTTAGCAAAATCTGAGATCTCAGAGCATGA 2804
Qy 81 ArgGlyValCys 84
Db 2805 AGAGTTATCTGT 2816
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RESULT 29
US-08-480-145-3
; Sequence 3, Application US/08480145
; Patent No. 5717067
; GENERAL INFORMATION:
; APPLICANT: DiFiore, Pier P
; APPLICANT: Fazioli, Francesca
; TITLE OF INVENTION: A Substrate for the Epidermal Growth
; TITLE OF INVENTION: Factor Receptor Kinase
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: United States of America
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,145
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/095,737
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH060.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 111..2802
;
US-08-480-145-3
Alignment Scores:
Pred. No.: 28.6 Length: 3033
Score: 67.50 Matches: 27
Percent Similarity: 37.50% Conservative: 12
Best Local Similarity: 25.96% Mismatches: 36
Query Match: 15.07% Indels: 29
DB: 2 Gaps: 4

US-10-757-745-2_COPY_54_140 (1-87) x US-08-480-145-3 (1-3033)
Qy 5 LeuAsnSerTyrPheGluPro---ProValGluSerAlaLeuGluArgProGlu 23
Db 2520 CTGAATGATCCATTTCCAGCTTTCCAGCAATGATAGTCCCAAGAAAAGATCCTGAT 2579
Qy 24 ThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrAspSerThr 43
Db 2580 ATGTTTGTGATCCATTCCTTCTTACCACTACCAATTAAGAGGCTGACCCAGCAAT 2639
Qy 44 ThrSerLysIleSer-----ProSerGluAsp----- 52
Db 2640 TTTCCTAACTTCAGTGTCTTATCCCTCTGAGAGAGATGATGATGAGCAAGGAA 2699

Qy 53 -----ThrGlnGlnGluAsnGlySerMet 60
Db 2700 AGTGAGCGGGAAGAAACAGAGGCTTGCACGACTAAATCAGCAGGACGAGCAAGACTTG 2759
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 2760 GAACTGGGCATT-----GCACCTTACCAATCTGAGATCTTCAGAGCATGA 2804
Qy 81 ArgGlyValCys 84
Db 2805 AGAGTATCTGT 2816

RESULT 30
US-08-477-389-3
; Sequence 3, Application US/08477389
; Patent No. 5872219
; GENERAL INFORMATION:
; APPLICANT: DiFiore, Pier P
; APPLICANT: Fazioli, Francesca
; TITLE OF INVENTION: A Substrate for the Epidermal Growth
; TITLE OF INVENTION: Factor Receptor Kinase
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, Sixteenth Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: United States of America
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,389
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/095,737
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH060.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3033 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 111..2802
;
US-08-477-389-3
Alignment Scores:
Pred. No.: 28.6 Length: 3033
Score: 67.50 Matches: 27
Percent Similarity: 37.50% Conservative: 12
Best Local Similarity: 25.96% Mismatches: 36
Query Match: 15.07% Indels: 29
DB: 2 Gaps: 4

US-10-757-745-2_COPY_54_140 (1-87) x US-08-477-389-3 (1-3033)
Qy 5 LeuAsnSerTyrPheGluPro---ProValGluSerAlaLeuGluArgProGlu 23
Db 2520 CTGAATGATCCATTTCCAGCTTTCCAGCAATGATAGTCCCAAGAAAAGATCCTGAT 2579
Qy 24 ThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrAspSerThr 43
Db 2580 ATGTTTGTGATCCATTCCTTCTTACCACTACCAATTAAGAGGCTGACCCAGCAAT 2639
Qy 44 ThrSerLysIleSer-----ProSerGluAsp----- 52
Db 2640 TTTCCTAACTTCAGTGTCTTATCCCTCTGAGAGAGATGATGATGAGCAAGGAA 2699
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```

Db      2520 CTGAATGATCCATTTTCAGCCTTTCCAGGCAATGATAGTCCCAAGAAAAAGATCCTGAT 2579
Qy      24  ThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThrAspSerThr 43
Db      2580 ATGTTTGTGATCCATTCACTTCTTCTACCACTACCAATAAAGAGGCTGACCCCAAGCAAT 2639
Qy      44  ThrSerLysIleSer-----ProSerGluAsp----- 52
Db      2640 TTTGCTAACTTCAGTGTCTTATCCCTCTGAGAAGATATGATTGAATGGGCAAAAAGGGAA 2699
Qy      53  -----ThrGlnGlnGluAsnGlySerMet 60
Db      2700 AGTGAGCGGGAGAGAACAGAGGCTTCCAGACTAAATCAGCAGGACCAAGAGACTTG 2759
Qy      61  PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db      2760 GAACTGGCCATT-----GCACCTTAGCAAATCTGAGATCTCAGNAGCATGA 2804
Qy      81  ArgGlyValCys 84
Db      2805 AGAGTTATCTGT 2816

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Search completed: December 4, 2005, 15:39:41
 Job time : 127.963 secs

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 4, 2005, 00:41:46 ; Search time 1849.19 Seconds
(without alignments)
2201.217 Million cell updates/sec

Title: US-10-757-745-2_COPY_54_140

Perfect score: 448

Sequence: 1 MERALNSYFPPVBSALER.....IDGLDNLNLSERARGVCSYL 87

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Command line parameters:

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-DB=EST -OPMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=500
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10757745 @CNG 1 1 8148 @runat_01122005_091749_10090 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: gb_est1:**
- 2: gb_est2:**
- 3: gb_est3:**
- 4: gb_hic:**
- 5: gb_est4:**
- 6: gb_est5:**
- 7: gb_est6:**
- 8: gb_est7:**
- 9: gb_gss1:**
- 10: gb_gss2:**
- 11: gb_gss3:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	448	100.0	429	BQ582059	ill2c11.y
2	448	100.0	471	CR543841	DKFZp4590
3	448	100.0	473	CB120234	K-EST0167
4	448	100.0	480	AI750554	cn04a01.y
5	448	100.0	485	AA486032	ab40b10.f
6	448	100.0	530	BM846221	K-EST0125
7	448	100.0	554	BP220985	BP220985

BP226620	BP226620	565	3	BP226620	448	100.0	565	3	BP226620
BP220508	BP220508	566	3	BP220508	448	100.0	566	3	BP220508
BP257211	BP257211	568	3	BP257211	448	100.0	568	3	BP257211
BP221518	BP221518	570	3	BP221518	448	100.0	570	3	BP221518
AU279894	AU279894	573	1	AU279894	448	100.0	573	1	AU279894
BP221260	BP221260	573	3	BP221260	448	100.0	573	3	BP221260
BP261500	BP261500	573	3	BP261500	448	100.0	573	3	BP261500
BP262642	BP262642	576	3	BP262642	448	100.0	576	3	BP262642
CN298919	17006001	577	7	CN298919	448	100.0	577	7	CN298919
BP274368	BP274368	580	3	BP274368	448	100.0	580	3	BP274368
BP207751	BP207751	581	3	BP207751	448	100.0	581	3	BP207751
BP225088	BP225088	581	3	BP225088	448	100.0	581	3	BP225088
BP262638	BP262638	581	3	BP262638	448	100.0	581	3	BP262638
BP270744	BP270744	581	3	BP270744	448	100.0	581	3	BP270744
BP379659	BP379659	581	3	BP379659	448	100.0	581	3	BP379659
BP219740	BP219740	582	3	BP219740	448	100.0	582	3	BP219740
BP261141	BP261141	582	3	BP261141	448	100.0	582	3	BP261141
BP270415	BP270415	582	3	BP270415	448	100.0	582	3	BP270415
BP275810	BP275810	582	3	BP275810	448	100.0	582	3	BP275810
BP195721	BP195721	583	3	BP195721	448	100.0	583	3	BP195721
BP262103	BP262103	583	3	BP262103	448	100.0	583	3	BP262103
BP262741	BP262741	583	3	BP262741	448	100.0	583	3	BP262741
BP319548	BP319548	583	3	BP319548	448	100.0	583	3	BP319548
BU783229	in01a08.y	583	5	BU783229	448	100.0	583	5	BU783229
BP263059	BP263059	584	3	BP263059	448	100.0	584	3	BP263059
BP348623	BP348623	584	3	BP348623	448	100.0	584	3	BP348623
BP236074	BP236074	588	3	BP236074	448	100.0	588	3	BP236074
AL703449	DKFZp686G	602	1	AL703449	448	100.0	602	1	AL703449
CB069952	ie3le10.y	621	6	CB069952	448	100.0	621	6	CB069952
CB157906	K-EST0217	634	6	CB157906	448	100.0	634	6	CB157906
CV023369	288 Full	634	7	CV023369	448	100.0	634	7	CV023369
BI333830	60299339	644	3	BI333830	448	100.0	644	3	BI333830
CR753214	DKFZp4691	652	7	CR753214	448	100.0	652	7	CR753214
CN298920	17006001	657	7	CN298920	448	100.0	657	7	CN298920
EG719113	602698045	678	2	EG719113	448	100.0	678	2	EG719113
BU661472	cl72d11.2	701	5	BU661472	448	100.0	701	5	BU661472
CN298922	170060000	719	7	CN298922	448	100.0	719	7	CN298922
CN298924	170004244	729	7	CN298924	448	100.0	729	7	CN298924
CX760857	AGENCOURT	731	8	CX760857	448	100.0	731	8	CX760857
BI258848	602969663	767	2	BI258848	448	100.0	767	2	BI258848
BI754101	603027659	774	3	BI754101	448	100.0	774	3	BI754101
BG719977	602691335	786	2	BG719977	448	100.0	786	2	BG719977
CX756424	AGENCOURT	799	8	CX756424	448	100.0	799	8	CX756424
CX166335	HESC2_39	810	8	CX166335	448	100.0	810	8	CX166335
BI908925	603067028	838	3	BI908925	448	100.0	838	3	BI908925
CR765451	DKFZp469E	846	7	CR765451	448	100.0	846	7	CR765451
BE784416	601473891	853	2	BE784416	448	100.0	853	2	BE784416
BI553412	603193358	858	3	BI553412	448	100.0	858	3	BI553412
BG740396	602634171	870	2	BG740396	448	100.0	870	2	BG740396
BU159911	AGENCOURT	870	5	BU159911	448	100.0	870	5	BU159911
BU169945	AGENCOURT	883	5	BU169945	448	100.0	883	5	BU169945
BU179107	AGENCOURT	906	6	BU179107	448	100.0	906	6	BU179107
CD251503	AGENCOURT	937	2	CD251503	448	100.0	937	2	CD251503
BI555333	AL555333	948	1	BI555333	448	100.0	948	1	BI555333
BI161201	602865659	959	2	BI161201	448	100.0	959	2	BI161201
BM468826	AGENCOURT	972	3	BM468826	448	100.0	972	3	BM468826
BI338160	603338160	981	5	BI338160	448	100.0	981	5	BI338160
BE892886	601435730	995	2	BE892886	448	100.0	995	2	BE892886
BI337141	60337141	1018	5	BI337141	448	100.0	1018	5	BI337141
BM554324	AGENCOURT	1035	3	BM554324	448	100.0	1035	3	BM554324
BI337905	60337905	1067	5	BI337905	448	100.0	1067	5	BI337905
BM555041	AGENCOURT	1089	11	BM555041	448	100.0	1089	11	BM555041
CR601303	full-leng	1103	3	CR601303	448	100.0	1103	3	CR601303
BM553049	AGENCOURT	1168	4	BM553049	448	100.0	1168	4	BM553049
CR592636	full-leng	1192	3	CR592636	448	100.0	1192	3	CR592636
CR597293	full-leng	1620	4	CR597293	448	100.0	1620	4	CR597293
CR595644	full-leng	1894	4	CR595644	448	100.0	1894	4	CR595644
AV717253	AV717253	1909	1	AV717253	445	99.3	1909	1	AV717253

81	444	99.1	582	3	BP234218	BP234218	BP234218	154	211.5	47.2	600	3	BI990829	BI990829	4081-88 M
82	443	98.9	582	3	BP233592	BP233592	BP233592	155	211.5	47.2	645	5	BY737520	BY737520	BY737520
83	440	98.2	572	3	BP262485	BP262485	BP262485	156	211.5	47.2	648	1	AW321603	AW321603	uo36606.Y
84	440	98.2	582	3	BP263516	BP263516	BP263516	157	211.5	47.2	691	3	BI648868	BI648868	303275826
85	440	98.2	626	2	BF977971	602148451	BF977971	158	211.5	47.2	767	8	CX226137	CX226137	MBM01355
86	440	98.2	942	5	BX358707	BX358707	BX358707	159	211.5	47.2	841	2	BF784792	BF784792	602111139
87	440	98.2	1046	3	BM926092	AGENCOURT	BM926092	160	211.5	47.2	942	2	BG298330	BG298330	602397112
88	440	98.2	1743	4	CR602029	full-16ng	CR602029	161	211.5	47.2	963	3	BI656151	BI656151	603283518
89	439	98.0	752	1	AU139147	AU139147	AU139147	162	211.5	47.2	1046	6	CA976386	CA976386	AGENCOURT
90	439	98.0	783	5	BX365835	BX365835	BX365835	163	210.5	47.0	615	6	CB577956	CB577956	AMGNNUC:N
91	438	97.8	739	7	CR791801	DKF2p468J	CR791801	164	210.5	47.0	627	6	CB577890	CB577890	AMGNNUC:N
92	437	97.5	310	8	T26956	11d155Droi	T26956	165	210.5	47.0	734	7	CV119018	CV119018	AGENCOURT
93	436	97.3	780	5	BX374579	BX374579	BX374579	166	206.5	46.1	639	6	CB545297	CB545297	AMGNNUC:N
94	435	97.1	580	3	BP261787	BP261787	BP261787	167	201	44.9	640	1	AL854676	AL854676	AL854676
95	433	96.7	704	2	BG119064	602347589	BG119064	168	201	44.9	842	8	CX958091	CX958091	JGI_CAAO9
96	432	96.4	704	3	BI334820	602998939	BI334820	169	201	44.9	866	8	CX843565	CX843565	JGI_CAAK1
97	431	96.2	581	3	BP199948	BP199948	BP199948	170	201	44.9	879	8	CX824886	CX824886	JGI_CAAK4
98	430	96.0	588	3	BP348796	BP348796	BP348796	171	199.5	44.5	712	2	BB609556	BB609556	BB609556
99	429	95.8	932	2	BG740339	602635289	BG740339	172	199	44.4	274	6	CD699206	CD699206	EST15729
100	429	95.8	1089	11	DQ049206	Pan.trog1	DQ049206	173	198.5	44.3	475	6	CB728877	CB728877	AMGNNUC:C
101	428	95.5	904	5	BX422491	BX422491	BX422491	174	195.5	43.6	703	5	BY719852	BY719852	BY719852
102	427	95.3	556	3	BP243301	BP243301	BP243301	175	194.5	43.4	600	2	BG800090	BG800090	2112-54 M
103	427	95.3	570	3	BM172060	imageqc_3	BM172060	176	193.5	43.2	621	2	BF182465	BF182465	601804232
104	421	94.0	584	3	BP274942	BP274942	BP274942	177	192	42.9	634	1	AL858410	AL858410	AL858410
105	421	94.0	757	3	BI760756	603044763	BI760756	178	192	42.9	638	1	AL901140	AL901140	AL901140
106	421	94.0	889	2	BG37046	602565130	BG37046	179	192	42.9	654	1	AL895081	AL895081	AL895081
107	415	92.6	581	3	BP264149	BP264149	BP264149	180	189	42.2	671	3	BU622975	BU622975	BU622975
108	415	92.6	1090	7	CN641671	ILLUMIGEN	CN641671	181	189	42.2	816	7	CK806777	CK806777	AGENCOURT
109	408	91.1	827	8	CV805216	AGENCOURT	CV805216	182	189	42.2	876	7	CK798287	CK798287	AGENCOURT
110	405.5	90.5	915	3	BI915865	603184527	BI915865	183	189	42.2	927	6	CA972607	CA972607	AGENCOURT
111	405	90.4	352	5	BQ787387	im09C09.Y	BQ787387	184	185	41.3	519	2	BB867803	BB867803	BB867803
112	401	89.5	922	7	CN801806	ILLUMIGEN	CN801806	185	184.5	41.2	425	6	CB696073	CB696073	AMGNNUC:N
113	400	89.3	347	5	BU070378	im09C09.X	BU070378	186	182.5	40.7	1289	4	AK009089	AK009089	Mus.muscu
114	389	86.8	793	2	BG533717	602562373	BG533717	187	181.5	40.5	718	4	CNS0ES51	CNS0ES51	Tetraodon
115	384	85.7	908	2	BG391213	602417244	BG391213	188	181	40.4	463	8	DN851694	DN851694	4147331 B
116	383	85.5	770	2	BG391295	602417344	BG391295	189	181	40.4	782	8	CX937111	CX937111	JGI_CAAO5
117	365	81.5	582	3	BM507091	ih24h01.Y	BM507091	190	179.5	40.1	736	5	BX306203	BX306203	BX306203
118	363	81.0	548	3	BF375391	BP375391	BP375391	191	179	40.0	444	10	AG204589	AG204589	Pan.trog1
119	361	80.6	816	1	AL516230	AL516230	AL516230	192	179	40.0	581	3	BI444674	BI444674	de27d10.Y
120	357	79.7	394	1	AV661333	AV661333	AV661333	193	179	40.0	688	2	BE189858	BE189858	db61e10.Y
121	338	75.4	325	8	T31666	EST36732.Hu	T31666	194	179	40.0	744	9	CE158280	CE158280	tigr-988-
122	331	73.9	674	7	CN791432	4126159.B	CN791432	195	179	40.0	750	8	CX135641	CX135641	AGENCOURT
123	329	73.4	388	1	AV659558	AV659558	AV659558	196	179	40.0	831	6	CA981008	CA981008	AGENCOURT
124	329	73.4	581	3	BP349936	BP349936	BP349936	197	179	40.0	879	7	CK797649	CK797649	AGENCOURT
125	327	73.0	467	6	CF788416	860364.MA	CF788416	198	179	40.0	896	6	CA971409	CA971409	AGENCOURT
126	327	73.0	798	8	DN122208	1122397.M	DN122208	199	179	40.0	909	6	CA982823	CA982823	AGENCOURT
127	325	72.5	648	6	CF764797	CES003181	CF764797	200	179	40.0	919	6	CA973696	CA973696	AGENCOURT
128	325	72.5	683	7	CN789157	4123581.B	CN789157	201	179	40.0	927	6	CA972288	CA972288	AGENCOURT
129	322	71.9	750	2	BI181461	UNL-P-FN-	BI181461	202	179	40.0	984	5	BX846715	BX846715	BX846715
130	321	71.7	378	1	AV655175	AV655175	AV655175	203	178.5	39.8	644	2	EG083167	EG083167	H3085C02-
131	312	69.6	368	2	BE694706	PMO-BT075	BE694706	204	177	39.5	992	9	CC216952	CC216952	CH261-110
132	312	69.6	581	6	CB286391	CMD36.CO9	CB286391	205	174	38.8	754	6	CD053018	CD053018	LITZHFO00
133	310	69.2	581	3	BP270589	BP270589	BP270589	206	174	38.8	842	6	DN597142	DN597142	AGENCOURT
134	310	69.2	952	5	BX433489	BX433489	BX433489	207	174	38.8	900	6	CA980929	CA980929	AGENCOURT
135	305	68.1	965	7	CN803230	ILLUMIGEN	CN803230	208	173	38.6	556	3	BM036121	BM036121	fu16b12.Y
136	298	66.5	365	7	CR767008	DKF7p469G	CR767008	209	173	38.6	644	3	BM860342	BM860342	fy36h04.Y
137	295	65.8	416	8	RI4990	YG45c11.r1	RI4990	210	173	38.6	699	1	AL722490	AL722490	AL722490
138	289.5	64.6	751	2	BF243327	601877278	BF243327	211	173	38.6	735	7	CK693033	CK693033	ZF101-P00
139	288	64.3	898	2	BG233866	602649018	BG233866	212	173	38.6	811	7	CV482470	CV482470	AGENCOURT
140	269	60.0	635	3	BM539358	BM539358	BM539358	213	173	38.6	834	7	CV482470	CV482470	AGENCOURT
141	229	51.1	409	2	BG900023	BM539358	BG900023	214	173	38.6	838	7	CV482470	CV482470	AGENCOURT
142	224	50.0	645	3	BM426270	pgf2n.pko	BM426270	215	173	38.6	846	7	CN175478	CN175478	AGENCOURT
143	221	49.3	1087	7	CN642527	ILLUMIGEN	CN642527	216	173	38.6	857	7	CN017421	CN017421	AGENCOURT
144	220	49.1	625	5	BU471395	603363114	BU471395	217	168.5	37.6	765	7	CN042095	CN042095	v11_p41_a
145	220	49.1	662	2	BI067773	pgfin.pko	BI067773	218	167	37.3	827	8	DN097147	DN097147	JGI_CABE7
146	219.5	49.0	946	5	BU468774	603371865	BU468774	219	165	36.8	491	1	AJ7681912	AJ7681912	AJ7681912
147	217.5	48.5	600	2	BI064472	pgfin.pko	BI064472	220	165	36.8	1236	8	DN716145	DN716145	CNB111-B0
148	217	48.4	577	9	BZ858137	CH240.232	BZ858137	221	164	36.6	544	1	AZ208842	AZ208842	mw73d02.r
149	213	47.5	549	1	AW669835	113421.MA	AW669835	222	162	36.2	666	7	CO050979	CO050979	Le_mx0.21
150	212.5	47.4	531	7	CN233559	RJA113F02	CN233559	223	160.5	35.8	641	2	BG977003	BG977003	602845553
151															

227	155	34.6	570	5	BU397611	603534313	BU397611	603534313	1	AL727624	AL727624
228	153.5	34.3	847	8	DR867246	JGI_CABG9	DR867246	JGI_CABG9	8	DR704222	Aen_04017
229	153	34.2	304	3	BEG19103	601472729	BEG19103	601472729	3	CN807482	HDAH03A07
230	153	34.2	312	3	EMI53209	TCHAP1Q14	EMI53209	TCHAP1Q14	3	BQ336306	PM1-MT014
231	153	34.2	480	6	CA777140	IP03F10.Y	CA777140	IP03F10.Y	6	BF140146	601786704
232	153	34.2	582	3	BP194502	BP194502	BP194502	BP194502	3	AA163045	mc28909.Y
233	153	34.2	685	7	CK981492	AL14013 B	CK981492	AL14013 B	7	CD509260	CDA93-D02
234	153	34.2	722	2	BF679649	602154095	BF679649	602154095	2	AJ398593	AJ398593
235	153	34.2	860	7	CO918949	AGENCOURT	CO918949	AGENCOURT	7	BY036773	BY036773
236	150.5	33.6	802	8	DN100293	JGI_CABE8	DN100293	JGI_CABE8	8	AJ458761	Thermotog
237	150.5	33.6	835	8	CK937110	JGI_CAA05	CK937110	JGI_CAA05	8	BI150788	602914879
238	149.5	33.4	456	1	AA839622	vw97e06.r	AA839622	vw97e06.r	1	DR946006	EST113754
239	148.5	33.1	757	10	BX198893	Danilo rer	BX198893	Danilo rer	10	BF992133	QV3-GN020
240	147.5	32.9	525	2	BE290901	601084205	BE290901	601084205	2	CV740501	SJAL_027
241	145.5	32.5	675	5	AL722584	AL722584	AL722584	AL722584	5	CV740501	SJAL_027
242	145.5	32.5	827	1	BQ443284	UI-M-EVO-	BQ443284	UI-M-EVO-	1	CV756544	ej16-010
243	145	32.4	537	7	CR774766	DKF2P469A	CR774766	DKF2P469A	7	AX863267	SJS_016_0
244	144	32.1	891	1	AL879624	AL879624	AL879624	AL879624	1	AY814979	SchiatoSo
245	144	32.1	909	5	BX780455	BX780455	BX780455	BX780455	5	BY028675	BY028675
246	143.5	32.0	799	1	AW199574	da05f07.Y	AW199574	da05f07.Y	1	CD321260	StrPus38.
247	140.5	31.4	672	11	DE094838	Oryzias 1	DE094838	Oryzias 1	11	CK682762	Yde05908.
248	140.5	31.4	894	5	BX776016	BX776016	BX776016	BX776016	5	BH207435	Sml-45M4.
249	137	30.6	563	8	DR003404	TC114160	DR003404	TC114160	8	BI789841	ic44b07.Y
250	136.5	30.5	352	6	BU235217	603791177	BU235217	603791177	6	BP262101	BP262101
251	136	30.4	1030	5	BG982031	MR3-CN014	BG982031	MR3-CN014	5	BF337260	602034615
252	134	29.9	237	2	BF170990	PCL1883 M	BF170990	PCL1883 M	2	BY101168	BY101168
253	131	29.2	860	8	CX958090	JGI_CAA09	CX958090	JGI_CAA09	8	AI208756	AI208756
254	127.5	28.5	808	8	DN932266	AGENCOURT	DN932266	AGENCOURT	8	BF893919	PM1-MT014
255	125	27.9	454	5	BG982031	MR3-CN014	BG982031	MR3-CN014	5	BI424242	eah67e02.
256	124.5	27.8	839	5	BX911124	BX911124	BX911124	BX911124	5	BM885374	sa199804.
257	124	27.7	623	1	AL725543	AL725543	AL725543	AL725543	1	CF712017	CCAF857TR
258	123.5	27.6	424	4	AK180792	MUS ruscu	AK180792	MUS ruscu	4	BF526774	602070322
259	123	27.6	760	5	BU204728	604152621	BU204728	604152621	5	AA982672	uh12a05.X
260	122	27.2	463	3	BF852284	MR3-EN008	BF852284	MR3-EN008	3	BE246685	uu25b12.Y
261	120	26.8	156	3	BQ331200	MR4-ET014	BQ331200	MR4-ET014	3	BP049364	BP049364
262	120	26.8	296	2	BF992136	QV3-GN020	BF992136	QV3-GN020	2	CF712017	CCAF857TR
263	120	26.8	422	2	BG982034	MR3-CN014	BG982034	MR3-CN014	2	AA536675	vj87h03.r
264	120	26.8	435	3	BQ332331	MR4-ET014	BQ332331	MR4-ET014	3	CU2905189	NAIstrap-
265	120	26.8	437	2	BF768820	PMO-IT001	BF768820	PMO-IT001	2	BU505745	AGENCOURT
266	120	26.8	440	2	BG982036	MR3-CN014	BG982036	MR3-CN014	2	CB209613	AGENCOURT
267	120	26.8	440	2	BF773259	PMO-IT001	BF773259	PMO-IT001	2	BI317492	sa66f606
268	120	26.8	453	2	BF773259	PMO-IT001	BF773259	PMO-IT001	2	CV246027	WS0111.B2
269	120	26.8	453	3	BQ315535	PMO-IT001	BQ315535	PMO-IT001	3	CV250470	WS0111.B2
270	120	26.8	456	2	BF986980	QV3-GN020	BF986980	QV3-GN020	2	CC477031	CH240_303
271	120	26.8	459	2	BG982034	MR3-CN014	BG982034	MR3-CN014	2	BI441344	ic52d10.Y
272	120	26.8	461	2	BG982012	MR3-CN020	BG982012	MR3-CN020	2	EQ852542	QCB18223.
273	120	26.8	579	2	BF997052	QV3-GN020	BF997052	QV3-GN020	2	BQ995001	QCB8M14.Y
274	119	26.6	247	2	BF768814	PMO-IT001	BF768814	PMO-IT001	2	DR950944	EST114248
275	119	26.6	460	2	BF893150	PM1-MT014	BF893150	PM1-MT014	2	CK863376	SJS_041.7
276	117	26.1	134	3	BJ061261	BU061261	BJ061261	BU061261	3	DR939601	EST113114
277	117	26.1	441	2	BF893925	PM1-MT014	BF893925	PM1-MT014	2	DR929708	EST112124
278	116.5	26.0	410	2	BG091909	mac18c11.	BG091909	mac18c11.	2	CR746747	CR746747
279	116.5	26.0	410	2	CC248786	KX529 Bay	CC248786	KX529 Bay	2	DT071039	AGENCOURT
280	116	25.9	574	3	BI345352	74149 MA	BI345352	74149 MA	3	CR17461	Tetraodon
281	116	25.9	640	6	CB505136	sealplnbs	CB505136	sealplnbs	6	CK100764	C079P13.5
282	115	25.7	463	2	BF852788	MR3-EN008	BF852788	MR3-EN008	2	BF891509	PM1-MT014
283	115	25.7	467	3	BQ329405	MR3-EN008	BQ329405	MR3-EN008	3	BU834029	T055F12 P
284	115	25.7	471	2	BF893924	PM1-MT014	BF893924	PM1-MT014	2	BU825565	UK110TD01
285	115	25.7	491	2	BI016235	MR4-ET014	BI016235	MR4-ET014	2	CH025685	TG8STyc8
286	112	25.0	458	3	BQ666782	QV3-GN020	BQ666782	QV3-GN020	3	BM691630	UI-E-C11-
287	109	24.3	431	3	CK695369	ZF101-P00	CK695369	ZF101-P00	3	CA394836	c657a06.Y
288	109	24.3	570	3	BF258309	BP258309	BF258309	BP258309	3	BM707845	UI-E-C11-
289	107	23.9	835	2	BF867245	JGI_CABG9	BF867245	JGI_CABG9	2	BQ340289	MR1-NN119
290	106	23.7	441	2	BF892415	PM1-MT014	BF892415	PM1-MT014	2	BF993341	MR2-GN012
291	104	23.2	153	2	BF992130	QV3-GN020	BF992130	QV3-GN020	2	CN312718	170004240
292	103.5	23.1	444	2	BF893187	PM1-MT014	BF893187	PM1-MT014	2	CF131579	UI-HF-FQ0
293	103	23.0	367	5	BY067359	BY067359	BY067359	BY067359	5	BQ639714	he19b10.Y
294	102	22.8	617	7	CN694288	E0348809-	CN694288	E0348809-	7	AL047251	DKF2P586B
295	101	22.5	680	7	CK952220	4091710 B	CK952220	4091710 B	7	CB188959	ks27D06.Y
296	100	22.3	935	11	CNS032UB	AL225311 Tetraodon	CNS032UB	AL225311 Tetraodon	11	AW247266	28200549.5
297	99.5	22.2	625	6	CB190354	pl2se10.Y	CB190354	pl2se10.Y	6	CN312708	170006001
298	98	21.9	382	5	BY070423	BY070423	BY070423	BY070423	5		
299	97	21.7	718	6	CB512714	sealrgb54	CB512714	sealrgb54	6		

AUTHORS
 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Searce, M., Brastelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, B., Wylie, T., Martin, J., Blisstein, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y., and Bowers, Y.

TITLE
 Endocrine Pancreas Consortium

JOURNAL
 Other_ESTS: il12c11.xl

COMMENT
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohpc.harvard.edu
 Library was constructed by Dr. J. Ferrer In vivo mass-excised to pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
 Seq primer: -40RP from Gibco.

FEATURES

source
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 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6029589"
 /tissue_type="insulinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="Human insulinoma"
 /note="Organ: pancreas; Vector: pBluescript SK-; Site 1: XhoI; Site 2: EcoRI; Constructed with lambda ZAPRI system (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to pBluescript SK- by Dr. H. Inoue following the Washington University protocol (http://genome.wustl.edu/est/lambda_protocol.shtml). Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permutt Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."

ORIGIN

Alignment Scores:
 Pred. No.: 5.92e-47 Length: 429
 Score: 448.00 Matches: 87
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BQ582059 (1-429)

Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
 Db 103 ATGGAAAGGGCTCTGAATCTCTACTTCGAGCCTCCGGTGGAGGAGCGCTTGGAAACGC 162
 Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAenGluThrThr 40
 Db 163 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTTACCAATGAAGAAACAAC 222
 Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAenGlySerMet 60
 Db 223 GATTCCACCACTTCTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGCATG 282
 Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAenAenLeuSerGluArgAla 80
 Db 283 TTCTCTCTCAATACCTGGAATATTGATGATTAGATCTAAACAATCTGTCTCAGAGAGGGCT 342
 Qy 81 ArgGlyValCysSerTyrLeu 87
 Db 343 CGAGGGGGTGTGTTCTCTACTTA 363

RESULT 2

CR543841

LOCUS

DEFINITION

DKFZp45900742_r1 459 (synonym: pcor1) Pongo pygmaeus cDNA clone

DKFZp45900742 5', mRNA sequence.

CR543841

VERSION

CR543841.1 GI:49895253

KEYWORDS

EST.

SOURCE

Pongo pygmaeus (orangutan)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Pongo.

REFERENCE

1 (bases 1 to 471)

AUTHORS

Bloeker, H., Boecker, M., Brandt, P., Mewes, H.W., Weil, B., Amid, C.,

Osanger, A., Fobos, G., Han, M. and Wiemann, S.

Pongo pygmaeus mRNA (Bloeker, H., Boecker, M., Brandt, P., et al.)

Unpublished (2004)

CONTACT: MIPS

JOURNAL

COMMENT

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert Clone from S. Wiemann,

Molecular Analysis, German Cancer Research Center (DKFZ);

Email s.wiemann@kfz-heidelberg.de; sequenced by GBF (National

Research Centre for Biotechnology Ltd., Braunschweig/Germany)

within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZp45900742) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further

information about the clone and the sequencing project is available

at http://mips.gsf.de/projects/cdna/.

FEATURES

source

1..471

Location/Qualifiers

/organism="Pongo pygmaeus"

/mol_type="mRNA"

/db_xref="taxon:9600"

/clone="DKFZp45900742"

/tissue_type="cortex"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="459 (synonym: pcor1)"

/notes="Vector: pSport1_Sfi; Site 1: SfiI; Site 2: SfiIb"

ORIGIN

Alignment Scores:

Pred. No.: 6.69e-47 Length: 471

Score: 448.00 Matches: 87

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CR543841 (1-471)

Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20

Db 161 ATGGAAAGGGCTCTGAATCTCTACTTCGAGCCTCCGGTGGAGGAGCGCTTGGAAACGC 220

Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAenGluThrThr 40

Db 221 CGCCCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTTACCAATGAAGAAACAAC 280

Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAenGlySerMet 60

Db 281 GATTCCACCACTTCTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGCATG 340

Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAenAenLeuSerGluArgAla 80

Db 341 TTCTCTCTCAATACCTGGAATATTGATGATTAGATCTAAACAATCTGTCTCAGAGAGGGCT 400

Qy 81 ArgGlyValCysSerTyrLeu 87

✓


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QY 61 PheSerLeuileThrTrpAsnileAapGlyLeuAapLeuAsnLeuSerGluArgAla 80
Db 334 TTTCTCTCATTACCTGGGAATATTGATGATTAGATCTAAACAATCTGTCTCAGAGGGCT 393

QY 81 ArgGlyValCysSerTyrLeu 87
Db 394 CGAGGGGTGTCTCTACTTA 414

RESULT 5
AA486032 485 bp mRNA linear EST 06-MAR-1998
LOCUS AB40b10.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone
DEFINITION IMAGE:843259 5', mRNA sequence.
ACCESSION AA486032
VERSION AA486032.1 GI:2216248
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 485)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kritzman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,P.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LML ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1913 Std Error: 0.00
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 444.
Location/Qualifiers
FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:843259"
/sex="female"
/dev stage="HeLa S3 cell line"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene HeLa cell s3 937216"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dt. HeLa S3
epithelioid carcinoma cells grown to semi-confluency
without induction. Average insert size: 1.5 kb; Uni-ZAP XR
vector. -5' adaptor sequence: 5' GAATTCGGACGAG 3' ~3'
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN
Alignment Scores: 6.95e-47 Length: 485
Pred. No.: 448.00 Matches: 87
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 1

US-10-757-745-2_COPY_54_140 (1-87) x AA486032 (1-485)

QY 1 MetGluArgAlaLeuAanSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 150 ATGGAAAGGGCTCTGAACTCTCTACTTCGAGCCTCCGGTGGAGGAGCGCTTGGAAACGC 209

QY 21 ArgProGluThrIleSerGluProValGluThrTyrValAspLeuThrAanGluGluThrThr 40

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Db 210 CGACCTGAAACCATCTCTGAGCCCAAGACCTATTGTTGACCTAACCAATGAAGAAACAAC 269
QY 41 AapSerThrThrSerIleSerProSerGluAapThrGlnGlnGlnGlnGlnGlnGlnGlnGln 60
Db 270 GATTCCACCACTTCTAAATATCAGCCCACTCTGAAGATCTCAGCAAGAAAATGGCAGCATG 329
QY 61 PheSerLeuileThrTrpAsnileAapGlyLeuAapLeuAsnLeuSerGluArgAla 80
Db 330 TTTCTCTCATTACCTGGGAATATTGATGATTAGATCTAAACAATCTGTCTCAGAGGGCT 389

QY 81 ArgGlyValCysSerTyrLeu 87
Db 390 CGAGGGGTGTGTCTCTACTTA 410

RESULT 6
BM846221 530 bp mRNA linear EST 06-MAR-2002
LOCUS K-EST0125204 S13KMS5 Homo sapiens cDNA clone S13KMS5-59-C04 5',
DEFINITION mRNA sequence.
ACCESSION BM846221
VERSION BM846221.1 GI:19202620
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 530)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 59 row: C column: 04
High quality sequence stop: 530.
Location/Qualifiers
FEATURES
Source
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/clone="S13KMS5-59-C04"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10P"
/clone_lib="S13KMS5"
/notes="Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly
(A)+ RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then decapped with tobacco acid
pyrophosphatase (TAP). The decapped intact mRNA was
ligated with DNA-RNA linker including EcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dt-selected mRNA by priming with
dt-tailed vector. The dt-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10P' by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."

ORIGIN
Alignment Scores: 7.81e-47 Length: 530
Pred. No.: 448.00 Matches: 87
Score:

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BM846221 (1-530)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
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Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 224 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAACAACACT 283

Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 284 GATTCCACCATCTCTAAATCAGCCATCTGAAGATACCTCAGCAAGAAAATGGCAGCATG 343

Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 344 TTCTCTCTCATACCTGGAATATTGATGGATTAGATCTAAACAATCTGTCTCAGAGAGGGCT 403

Qy 81 ArgGlyValCysSerTyrLeu 87
Db 404 CGAGGGGTGTGTTCTTACTTA 424

RESULT 7
BP220985 554 bp mRNA linear EST 15-SEP-2004
LOCUS BP220985 Sugano cDNA library, colon Homo sapiens cDNA clone
DEFINITION COL06450, mRNA sequence.
ACCESSION BP220985
VERSION BP220985.1 GI:52093890
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
AUTHORS Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

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/clone="COL06450"
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Pred. No.: 8,28e-47 Length: 554
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP220985 (1-554)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20

US-10-757-745-2_COPY_54_140 (1-87) x BP226620 (1-565)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
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Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 221 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAACAACACT 280

Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60

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Db 69 ATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCCGGTGGAGGAGCGCTTGGAAACGC 128
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 129 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAACAACACT 188
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 189 GATTCCACCATCTCTAAATCAGCCATCTGAAGATACCTCAGCAAGAAAATGGCAGCATG 248
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 249 TTCTCTCTCATACCTGGAATATTGATGGATTAGATCTTAACAATCTGTCTCAGAGAGGGCT 308
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 309 CGAGGGGTGTGTTCTTACTTA 329

RESULT 8
BP226620 565 bp mRNA linear EST 15-SEP-2004
LOCUS BP226620 Sugano cDNA library, dermoid cancer Homo sapiens cDNA
DEFINITION clone DMC03190, mRNA sequence.
ACCESSION BP226620
VERSION BP226620.1 GI:52099525
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
AUTHORS Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DMC03190"
/clone_lib="Sugano cDNA library, dermoid cancer"
/note="dermoid cancer"

ORIGIN
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Alignment Scores:
Pred. No.: 8,49e-47 Length: 565
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP226620 (1-565)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 161 ATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCCGGTGGAGGAGCGCTTGGAAACGC 220
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 221 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAACAACACT 280
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60

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Db 281 GATTCACCACTTCTAAATACGCCATCTGAGATACTCAGCAAGAAATGCGACGATG 340
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Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
|||||
Db 341 TTCTCTCTCAATACCTGGAATATTGATGGATTAGATCTAAACAATCTGTGAGAGGGCT 400
|||||
Qy 81 ArgGlyValCysSerTyrLeu 87
|||||
Db 401 CGAGGGGTGTGTTCTACTTAA 421
|||||

RESULT 9
BP220508
LOCUS
DEFINITION
BP220508 Sugano cDNA library, colon Homo sapiens cDNA clone
COL03160, mRNA sequence.

ACCESSION
BP220508
VERSION
BP220508.1 GI:52093413
KEYWORDS
EST.

SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 566)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

PUBMED
15342556
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

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/clone="COL03160"
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ORIGIN

Alignment Scores:
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB.: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP220508 (1-566)

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Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThr 40
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Db 139 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTGACCTTAACCAATGAAGAAACAACT 198
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Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
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Db 199 GATTCACCACTTCTAAATACGCCATCTGAAGATACTCAGCAAGAAATGGCAGCATG 258
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Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
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Qy 81 ArgGlyValCysSerTyrLeu 87
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Db 319 CGAGGGGTGTGTTCTACTTAA 339
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RESULT 10
BP257211
LOCUS

DEFINITION
BP257211 Sugano cDNA library, heart Homo sapiens cDNA clone
HRT00430, mRNA sequence.

ACCESSION
BP257211
VERSION
BP257211.1 GI:52172441
KEYWORDS
EST.

SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 568)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL
PUBMED
15342556
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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/db_xref="taxon:9606"
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Query Match: 100.00% Indels: 0
DB.: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP257211 (1-568)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluSerAlaLeuGluArg 20
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Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThr 40
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Db 190 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTGACCTTAACCAATGAAGAAACAACT 249
|||||

Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
|||||
Db 250 GATTCACCACTTCTAAATACGCCATCTGAAGATACTCAGCAAGAAATGGCAGCATG 309
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Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
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Qy 81 ArgGlyValCysSerTyrLeu 87
|||||
Db 370 CGAGGGGTGTGTTCTACTTAA 390
|||||

RESULT 11
BP221518
LOCUS

DEFINITION
BP221518 Sugano cDNA library, colon Homo sapiens cDNA clone
COL09203, mRNA sequence.

ACCESSION
BP221518
VERSION
BP221518.1 GI:52172441
KEYWORDS
EST.

SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 570)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL
PUBMED
15342556
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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/db_xref="taxon:9606"
/clone="HRT00430"
/tissue_type="heart"
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Score: 448.00 Matches: 87
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Query Match: 100.00% Indels: 0
DB.: 3 Gaps: 0

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Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThr 40
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Db 190 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTGACCTTAACCAATGAAGAAACAACT 249
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Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
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Db 250 GATTCACCACTTCTAAATACGCCATCTGAAGATACTCAGCAAGAAATGGCAGCATG 309
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Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
|||||
Db 310 TTCTCTCTCAATACCTGGAATATTGATGGATTAGATCTAAACAATCTGTGAGAGGGCT 369
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Qy 81 ArgGlyValCysSerTyrLeu 87
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Db 370 CGAGGGGTGTGTTCTACTTAA 390
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ACCESSION BP221518
VERSION BP221518.1 GI:52094423
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 570)
AUTHORS Suzuki,I., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES             Location/Qualifiers
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Pred. No.:      8,598-47      Length:      570
Score:          448.00      Matches:      87
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
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US-10-757-745-2_COPY_54_140 (1-87) x BP221518 (1-570)
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DB 68 ATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCGGTGGAGGAGCGCTTGGACGC 127
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
DB 128 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTGTGACCTAACCAATGAAGAACAACT 187
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnAsnGlySerMet 60
DB 188 GATTCACACATCTTAAATCAGCCCATCTGAGATCTCAGCAAGAAAATGGCAGCATG 247
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 248 TTCTCTCTCATTCACCTGGAATATTGATGATTAGATCTAAACAATCTGTCTCAGAGGGCT 307
QY 81 ArgGlyValCysSerTyrIleu 87
DB 308 CGAGGGGTGTGTTCTACTTAA 328

RESULT 12
LOCUS AU279894
DEFINITION AU279894 CHONS2 Homo sapiens cDNA clone CHONS2002038 5', mRNA
sequence.
ACCESSION AU279894
VERSION AU279894.1 GI:28299121
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

BP221518
BP221518.1 GI:52094423
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 570)
Suzuki,I., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
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/db_xref="taxon:9606"
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QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
DB 257 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTGTGACCTAACCAATGAAGAACAACT 316
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnAsnGlySerMet 60
DB 317 GATTCACACATCTTAAATCAGCCCATCTGAGATCTCAGCAAGAAAATGGCAGCATG 376
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 377 TTCTCTCTCATTCACCTGGAATATTGATGATTAGATCTAAACAATCTGTCTCAGAGGGCT 436
QY 81 ArgGlyValCysSerTyrLeu 87
DB 437 CGAGGGGTGTGTTCTACTTAA 457

RESULT 13
LOCUS BP221260
DEFINITION BP221260 Sugano cDNA library, colon Homo sapiens cDNA clone
COL08083, mRNA sequence.
ACCESSION BP221260
VERSION BP221260.1 GI:52094165
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

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REFERENCE
AUTHORS  Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
          Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE     Sequence comparison of human and mouse genes reveals a homologous
          block structure in the promoter regions
JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
PUBMED    15342556
COMMENT   Contact: Yutaka Suzuki
          Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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ORIGIN
Alignment Scores:
Pred. No.:      8,65e-47      Length:      573
Score:          448.00      Matches:      87
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             3           Gaps:          0

US-10-757-745-2_COPY_54_140 (1-87) x BP221260 (1-573)
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QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
   |||||
Db 142 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTGTGACCTAAACCAATGAAGAAACAAC 201
   |||||
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
   |||||
Db 202 GATTCACCACTTCTTAATACGCCATCTGAGATACTCAGCAAGAAATGCGCAGCATG 261
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QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
   |||||
Db 262 TTCTCTCTATTACCTGGATATTGATGGATTAGATCTAAACAATCTGTCTGAGAGGGCT 321
   |||||
QY 81 ArgGlyValCysSerTyrLeu 87
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Db 322 CGAGGGGTGTGTTCTCTACTTA 342
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RESULT 14
BP261500 573 bp mRNA linear EST 16-SEP-2004
LOCUS    BP261500 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION
clone HS103816, mRNA sequence.
ACCESSION BP261500
VERSION    BP261500.1 GI:52176731
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Homiidae; Homo.
REFERENCE 1 (bases 1 to 573)
AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
          Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE     Sequence comparison of human and mouse genes reveals a homologous
          block structure in the promoter regions
JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
PUBMED    15342556
COMMENT   Contact: Yutaka Suzuki
          Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source    Location/Qualifiers
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US-10-757-745-2_COPY_54_140 (1-87) x BP261500 (1-573)
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QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
   |||||
Db 126 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTGTGACCTAAACCAATGAAGAAACAAC 185
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QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
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Db 186 GATTCACCACTTCTTAATACGCCATCTGAGATACTCAGCAAGAAATGCGCAGCATG 245
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QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
   |||||
Db 246 TTCTCTCTATTACCTGGATATTGATGGATTAGATCTAAACAATCTGTCTGAGAGGGCT 305
   |||||
QY 81 ArgGlyValCysSerTyrLeu 87
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Db 306 CGAGGGGTGTGTTCTCTACTTA 326
   |||||

RESULT 15
BP262642 576 bp mRNA linear EST 16-SEP-2004
LOCUS    BP262642 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION
clone HS107584, mRNA sequence.
ACCESSION BP262642
VERSION    BP262642.1 GI:52177873
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Homiidae; Homo.
REFERENCE 1 (bases 1 to 576)
AUTHORS   Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
          Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE     Sequence comparison of human and mouse genes reveals a homologous
          block structure in the promoter regions
JOURNAL   Genome Res. 14 (9), 1711-1718 (2004)
PUBMED    15342556
COMMENT   Contact: Yutaka Suzuki
          Department of Virology
          Institute of Medical Science, University of Tokyo
          4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
          Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source    Location/Qualifiers
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Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
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US-10-757-745-2_COPY_54_140 (1-87) x BP274368 (1-580)

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QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
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QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
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 DB 300 GATTCACCACTTCTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAAATGCGACATG 359
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QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
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QY 81 ArgGlyValCysSerTyrLeu 87
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 DB 420 CGAGGGGTGTGTTCTTACTTA 440
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RESULT 18
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 LOCUS BP207751 581 bp mRNA linear EST 14-SEP-2004
 DEFINITION Homo sapiens cDNA library, coronary artery smooth muscle cell
 BP207751
 ACCESSION BP207751
 VERSION BP207751.1 GI:52064157
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1 (bases 1 to 581)
 AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 TITLE Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
 source
 1..581
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="CAS11735"
 /tissue_type="coronary artery"
 /cell_type="smooth muscle cell"
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 muscle cell"

ORIGIN
 Alignment Scores: 8.81e-47 Length: 581
 Pred. No.: 448.00 Matches: 87
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 100.00% Gaps: 0
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US-10-757-745-2_COPY_54_140 (1-87) x BP207751 (1-581)

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QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
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 DB 128 CGACCTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 187
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QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
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 DB 188 GATTCACCACTTCTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAAATGCGACATG 247
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QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
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 DB 248 TTCTCTCTCATTACCTGGAAATATTGATGGATTAGATCTAAACAATCTGTGAGAGAGGGCT 307
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QY 81 ArgGlyValCysSerTyrLeu 87
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 DB 308 CGAGGGGTGTGTTCTTACTTA 328
 |||||

RESULT 19
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 DEFINITION clone DAT05184, mRNA sequence.
 BP225088
 ACCESSION BP225088
 VERSION BP225088.1 GI:52097993
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1 (bases 1 to 581)
 AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 TITLE Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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 /clone="DAT05184"
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 /note="Burkitt's lymphoma"

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 Percent Similarity: 100.00% Mismatches: 0
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QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
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Qy 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGluAsnGlySerMet 60
Db 301 GATTCACCACTTCTAATCAGCCCACTGAGATCTCAGCAAGAAATGGCAGCATG 360
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
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Qy 81 ArgGlyValCysSerTyrLeu 87
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RESULT 20
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LOCUS BP262638 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION clone HS107576, mRNA sequence.
ACCESSION BP262638
VERSION BP262638.1 GI:52177869
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 581)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
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/clone="HS107576"
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/clone_lib="Sugano cDNA library, small intestine"
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Pred. No.: 8,81e-47 Length: 581
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Qy 21 ArgProGluThrIleSerGluProIlyThrTyrValAspLeuThrAsnGluThrThr 40
Db 137 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTGACCAACAAATGAAGAACT 196
Qy 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGluAsnGlySerMet 60
Db 197 GATTCACCACTTCTAATCAGCCCACTGAGATCTCAGCAAGAAATGGCAGCATG 256
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
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Db 257 TTCTCTCTCATTCCTGAATATTGATGATTAGATCTAAACAATCTCTCAGAGAGGCT 316
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 317 CGAGGGGTGTGTCTCTACTTA 337

RESULT 21
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LOCUS BP270744 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION clone KAR05146, mRNA sequence.
ACCESSION BP270744
VERSION BP270744.1 GI:52220093
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 581)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
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Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Db 128 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTGACCAACAAATGAAGAACT 187
Qy 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGluAsnGlySerMet 60
Db 188 GATTCACCACTTCTAATCAGCCCACTGAGATCTCAGCAAGAAATGGCAGCATG 247
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 248 TTCTCTCTCATTCCTGAATATTGATGATTAGATCTAAACAATCTCTCAGAGAGGCT 307
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 308 CGAGGGGTGTGTCTCTACTTA 328

RESULT 22
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JOURNAL
PUBMED
COMMENT
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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/db_xref="taxon:9606"
/clone="HS102506"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

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Alignment Scores:
Pred. No.: 8.83e-47 Length: 582
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

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Db 126 CGACCTGAACCATCTCTGAGCCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACT 185
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
|||||
Db 186 GATTCACCACTTCTAAATCAGCCCATCTGAAGATATCTCAGCAAGAAAATGGCAGCATG 245
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Db 246 TTCTCTCTCAATACCTCGAATATTGATGATTAGATCTAAACATCTCTCAGAGAGGGCT 305
Qy 81 ArgGlyValCysSerTyrLeu 87
|||||
Db 306 CGAGGGGTGTGTTCTACTTA 326

RESULT 25
BP270415
LOCUS
DEFINITION
BP270415 Sugano cDNA library, small intestine Homo sapiens cDNA
clone KAR02166, mRNA sequence.

ACCESSION
BP270415
VERSION
BP270415.1 GI:52219764
KEYWORDS
EST.
SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo

REFERENCE
AUTHORS
1 (bases 1 to 582)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions

JOURNAL
PUBMED
COMMENT
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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/mol_type="mRNA"
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Alignment Scores:
Pred. No.: 8.83e-47 Length: 582
Score: 448.00 Matches: 87
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-757-745-2_COPY_54_140 (1-87) x BP270415 (1-582)

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Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
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Db 218 CGACCTGAACCATCTCTGAGCCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACT 277
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Db 278 GATTCACCACTTCTAAATCAGCCCATCTGAAGATATCTCAGCAAGAAAATGGCAGCATG 337
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Qy 81 ArgGlyValCysSerTyrLeu 87
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Db 398 CGAGGGGTGTGTTCTACTTA 418

RESULT 26

BP275810

LOCUS

DEFINITION

BP275810 Sugano cDNA library, kidney Homo sapiens cDNA clone

KDN04583, mRNA sequence.

ACCESSION

BP275810

VERSION

BP275810.1 GI:52189542

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo

REFERENCE

AUTHORS

1 (bases 1 to 582)

Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,

Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

15342556

Contact: Yutaka Suzuki

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Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

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Location/Qualifiers

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Score: 448.00 Matches: 87
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Best Local Similarity: 100.00% Mismatches: 0
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DB 209 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACA 268
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 269 GATTCACCACTTCTAAATCAGCCCATCTGAGATCTAGATCTAGCAAGAAATGCGACATG 328
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 329 TTCTCTCTCATTACCTGGGAATATTGATGATTAGATCTAAACAATCTGTGAGAGGGCT 388
QY 81 ArgGlyValCysSerTyrLeu 87
DB 389 CGAGGGGTGTGTTCTACTTA 409
RESULT 27
BP195721 583 bp mRNA linear EST 14-SEP-2004
LOCUS BP195721 Sugano cDNA library, brain Homo sapiens cDNA clone
DEFINITION ADB08961, mRNA sequence.
ACCESSION BP195721
VERSION BP195721.1 GI:52039998
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 583)
AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
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Location/Qualifiers
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/clone="ADB08961"
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Alignment Scores:
Pred. No.: 8.85e-47 Length: 583
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Query Match: 100.00% Indels: 0
US-10-757-745-2_COPY_54_140 (1-87) x BP275810 (1-582)
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DB 94 ATGGAAGGGCTCTGAACCTCTTCTGAGCCTCCGGTGAGGAGGCGCCTTGGACGC 153
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Alignment Scores:
Pred. No.: 8.85e-47 Length: 583
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservativeness: 0
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Qy 41 AspSerThrThrSerIlySerProSerGluAspThrGlnGlnAsnGlySerMet 60
Db 214 GATTCACCACTTCTAAATCAGCCATCTGAAGTACTCAGCAAGAAAATGGCAGCATG 273

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Qy 81 ArgGlyValCysSerTyrLeu 87
Db 334 CGAGGGGTGTGTTCTACTTA 354

RESULT 29
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DEFINITION BP262741 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS107919, mRNA sequence.
ACCESSION BP262741
VERSION BP262741.1 GI:52177972
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 583)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp.
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US-10-757-745-2_COPY_54_140 (1-87) x BP262741 (1-583)

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Qy 41 AspSerThrThrSerIlySerProSerGluAspThrGlnGlnAsnGlySerMet 60
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Qy 81 ArgGlyValCysSerTyrLeu 87
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RESULT 30
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DEFINITION BP319548 Sugano cDNA library, pericardium Homo sapiens cDNA
clone PCD1128, mRNA sequence.
ACCESSION BP319548
VERSION BP319548.1 GI:52248523
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 583)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp.
FEATURES
source
1..583
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="PCD1128"
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Alignment Scores:
Pred. No.: 8,85e-47 Length: 583
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP319548 (1-583)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
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Qy 21 ArgProGluThrIleSerGluProIlyThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 269 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACAATGAAGAACAAC 328

Qy 41 AspSerThrThrSerIlySerProSerGluAspThrGlnGlnAsnGlySerMet 60
Db 329 GATTCACCACTTCTAAATCAGCCATCTGAAGTACTCAGCAAGAAAATGGCAGCATG 388

Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 389 TTCTCTCTCAATACCTGGAATATTGATGGATTAGATCTAAACAATCTGTCTCAGAGGGCT 448

Qy 81 ArgGlyValCysSerTyrLeu 87
Db 449 CGAGGGGTGTGTTCTACTTA 469
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 3, 2005, 23:33:41 ; Search time 270.055 Seconds
(without alignments)
2147.074 Million cell updates/sec

Title: US-10-757-745-2_COPY_54_140

Perfect score: 448

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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

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- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	448	100.0	483	2	AAAX40590
2	448	100.0	1296	3	AAC98160 Human col
3	448	100.0	1920	3	AAZ47118 Human CD4
4	448	100.0	1936	10	AD019013 Human dis

5	448	100.0	1936	13	ADP25361
6	448	100.0	1940	14	ADP06356
7	448	100.0	1948	4	AAI58997
8	448	100.0	1948	5	ADQ99219
9	448	100.0	1948	9	ABE48979
10	448	100.0	1958	4	AAI60783
11	448	100.0	2499	2	AAAX28153
12	448	100.0	3152	9	ADA10970
13	-439	98.0	752	4	AAH08073
14	439	98.0	1898	4	AAH15146
c 15	414	92.4	391	11	ADT95307
c 16	414	92.4	391	11	ADT95307
c 17	332.5	74.2	1227	5	AAH41789
18	211.5	47.2	1312	3	AAZ47119
19	178.5	39.8	602	10	ADD34376
20	114	25.4	725	6	ABQ34465
c 21	114	25.4	725	6	ABQ34465
c 22	113	25.2	258	2	AAAX1008
23	101	22.5	60	6	ABN41860
24	84.5	18.9	1589	5	AAH87500
25	84.5	18.9	2228	5	AAH87499
c 26	84.5	18.9	2717	5	AAH82908
c 27	84.5	18.9	4002	5	AAH75995
c 28	84.5	18.9	4890	5	AAH87489
29	84.5	18.9	6448	5	AAH82911
30	84.5	18.9	7197	5	AAH87485
c 31	84.5	18.9	7556	5	AAH82893
c 32	84.5	18.9	7731	5	AAH87486
33	84.5	18.9	11742	5	AAH87514
34	84.5	18.9	12036	5	AAH75996
35	84.5	18.9	23157	5	AAH75998
36	84.5	18.9	32313	5	AAH82912
37	83	18.5	6115	10	ADF90711
38	83	18.5	37741	14	ABE47090
c 39	81.5	18.2	826	10	ADD34445
40	81.5	18.2	3321	3	AAC81290
41	81.5	18.2	6763	3	AAC81309
c 42	79	17.6	1473	6	AD41820
c 43	79	17.6	1703	8	ABZ80231
c 44	79	17.6	2456	13	ADP07759
c 45	79	17.6	3558	12	ADQ67469
c 46	78	17.4	480	6	ABQ55431
47	78	17.4	1142	9	ADA24517
48	78	17.4	3672	10	ABZ77286
49	78	17.4	3672	13	ADR24529
50	78	17.4	3672	14	ADY61760
51	78	17.4	4180	13	ACN37824
52	78	17.4	4194	10	AAI60051
53	78	17.4	4750	2	AAZ41297
54	78	17.4	5511	8	ABX77514
55	78	17.4	5511	8	ABX63285
56	78	17.4	5511	9	ACH04033
57	78	17.4	5511	10	ADJ56346
c 58	78	17.4	6115	10	ADF90711
59	78	17.4	6316	12	ADP07274
60	78	17.4	6316	12	ADP07323
61	77	17.2	894	6	ABQ34415
c 62	77	17.2	894	6	ABQ34415
63	75.5	16.9	10506	8	ABQ52973
64	75.5	16.9	10506	12	ADP09724
65	75.5	16.9	10506	13	ADQ96719
66	75.5	16.9	10506	13	ADT91343
67	75.5	16.9	10617	8	AAU52982
68	75.5	16.9	10617	12	ADP09737
69	75.5	16.9	10617	13	ADQ96732
70	75.5	16.9	10617	13	ADT91356
71	75	16.7	2601	12	ADQ08623
c 72	74	16.5	2488	4	AAE57111
c 73	74	16.5	2490	5	AAE73107
c 74	74	16.5	2547	4	AAE58469
c 75	74	16.5	5996	4	AAE58468
76	73.5	16.4	893	3	AAE58808
77	73.5	16.4	5713	14	ADW14324

c	78	72	16.1	1339	6	ABQ34020	Abq34020 Oligonucl	c	151	68.5	15.3	6698	6	ABL32856	Ab132856 Human imm
	79	72	16.1	1339	6	ABQ34021	Abq34021 Oligonucl		152	68.5	15.3	305107	4	AAH62689	Aah62689 Shrimp wh
	80	72	16.1	2555	4	ABL24680	Ab124680 Drosophil		153	68	15.2	692	6	ABQ52465	Abq52465 Oligonucl
	81	72	16.1	3748	4	ABL110964	Ab1110964 Drosophil	c	154	68	15.2	692	6	ABQ52464	Abq52464 Oligonucl
	82	72	16.1	4964	13	ADS48480	Ads48480 Bacterial		155	68	15.2	1467	12	ADO30254	Ado30254 Mouse GPC
	83	71.5	16.0	822	6	ABN67632	Abn67632 Streptoco		156	68	15.2	2229	4	ABL06985	Ab106985 Drosophil
	84	71.5	16.0	921	6	ABK95351	Abk95351 DNA encod		157	68	15.2	2796	4	AAS51941	Aas51941 Staphyloc
	85	71.5	16.0	4320	4	ABL06555	Ab106555 Drosophil		158	68	15.2	2799	4	AAS44703	Aas44703 Staphyloc
c	86	71.5	16.0	139613	13	ABD32606	Abd32606 Mouse can		159	68	15.2	2817	2	AAQ54844	Aas54844 Collagena
	87	71	15.8	725	6	ABQ34462	Abq34462 Oligonucl	c	160	68	15.2	3356	5	AAH47748	Aah47748 C. histol
c	88	71	15.8	725	6	ABQ34463	Abq34463 Oligonucl		161	68	15.2	4291	4	ABL06984	Ab106984 Drosophil
c	89	71	15.8	24459	14	ACL68541	Acl68541 M. xanthu		162	68	15.2	4358	2	AAV35415	Aav35415 C. histol
	90	71	15.8	32241	14	ACL64784	Acl64784 M. xanthu		163	68	15.2	5914	10	ADG73655	Adg73655 C. histol
c	91	71	15.8	110000	6	ABA03041_10	Continuation (11 o		164	68	15.2	144179	11	ACN44388	Actn44388 Mouse gen
c	92	70.5	15.7	1772	13	ADT19616	Adt19616 Plant cDN		165	67.5	15.1	522	12	ACH72860	Ach72860 Human gen
	93	70.5	15.7	6012	10	ABX06685	Abx06685 S. pneumo		166	67.5	15.1	699	8	ABT18269	Abt18269 Aspergill
	94	70.5	15.7	6012	12	ADM91930	Adm91930 S. pneumon		167	67.5	15.1	659	8	ABT18863	Abt18863 Aspergill
	95	70.5	15.7	6012	13	ADT49970	Adt49970 S. pneumon		168	67.5	15.1	1599	8	ABT20683	Abt20683 Aspergill
	96	70.5	15.7	6014	3	ADU48333	Adu48333 Streptoco		169	67.5	15.1	1656	8	ABT20085	Abt20085 Aspergill
c	97	70.5	15.7	15213	2	AAV52159	Aav52159 Streptoco		170	67.5	15.1	1857	8	ABT14864	Abt14864 Pathogen
	98	70.5	15.7	110000	10	ABS56454_09	Continuation (10 o		171	67.5	15.1	1857	8	ACF74277	Acf74277 Staphyloc
	99	70	15.6	835	2	AAV27370	Aav27370 Streptoco		172	67.5	15.1	1886	3	AAC35974	Aac35974 Arabidops
	100	70	15.6	835	6	ABQ84838	Abq84838 S. pneumo		173	67.5	15.1	2019	13	ADS50827	AdS50827 Bacterial
	101	70	15.6	835	10	ADC45174	Adc45174 S. pneumo		174	67.5	15.1	2310	5	ADM19563	Adm19563 Novel hum
	102	70	15.6	1714	2	RAV27324	Rav27324 Streptoco	c	175	67.5	15.1	2319	4	ABL22773	Ab122773 Drosophil
	103	70	15.6	1714	6	ABQ84793	Abq84793 S. pneumo		176	67.5	15.1	2361	8	ADA89881	Ada89881 Staphyloc
	104	70	15.6	1714	10	ADC45084	Adc45084 S. pneumo		177	67.5	15.1	2583	5	ADM19268	Adm19268 Novel hum
	105	70	15.6	2450	4	ABL229977	Ab1229977 Drosophil		178	67.5	15.1	2699	8	ABT17675	Abt17675 Aspergill
	106	70	15.6	3532	10	ADE15671	Adel5671 Human str		179	67.5	15.1	3033	2	AAV16484	Aat16484 cDNA enco
	107	70	15.6	3640	6	RA599915	Ras99915 Polynucle		180	67.5	15.1	3033	2	AAV13999	Aav13999 Murine ep
	108	70	15.6	3640	12	ADL13159	Adl13159 Human ste		181	67.5	15.1	3033	2	AAV04192	Aax04192 Murine ep
	109	70	15.6	3875	13	ADR24178	Adr24178 Breast ca		182	67.5	15.1	3522	13	ADU25445	Adu25445 cDNA enco
	110	70	15.6	3950	14	AEA19702	Aea19702 Novel hum		183	67.5	15.1	3594	8	ACC80945	Acc80945 Human nil
	111	70	15.6	4058	14	AEA19701	Aea19701 Novel hum		184	67.5	15.1	3656	8	ABT19489	Abt19489 Aspergill
	112	70	15.6	4061	4	AAI58478	Aai58478 Human pol		185	67.5	15.1	5340	4	ABL22772	Ab122772 Drosophil
	113	70	15.6	4061	5	ADQ98693	Adq98693 DNA encod	c	186	67.5	15.1	9623	2	AAV74477	Aav74477 Staphyloc
	114	70	15.6	4061	9	ADB48453	Adb48453 Novel hum		187	67	15.0	337	6	RAI90336	Rai90336 Human pol
	115	70	15.6	4150	4	AAK51922	Aak51922 Human pol		188	67	15.0	610	6	ABK30252	Abk30252 Human G-p
c	116	70	15.6	4176	4	AAK52905	Aak52905 Human pol		189	67	15.0	693	13	ADR62879	Adr62879 Cotton cd
c	117	70	15.6	4176	4	AAK52906	Aak52906 Human pol		190	67	15.0	756	12	ADP98597	Adp98597 C. albica
c	118	70	15.6	4176	4	AAI60264	Aai60264 Human pol		191	67	15.0	761	4	AAK73882	Aak73882 Human imm
c	119	70	15.6	4176	14	AEA20688	Aea20688 Novel hum		192	67	15.0	1059	12	ACH89475	Ach89475 Human gen
c	120	70	15.6	4176	14	AEA20689	Aea20689 Novel hum		193	67	15.0	1392	12	ADP05796	Adp05796 Mouse nuc
	121	70	15.6	4231	5	RA587070	Ras87070 DNA encod		194	67	15.0	1488	2	AAQ45960	Aaq45960 mRXR-gamm
	122	70	15.6	4258	4	AAK51921	Aak51921 Human pol		195	67	15.0	1488	12	ADF91837	Adf91837 Mouse rec
	123	70	15.6	5048	14	ADX07700	Adx07700 Cyclin-de		196	67	15.0	1506	13	ADT19451	Adt19451 Plant cDN
	124	70	15.6	5077	14	ADZ49482	Adz49482 Insulin s		197	67	15.0	1518	2	AAV01870	Aav01870 Human bra
c	125	70	15.6	110000	12	ADN46845_04	Continuation (5 of		198	67	15.0	1518	8	ACC69961	Acc69961 Human bra
	126	70	15.6	110000	12	ADN47591_16	Continuation (17 o		199	67	15.0	1518	13	ADQ76499	Adq76499 Nucleotid
c	127	70	15.6	110000	12	ADN46123_04	Continuation (5 of		200	67	15.0	1662	2	AAQ13388	Aaq13388 Mouse RXR
	128	70	15.6	110000	12	ADN47209_16	Continuation (17 o		201	67	15.0	1963	4	ABA26693	AbA26693 Probe #51
c	129	70	15.6	110000	12	ADN46464_04	Continuation (5 of		202	67	15.0	2634	14	ADY15399	Ady15399 DNA enco
	130	70	15.6	110000	12	ADN47960_16	Continuation (17 o		203	67	15.0	2636	2	AAV01871	Aav01871 Human bra
	131	69.5	15.5	871	6	ABQ45309	Abq45309 Oligonucl		204	67	15.0	2636	8	ACC69962	Acc69962 Human bra
c	132	69.5	15.5	871	6	ABQ45308	Abq45308 Oligonucl		205	67	15.0	2636	13	ADQ76500	Adq76500 Nucleotid
	133	69.5	15.5	2845	12	ADG73843	Adg73843 Candida c	c	206	67	15.0	4031	2	AAV69717	Aav69717 Tumour re
	134	69.5	15.5	3998	4	AAH29827	Aah29827 S cerevis	c	207	67	15.0	4031	8	ABX93690	Abx93690 Human tum
	135	69.5	15.5	25569	14	ADV97728	Adv97728 cDNA sequ	c	208	67	15.0	4031	10	ADG18038	Adg18038 MAGE-A1 p
	136	69	15.4	231	10	ADF01095	Adf01095 Bacterial	c	209	67	15.0	4031	11	ADM33160	Adm33160 Human MAG
	137	69	15.4	291	2	AAV44907	Aat44907 Partial s	c	210	67	15.0	4031	12	ADI79393	Adi79393 Human MAG
	138	69	15.4	645	6	ABQ45229	Abq45229 Oligonucl	c	211	67	15.0	4225	2	AAV69720	Aav69720 Tumour re
c	139	69	15.4	645	6	ABQ45228	Abq45228 Oligonucl		212	67	15.0	4225	8	ABX33697	Abx33697 cDNA enco
	140	69	15.4	1049	13	ADX46456	Adx46456 Plant ful	c	213	67	15.0	4225	10	ADG18027	Adg18027 MAGE-C1 p
	141	69	15.4	2720	1	AAH81657	Aan81657 HVT TK ge	c	214	67	15.0	4225	11	ADM33109	Adm33109 Human MAG
	142	68.5	15.3	438	6	ABL94194	Ab194194 Arabidops	c	215	67	15.0	4225	12	ADI79401	Adi79401 Human MAG
	143	68.5	15.3	894	4	AAH62767	Aah62767 Shrimp wh	c	216	67	15.0	4265	3	AAZ36149	Aaz36149 DNA enco
	144	68.5	15.3	1185	13	ADV95365	Adv95365 cDNA enco	c	217	67	15.0	4265	5	AAS88353	Aas88353 DNA enco
c	145	68.5	15.3	1215	5	AAF27964	Aaf27964 Arabidops		218	67	15.0	4265	12	ADJ54129	Adj54129 Human CT7
	146	68.5	15.3	1342	3	AAC38000	Aac38000 Arabidops	c	219	67	15.0	4265	12	ADM68725	Adm68725 Human MAG
	147	68.5	15.3	1383	2	AAQ03809	Aaq03809 Thymidine	c	220	67	15.0	4265	14	ADV85852	Adv85852 Human CT7
	148	68.5	15.3	1915	3	AAC48203	Aac48203 Arabidops	c	221	67	15.0	4720	8	ABX95023	Abx95023 DNA enco
	149	68.5	15.3	3505	2	AAQ03818	Aaq03818 Turkey he	c	222	67	15.0	6471	10	ADP25517	Adp25517 Binding d
c	150	68.5	15.3	3587	13	ADT14743	Adt14743 Plant cDN		223	67	15.0	7636	4	AAK73881	Aak73881 Human imm

c 224	67	15.0	7806	5	AA588354	Aaa88354 DNA encod	c 297	65.5	14.6	791	6	ABQ68801	Abq68801 Listeria
c 225	67	15.0	8577	4	ABL28667	Abi28667 Drosophi	c 298	65.5	14.6	855	4	AAH03785	Aah03785 Human cDN
c 226	67	15.0	9295	4	ABL02495	Abi02495 Drosophi	c 299	65.5	14.6	1085	6	ABQ15084	Abq15084 Oligonuc
c 227	67	15.0	12294	4	ABL28666	Abi28666 Drosophi	c 300	65.5	14.6	1085	6	ABQ15085	Abq15085 Oligonuc
c 228	67	15.0	21230	11	ACN44248	Actn44248 Mouse gen	c 301	65.5	14.6	1137	8	ABQ49999	Abq49999 Rice gene
c 229	67	15.0	21314	4	ABL02494	Abi02494 Drosophi	c 302	65.5	14.6	1235	6	ABQ70433	Abq70433 Listeria
c 230	67	15.0	110000	6	ABQ69245_10	Continuation (11 o	c 303	65.5	14.6	1317	10	ADH85267	Adh85267 Enterococ
c 231	67	15.0	110000	6	ABQ67197_09	Continuation (10 o	c 304	65.5	14.6	1368	12	ADH79616	Adh79616 Glyphosat
c 232	66.5	14.8	468	5	AA564306	Aaa64306 DNA encod	c 305	65.5	14.6	1377	2	AAQ27201	Aaq27201 CP4-EPSPS
c 233	66.5	14.8	468	14	AEA20510	Aea20510 Novel hum	c 306	65.5	14.6	1377	2	AAQ23531	Aaq23531 Synthetic
c 234	66.5	14.8	468	14	AEA20509	Aea20509 Novel hum	c 307	65.5	14.6	1377	2	AAQ23531	Aaq23531 Synthetic
c 235	66.5	14.8	488	10	ADB57301	Adb57301 Toxicity-	c 308	65.5	14.6	1377	2	AAV77314	Aav77314 EPSPS DNA
c 236	66.5	14.8	550	6	ABQ34842	Abq34842 Oligonuc	c 309	65.5	14.6	1377	2	AAV58013	Aav58013 Synthetic
c 237	66.5	14.8	550	6	ABQ34843	Abq34843 Oligonuc	c 310	65.5	14.6	1377	2	AAV58013	Aav58013 Synthetic
c 238	66.5	14.8	1950	5	AA581702	Aaa81702 DNA encod	c 311	65.5	14.6	1377	2	AAO09719	Aao09719 CP4-EPSPS
c 239	66.5	14.8	1950	5	AA580755	Aaa80755 DNA encod	c 312	65.5	14.6	1377	10	AAO09757	Aao09757 Agrobacte
c 240	66.5	14.8	3119	2	AAX06981	Aax06981 Candida a	c 313	65.5	14.6	1701	14	ADZ72262	Adz72262 Plasmodi
c 241	66.5	14.8	8561	2	AAX06982	Aax06982 Candida a	c 314	65.5	14.6	1730	5	AAZ52316	Aaz52316 DNA encod
c 242	66.5	14.8	110000	6	ABA03041_01	Continuation (2 of	c 315	65.5	14.6	1829	3	AAZ52449	Aaz52449 HTRM clon
c 243	66	14.7	581	6	ABQ40107	Abq40107 Oligonuc	c 316	65.5	14.6	2082	4	AAH13844	Aah13844 Human cDN
c 244	66	14.7	581	6	ABQ40106	Abq40106 Oligonuc	c 317	65.5	14.6	2198	12	ADN35055	Adn35055 HAND1 gen
c 245	66	14.7	603	6	ABQ13694	Abq13694 Oligonuc	c 318	65.5	14.6	2211	14	ADV16324	Adv16324 E. faecal
c 246	66	14.7	603	6	ABQ13695	Abq13695 Oligonuc	c 319	65.5	14.6	2820	11	ADJ11533	Adj11533 Rice DNA
c 247	66	14.7	609	6	ABQ35356	Abq35356 Oligonuc	c 320	65.5	14.6	3156	5	ADL45783	Adl45783 Human ova
c 248	66	14.7	609	6	ABQ35357	Abq35357 Oligonuc	c 321	65.5	14.6	3486	12	ADN04169	Adn04169 Antipsoi
c 249	66	14.7	674	13	ADO82968	Ado82968 Plant ful	c 322	65.5	14.6	3486	13	ADP23894	Adp23894 PRO polyp
c 250	66	14.7	801	2	AAX98246	Aax98246 Nucleotid	c 323	65.5	14.6	3486	14	ADY15603	Ady15603 DNA encod
c 251	66	14.7	823	4	AAI97371	Aai97371 Human neu	c 324	65.5	14.6	5362	12	ADQ64397	Adq64397 Novel hum
c 252	66	14.7	870	6	ABK31754	Abk31754 DNA encod	c 325	65.5	14.6	8012	2	AAV57305	Aav57305 Sugar bee
c 253	66	14.7	891	11	ABD14835	Abd14835 Pseudomon	c 326	65.5	14.6	8160	6	AAH13096	Aah13096 Enterococ
c 254	66	14.7	1139	5	AAV54950	Aav54950 Nucleotid	c 327	65.5	14.6	8160	6	ABV57309	Abv57309 Sugar bee
c 255	66	14.7	1139	5	AAV54949	Aav54949 Nucleotid	c 328	65.5	14.6	8418	2	AAV57309	Abv57309 Sugar bee
c 256	66	14.7	1139	6	ABV54952	Abv54952 Coat prot	c 329	65.5	14.6	8798	2	AAV57309	Abv57309 Sugar bee
c 257	66	14.7	1139	6	ABV54953	Abv54953 Coat prot	c 330	65.5	14.6	8798	2	AAV57309	Abv57309 Sugar bee
c 258	66	14.7	1229	3	AAV47405	Aav47405 Arabidops	c 331	65.5	14.6	10846	6	ABV54336	Abv54336 Vector co
c 259	66	14.7	1275	11	ABD15034	Abd15034 Pseudomon	c 332	65.5	14.6	10847	2	AAV54337	Aav54337 E. coli f
c 260	66	14.7	1314	4	AAH43489	Aah43489 Clone 333	c 333	65.5	14.6	10900	2	AAV54337	Aav54337 E. coli f
c 261	66	14.7	1386	4	AAO09542	Aao09542 Human pro	c 334	65.5	14.6	12860	6	ABV54337	Abv54337 E. coli f
c 262	66	14.7	1418	13	ACN38517	Actn38517 Tumour-as	c 335	65.5	14.6	12860	6	ABV54337	Abv54337 E. coli f
c 263	66	14.7	1632	6	ABZ11415	Abz11415 Human pol	c 336	65.5	14.6	12860	6	ABV54337	Abv54337 E. coli f
c 264	66	14.7	1632	12	ADM43933	Adm43933 Novel hum	c 337	65.5	14.6	110000	6	ABV54337	Abv54337 E. coli f
c 265	66	14.7	1685	13	ADK54458	Adk54458 Plant ful	c 338	65.5	14.6	110000	11	ADM27081_12	Adm27081_12
c 266	66	14.7	1701	4	AAH43488	Aah43488 Clone 333	c 339	65	14.5	204	12	ADP94883	Adp94883 Cotton ex
c 267	66	14.7	1875	8	ACA23900	Acta23900 Prokaryot	c 340	65	14.5	387	10	ABX07151	Abx07151 S. pneumo
c 268	66	14.7	2032	2	AAV10117	Aav10117 Drosophi	c 341	65	14.5	387	13	ADT50022	Adt50022 S. pneumo
c 269	66	14.7	2032	6	ABV53745	Abv53745 cDNA encod	c 342	65	14.5	390	3	AAA05409	Aaa05409 Streptoco
c 270	66	14.7	2032	6	ABV53745	Abv53745 cDNA encod	c 343	65	14.5	455	9	ACH25223	Ach25223 Human adu
c 271	66	14.7	2048	2	AAV98244	Aav98244 Contig 13	c 344	65	14.5	834	4	ABL26751	Abi26751 Drosophi
c 272	66	14.7	2352	6	ABK31751	Abk31751 DNA encod	c 345	65	14.5	1024	3	AAA93421	Aaa93421 DNA encod
c 273	66	14.7	2442	10	ADH63038	Adh63038 Human 333	c 346	65	14.5	1024	3	AAV27621	Aav27621 Projectio
c 274	66	14.7	2445	4	AAH43491	Aah43491 Clone 333	c 347	65	14.5	1024	6	ABV27361	Abv27361 DNA encod
c 275	66	14.7	2470	4	ABA77002	Abat77002 Rat TRDH-	c 348	65	14.5	1079	14	ABV29280	Abv29280 Streptoco
c 276	66	14.7	2736	4	AAH43490	Aah43490 Clone 333	c 349	65	14.5	1102	6	ABQ29280	Abq29280 S. pneumo
c 277	66	14.7	2736	10	ADH63036	Adh63036 Human 333	c 350	65	14.5	1102	6	ABQ29280	Abq29280 S. pneumo
c 278	66	14.7	3566	14	ADW78770	Adw78770 Human bil	c 351	65	14.5	1102	6	ABQ29280	Abq29280 S. pneumo
c 279	66	14.7	4008	14	ADW78772	Adw78772 Human var	c 352	65	14.5	1102	6	ABQ29280	Abq29280 S. pneumo
c 280	66	14.7	4068	14	ADW78776	Adw78776 Human var	c 353	65	14.5	1102	6	ABQ29280	Abq29280 S. pneumo
c 281	66	14.7	4776	3	AAZ94744	Aaz94744 Human ATP	c 354	65	14.5	1102	6	ABQ29280	Abq29280 S. pneumo
c 282	66	14.7	5329	3	AAH88900	Aah88900 Mouse lam	c 355	65	14.5	1102	6	ABQ29280	Abq29280 S. pneumo
c 283	66	14.7	5329	3	AAH88900	Aah88900 Mouse lam	c 356	65	14.5	1102	6	ABQ29280	Abq29280 S. pneumo
c 284	66	14.7	5329	3	AAH88900	Aah88900 Mouse lam	c 357	65	14.5	1102	6	ABQ29280	Abq29280 S. pneumo
c 285	66	14.7	5689	3	AAH88900	Aah88900 Mouse lam	c 358	65	14.5	1102	6	ABQ29280	Abq29280 S. pneumo
c 286	66	14.7	5689	3	AAH88900	Aah88900 Mouse lam	c 359	65	14.5	1102	6	ABQ29280	Abq29280 S. pneumo
c 287	66	14.7	5689	3	AAH88900	Aah88900 Mouse lam	c 360	65	14.5	1102	6	ABQ29280	Abq29280 S. pneumo
c 288	66	14.7	6115	12	ADQ25499	Adq25499 Human sof	c 361	65	14.5	1139	6	ABV64049	Abv64049 Coat prot
c 289	66	14.7	154504	12	ADQ59431	Adq59431 Human can	c 362	65	14.5	1139	6	ABV64049	Abv64049 Coat prot
c 290	66	14.7	154504	14	ADZ13732	Adz13732 Murine ca	c 363	65	14.5	1139	6	ABV64049	Abv64049 Coat prot
c 291	65.5	14.6	707	6	ABQ13716	Abq13716 Oligonuc	c 364	65	14.5	1139	6	ABV64049	Abv64049 Coat prot
c 292	65.5	14.6	707	6	ABQ13717	Abq13717 Oligonuc	c 365	65	14.5	1164	9	ADB08110	Adb08110 Allolococ
c 293	65.5	14.6	740	6	ABQ17065	Abq17065 Oligonuc	c 366	65	14.5	1164	9	ADB08111	Adb08111 Allolococ
c 294	65.5	14.6	740	6	ABQ17064	Abq17064 Oligonuc	c 367	65	14.5	1164	9	ADB08111	Adb08111 Allolococ
c 295	65.5	14.6	741	6	ABQ39175	Abq39175 Oligonuc	c 368	65	14.5	1164	9	ADB08113	Adb08113 Allolococ
c 296	65.5	14.6	741	6	ABQ39174	Abq39174 Oligonuc	c 369	65	14.5	1192	6	ABK47579	Abk47579 cDNA enco

370	65	14.5	1392	10	ABZ23624	Abz23624 RXR gamma	443	64.5	14.4	1696	6	ABQ84900	Abq84900 S. pneumo
371	65	14.5	1392	12	ADJ92825	Adj92825 Human ret	444	64.5	14.4	1696	10	ADC45298	Adc45298 S. pneumo
372	65	14.5	1392	12	ADP05794	Adp05794 Human nuc	445	64.5	14.4	1722	14	ACL63769	Ac163769 M. xanthu
373	65	14.5	1450	13	ADS50354	Ads50354 Bacterial	446	64.5	14.4	1848	5	AAS90056	Aas90056 DNA encod
374	65	14.5	1497	5	AAS71271	Aas71271 DNA encod	447	64.5	14.4	1913	10	ADS61876	Ads61876 Human gen
375	65	14.5	1507	10	ADD30687	Add30687 Plant yie	448	64.5	14.4	1913	10	ADD48886	Add48886 Human gen
376	65	14.5	1507	12	ADI43536	Adi43536 Plant tra	449	64.5	14.4	1913	10	ADD47834	Add47834 Human gen
377	65	14.5	1507	12	ADO03364	Ado03364 Thalecres	450	64.5	14.4	1930	6	ABQ70440	Abq70440 Listeria
378	65	14.5	1507	14	AEA26766	Aea26766 Stress to	451	64.5	14.4	2065	5	AAS73478	Aas73478 DNA encod
379	65	14.5	1594	2	RAT35787	Rat35787 Human ret	452	64.5	14.4	2148	8	ACA22475	Aca22475 Prokaryot
380	65	14.5	1594	6	ABL67525	Ab167525 Thyroid c	453	64.5	14.4	2304	10	ADF02011	Adf02011 Bacterial
381	65	14.5	1594	10	ACA56461	Aca56461 Human sig	c 454	64.5	14.4	2834	4	AAK73215	Aak73215 Human imm
382	65	14.5	1594	12	ADI56257	Adi56257 Human pol	c 455	64.5	14.4	2834	4	AAK73218	Aak73218 Human imm
383	65	14.5	1698	10	ADC22171	Adc22171 Subcellul	456	64.5	14.4	3159	4	ABL26017	Ab126017 Drosophil
384	65	14.5	1730	14	AEA81158	Aea81158 Human ret	c 457	64.5	14.4	3209	4	ABL23572	Ab123572 Drosophil
385	65	14.5	1742	10	ACC72852	Acc72852 Human can	458	64.5	14.4	3930	12	ADO30970	Ado30970 Human Pol
386	65	14.5	1827	9	ACF36094	Acf36094 Human RXR	459	64.5	14.4	3930	13	ADS46913	Ads46913 Bacterial
387	65	14.5	1827	9	ACF04420	Acf04420 Human ret	460	64.5	14.4	5292	12	ADM78417	Adm78417 Newcastle
388	65	14.5	1841	6	AAS94767	Aas94767 Human DNA	c 461	64.5	14.4	5409	4	ABL26016	Ab126016 Drosophil
389	65	14.5	1841	10	ADJ56361	Adj56361 Murine cD	462	64.5	14.4	5643	10	ABX06330	Abx06330 S. pneumo
390	65	14.5	1841	13	ADX31153	Adx31153 Plant ful	463	64.5	14.4	5643	12	ADM91882	Adm91882 S.pneumon
391	65	14.5	1861	13	ACN11688	Acn11688 Human dia	464	64.5	14.4	5646	13	ADT49957	Adt49957 S.pneumon
392	65	14.5	2342	13	ADX65234	Adx65234 Plant ful	465	64.5	14.4	5646	3	AAZ29882	Aaz29882 Streptoco
393	65	14.5	2439	3	AAA93353	Aaa93353 EYFP-DEVD	466	64.5	14.4	8298	4	ABL20832	Ab120832 Drosophil
394	65	14.5	2439	3	AAA93352	Aaa93352 EYFP-DEVD	467	64.5	14.4	8673	4	ABL20834	Ab120834 Drosophil
395	65	14.5	2439	3	AAA27628	Aaa27628 DNA encod	468	64.5	14.4	12319	4	ABL17720	Ab117720 Drosophil
396	65	14.5	2439	3	AAA27629	Aaa27629 DNA encod	469	64.5	14.4	12319	4	ABL20830	Ab120830 Drosophil
397	65	14.5	2439	6	ABS71471	Abs71471 DNA encod	c 470	64.5	14.4	13926	2	AAV52138	Aav52138 Streptoco
398	65	14.5	2439	6	ABS71470	Abs71470 DNA encod	471	64.5	14.4	27845	4	ABL20591	Ab120591 Drosophil
399	65	14.5	2834	4	ABL26750	Ab126750 Drosophil	472	64.5	14.4	48718	4	ABL20590	Ab120590 Drosophil
400	65	14.5	3112	2	AAV52249	Aav52249 Streptoco	473	64.5	14.4	63284	4	ABL20688	Ab120688 Drosophil
401	65	14.5	3171	3	AAA93366	Aaa93366 NLS-EYFP-	474	64.5	14.4	71962	4	ABL19340	Ab119340 Drosophil
402	65	14.5	3171	3	AAA27642	Aaa27642 DNA encod	c 475	64.5	14.4	73100	14	ADZ42280	Adz42280 Human end
403	65	14.5	3171	6	ABS71484	Abs71484 DNA encod	476	64.5	14.4	101000	14	ADZ42285_3	Adz42285 Human end
404	65	14.5	3378	3	AAA93425	Aaa93425 DNA encod	477	64.5	14.4	109906	6	ABK94411	Abk94411 DNA encod
405	65	14.5	3378	3	AAA27626	Aaa27626 Microtubu	478	64.5	14.4	109906	12	ADL08112	Adl08112 Human gen
406	65	14.5	3378	6	ABS71544	Abs71544 DNA encod	479	64.5	14.4	110000	10	ABS56454_05	Ab56454 Human gen
407	65	14.5	3378	10	ADC18463	Adc18463 DNA encod	480	64.5	14.4	129297	14	AEA61179	Aea61179 Human FBR
408	65	14.5	4833	3	AAA93361	Aaa93361 EYFP-DEVD	481	64.5	14.4	149062	13	ABD32608	Abd32608 Human can
409	65	14.5	4833	3	AAA27637	Aaa27637 DNA encod	482	64	14.3	453	6	ABV96665	Abv96665 Human pan
410	65	14.5	4833	6	ABS71479	Abs71479 DNA encod	c 483	64	14.3	517	13	ACN55430	Acn55430 Cotton an
411	65	14.5	4872	4	ABL30025	Ab130025 Drosophil	484	64	14.3	548	5	ABV60832	Abv60832 Human pro
412	65	14.5	6082	13	ADT66711	Adt66711 Murine mi	c 485	64	14.3	600	6	ABQ23596	Abq23596 Oligonucl
413	65	14.5	7319	6	ABL34044	Ab134044 Human imm	486	64	14.3	600	6	ABQ23597	Abq23597 Oligonucl
414	65	14.5	20158	4	AAK82721	Aak82721 Human imm	487	64	14.3	602	13	ACN54301	Acn54301 Cotton an
415	65	14.5	110000	9	ABE12064_05	Continuation (6 of	488	64	14.3	610	13	ACN62448	Acn62448 Cotton de
416	65	14.5	110000	10	ABS56454_12	Continuation (13 o	c 489	64	14.3	656	6	ABT09986	Abt09986 Human bre
417	65	14.5	110000	14	AEA24401_26	Continuation (27 o	490	64	14.3	665	13	ADR63243	Adr63243 Cotton cd
418	65	14.5	123526	10	ADJ79962	Adj79962 Human gli	491	64	14.3	703	6	ABQ33581	Abq33581 Oligonucl
419	64.5	14.4	401	4	AAK96722	Aak96722 Human neu	c 492	64	14.3	703	6	ABQ33580	Abq33580 Oligonucl
420	64.5	14.4	401	4	AAK98215	Aak98215 Human neu	c 493	64	14.3	975	5	AAH68088	Aah68088 C glutami
421	64.5	14.4	401	6	ABT01492	Abt01492 Human neu	c 494	64	14.3	1098	4	AAK71208	Aak71208 Corynebac
422	64.5	14.4	401	6	ABT02985	Abt02985 Human neu	c 495	64	14.3	1118	6	ABQ45160	Abq45160 Oligonucl
423	64.5	14.4	401	12	ADH77747	Adh77747 Human neu	496	64	14.3	1118	6	ABQ45161	Abq45161 Oligonucl
424	64.5	14.4	411	6	ABN24908	Abn24908 Human ORF	497	64	14.3	1299	6	ABQ21861	Abq21861 Oligonucl
425	64.5	14.4	467	3	AAH30957	Aah30957 Human col	c 498	64	14.3	1299	6	ABQ21860	Abq21860 Oligonucl
426	64.5	14.4	567	13	ACN49207	Acn49207 Cotton pr	c 499	64	14.3	1331	13	ADT17925	Adt17925 Plant cdN
427	64.5	14.4	576	13	ADS62942	Ads62942 Bacterial	c 500	64	14.3	1371	13	ADR63305	Adr63305 Cotton cd
428	64.5	14.4	598	13	ADS62789	Ads62789 Bacterial							
429	64.5	14.4	676	6	ABQ71153	Abq71153 Listeria							
430	64.5	14.4	683	3	AAF14705	Aaf14705 Aspergill							
431	64.5	14.4	683	13	ADU58746	Adu58746 Aspergill							
432	64.5	14.4	683	14	ADZ96749	Adz96749 Aspergill							
433	64.5	14.4	775	2	AAV27368	Aav27368 streptoco							
434	64.5	14.4	775	6	ABQ84836	Abq84836 S. pneumo	XX						
435	64.5	14.4	775	10	ADC45170	Adc45170 S. pneumo	XX						
436	64.5	14.4	898	13	ADT18397	Adt18397 plant cDN	XX						
437	64.5	14.4	946	6	ABQ31330	Abq31330 Oligonucl	DT						
438	64.5	14.4	946	6	ABQ31331	Abq31331 Oligonucl	XX						
439	64.5	14.4	1117	13	ADS59765	Ads59765 Bacterial	XX						
440	64.5	14.4	1209	4	ABL23573	Ab123573 Drosophil	DE						
441	64.5	14.4	1689	14	ACL69557	Ac169557 M. xanthu	XX						
442	64.5	14.4	1696	2	AAV27432	Aav27432 Streptoco	KW						

ALIGNMENTS

RESULT 1

AAK40590
ID AAK40590 standard; cDNA; 483 BP.

XX AAK40590;

XX DT 18-JUN-1999 (first entry)

XX DE Human secreted protein 5' EST SEQ ID No: 190.

XX KW Human; secreted protein; EST; expressed sequence tag; diagnosis;

KW forensic; gene therapy; chromosome mapping; signal peptide; prostate;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition; db.
XX
XX Homo sapiens.
OS
XX WO9906550-A2.
PN
XX
XX 11-FEB-1999.
PD
XX
XX 31-JUL-1998; 98WO-IB001232.
PF
XX
XX 01-AUG-1997; 97US-00905144.
PR
XX
XX (GEST) GENSET.
PA
XX Dumas Milne Edwards J, Duclert A, Lacroix B;
PI
XX WPI; 1999-153780/13.
XX P-PSDB; AAV11868.
DR
XX
XX New isolated prostate-derived nucleic acids - used to develop products
PT which may have cytokine, immune regulatory, haematopoiesis regulating,
PT anti-inflammatory or tumour inhibition activity.
PT
XX
XX Claim 1; Page 298; 675pp; English.
PS
XX
XX AAX04038 to AAX40715 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins expressed in prostate, and encode the proteins
CC given in AAY11716 to AAY1193 respectively. The proteins given represent
CC the signal peptide and an N-terminal fragment of a secreted protein. The
CC nucleic acid sequences can be used for producing secreted human gene
CC products. They can also be used to develop products for diagnosis and
CC therapy. The proteins obtained may have cytokine activity, cell
CC proliferation and differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptides can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell
XX
XX Sequence 483 BP; 123 A; 111 C; 139 G; 110 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 4.22e-51 Length: 483
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AAX40590 (1-483)

Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 160 ATGGAAGGGCTCTGAACCTCTACTTCCAGCCCTCCGGTGGAGAGGGCGCTTGGACGC 219

Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAenGluThrThr 40
Db 220 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 279

Qy 41 AspSerThrThrSerIysIleSerProSerGluAspThrGlnGlnGluAenGlySerMet 60
Db 280 GATTCCACCACTTCTAAATTCAGCCCATCTGGAAGATACTCAGCAAGAAATGCGCAGATG 339

Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAenAsnLeuSerGluArgAla 80
|||||

Db 340 TTCTCTCTCTATTACTCTGGAATATTGATGGATTAGATCTTAACAATCTCTCAGAGGGCT 399
Qy 81 ArgGlyValCysSerTyrLeu 87
|||||
Db 400 CGAGGGGTGTCTTCTACTTA 420

RESULT 2
AAC98160
ID AAC98160 standard; cDNA; 1296 BP.
XX
AC AAC98160;
XX
XX 09-MAR-2001 (first entry)
XX
XX Human colon cancer antigen nucleotide sequence SEQ ID NO:170.
XX
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW identification; cytostatic; cardioactive; neuroprotective; vulnary;
KW immunomodulatory; muscular; gynaecological; gastrointestinal;
KW nephrotropic; antinefactive; antibacterial; gene therapy; wound;
KW neural disorder; immune system disorder; muscular disorder;
KW reproductive disorder; gastrointestinal disorder; renal disorder;
KW infectious disease; cardiovascular disorder; ss.
XX
XX Homo sapiens.
OS
XX WO200055351-A1.
PN
XX
XX 21-SEP-2000.
PD
XX
XX 08-MAR-2000; 2000WO-US005883.
PF
XX
XX 12-MAR-1999; 99US-0124270P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Ruben SM;
PI
XX WPI; 2000-587534/55.
DR P-PSDB; AAB53403.
DR
XX
XX Colon cancer associated gene sequences, referred to as colon cancer
PT antigens, useful for the treatment, prevention, and diagnosis of colon
PT disorders such as colon cancer.
XX
XX Claim 1; Page 597; 2104pp; English.
XX
XX AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC called human colon cancer antigens, given in AAB53334 to AAB54006. The
CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
CC vulnary, nephrotropic, antinefactive and antibacterial activities, and
CC can be used in gene therapy. The colon cancer antigen polynucleotides,
CC proteins and antibodies to the proteins are useful for the prevention,
CC treatment and diagnosis of colon disorders, such as colon cancer. The
CC polynucleotides may be used in diagnostics and research, such as for
CC chromosome identification, and as hybridisation probes. The proteins may
CC also be used to prevent diseases such as neural disorders, immune system
CC disorders, muscular disorders, reproductive disorders, gastrointestinal
CC disorders, wounds, renal disorders, infectious diseases, and
CC cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent
CC sequences used in the exemplification of the present invention
XX
XX Sequence 1296 BP; 376 A; 250 C; 326 G; 333 T; 0 U; 11 Other;
SQ

Alignment Scores:
Pred. No.: 1.57e-50 Length: 1296
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AAC98160 (1-1296)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 183 ATGGAAGGGCTCTGAACCTCTACTTCGAGGCTCGGTGGAGAGCGCTTGGAAACGC 242
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 243 CGACCTGAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAACCT 302
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 303 GATTCCACCACTTCTAAAATCAGCCATCTCAAGATACTCAGCAAGAAAATGGCAGCATG 362
QY 61 PheSerIleuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 363 TTCTCTCTCAVTACCTGGAATATTGATGATTAGATTCTAAACAATCTGTCTAGAGGGCT 422
QY 81 ArgGlyValCysSerTyrLeu 87
Db 423 CGAGGGGTGTCTCTACTTTA 443

RESULT 3

ID AAZ47118
XX AAZ47118 standard; cDNA; 1920 BP.

AC AAZ47118;

DT 15-MAR-2000 (first entry)

DE Human CD40 receptor associated protein gene.

KW Antiarteriosclerotic; antiarthritic; neuroprotective; dermatological;
KW immunosuppressive; antiinflammatory; immunosuppressive; antiallergic;
KW human; CD40 receptor associated protein; CRAP; cytoplasmic domain;
KW tumor necrosis factor; TNF; receptor; superfamily; CD30; homology;
KW TNF receptor associated factor; TRAP; modulator; signalling pathway;
KW diagnosis; NF-kappaB; Jun; kinase; atherosclerosis; multiple sclerosis;
KW arthritis; systemic lupus erythematosus; graft rejection; allergy;
KW graft versus host disease; autoimmune disease; ds.

XX Homo sapiens.

XX WO9555859-A2.

XX 04-NOV-1999.

XX 28-APR-1999; 99WO-EP003025.

XX 29-APR-1998; 98EP-00201392.

XX (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

XX PYPE SMC, Remacle JEFUG, Huylebroeck DFE;

XX WPI; 2000-062029/05.

XX P-FSDS; AAY56019.

XX Novel proteins used to treat inflammatory diseases, NF-kappaB related

XX diseases and for improvement of anti-tumor treatments.

XX Claim 9; Page 37-39; 48pp; English.

XX This sequence represents the gene encoding human CD40 receptor associated
XX protein (CRAP). CRAP is a functional protein capable of interacting with
XX the cytoplasmic domain of CD40 and/or other receptors of the tumour
XX necrosis factor (TNF) receptor superfamily such as CD30 and TNF receptor
XX I, where the protein has no homology to TNF receptor associated factor
XX (TRAF)-proteins. The CD40 binding proteins can be used as modulators of
XX the CD40 signalling pathway, especially to diagnose and treat TRAF-
XX related, CD40-related, NF-kappaB related and/or Jun (kinase)-related
XX diseases, and for the improvement of anti-tumour diseases. Diseases which
XX may be treated include atherosclerosis, arthritis, multiple sclerosis,

CC systemic lupus erythematosus, graft rejection, graft versus host disease,
CC allergy, and autoimmune disease. The proteins can be used to sensitize
CC tumour cells to anti-tumour treatments and to screen for compounds which
CC interfere with the interaction of the proteins with other protein
CC components of the TRAF, CD40 or NF-kappaB related pathway
XX
SQ Sequence 1920 BP; 599 A; 327 C; 435 G; 557 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.: 2,66e-50 Length: 1920
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AAZ47118 (1-1920)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 179 ATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCCGGTGGAGAGCGCTTGGAAACGC 238

QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 239 CGACCTGAACCACTCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAACCT 298

QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 299 GATTCCACCACTTCTAAAATCAGCCATCTCAAGATACTCAGCAAGAAAATGGCAGCATG 358

QY 61 PheSerIleuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 359 TTCTCTCTCAVTACCTGGAATATTGATGATTAGATTCTAAACAATCTGTCTAGAGGGCT 418

QY 81 ArgGlyValCysSerTyrLeu 87

Db 419 CGAGGGGTGTCTCTACTTTA 439

RESULT 4

ADD19013

ID ADD19013 standard; DNA; 1936 BP.

XX AC ADD19013;

XX 15-JAN-2004 (first entry)

XX Human disease related protein DNA sequence SeqID502.

KW human; disease state; cytostatic; antiinflammatory; ophthalmological;
KW antiarteriosclerotic; vulnery; gene therapy;
KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
KW glucose transportation; catecholamine synthesis; iron transport;
KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
KW inflammatory condition; wound healing; gene; ds.

XX Homo sapiens.

XX WO2003018621-A2.

XX 06-MAR-2003.

XX 23-AUG-2002; 2002WO-GB003892.

XX 23-AUG-2001; 2001GB-00020558.

XX 05-OCT-2001; 2001GB-00024037.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;

XX WPI; 2003-290046/28.

DR P-PSDB; ADD19012.
XX
XX New substantially purified polypeptide, useful for diagnosing or treating
PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
PT wound healing.
XX
XX
PS Claim 27; SEQ ID NO 502; 424pp; English.
XX
XX This invention relates to novel human genes and gene product which are
CC implicated in certain disease states. Compounds which modulate the
CC proteins of the invention may have cytosolic, antiinflammatory,
CC opthalmological, antiarteriosclerotic or vulnerary activities. The
CC sequences of the invention may be useful for gene therapy. The invention
CC may be useful for diagnosing or treating a hypoxia-regulated condition,
CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
CC erythropoiesis, or the biological response to hypoxia conditions
CC including processes such as glycolysis, gluconeogenesis, glucose
CC transportation, catecholamine synthesis, iron transport or nitric oxide
CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
CC inflammatory conditions or wound healing. The present sequence is that of
CC a disease related protein encoding DNA sequence of the invention.
XX
SQ Sequence 1936 BP; 617 A; 330 C; 431 G; 558 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,69e-50 Length: 1936
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x ADD19013 (1-1936)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluSerAlaLeuGluArg 20
DB 176 ATGGAAGGGCTCTGAACCTCTGAGCCTCCGGTGGAGAGAGCCCTTGGAAACG 235
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
DB 236 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACA 295
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnAsnGlySerMet 60
DB 296 GATTCCACCACCTCTCTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAAATGCGACATG 355
QY 61 PheSerLeuIleThrTrpIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 356 TTCTCTCTCATTAACCTGGGAATATGATGGATTAGATCTAAACAATCTGTGAGAGGGCT 415

QY 81 ArgGlyValCysSerTyrLeu 87
DB 416 CGAGGGGTGTCTCTACTTA 436

RESULT 5
ADP25361

ID ADP25361 standard; cDNA; 1936 BP.

XX
AC ADP25361;

XX 18-NOV-2004 (first entry)

XX PRO polypeptide encoding cDNA SEQ ID NO:475.

XX ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
KW immunosuppressive; osteopathic; antidiabetic; dermatological;
KW antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
KW gene therapy; immune system.

XX Unidentified.

OS
XX

PN WO2004041170-A2.
XX
XX 21-MAY-2004.
XX 30-OCT-2003; 2003WO-US034312.
XX
XX 01-NOV-2002; 2002US-0423394P.
XX (GETH) GENENTECH INC.
XX
XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;
XX
XX WPI; 2004-419628/39.
DR P-PSDB; ADP25362.
XX
XX New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
PS Claim 1; SEQ ID NO 475; 2940pp; English.

XX The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence encodes a PRO protein of
CC the invention.

XX Sequence 1936 BP; 617 A; 330 C; 431 G; 558 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,69e-50 Length: 1936
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x ADP25361 (1-1936)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluSerAlaLeuGluArg 20
DB 176 ATGGAAGGGCTCTGAACCTCTGAGCCTCCGGTGGAGAGAGCCCTTGGAAACG 235
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40
DB 236 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACA 295
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnAsnGlySerMet 60

Db 296 GATTCCACCACTTCTAAATCAGCCCTCTGAAGATACCTCAGCAAGAAATGGCAGCATG 355
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 356 TTCTCTCTCAATACCTGGAATATTGATGATTAGATCTAAACAATCTGTTCAGAGAGGCT 415
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 416 CGAGGGGTGTCTCTACTTA 436
RESULT 6
ID ADX06356 standard; DNA; 1940 BP.
XX
AC ADX06356;
XX
DT 21-APR-2005 (first entry)
XX
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 921.
XX
KW cyctostatic; cyclin-dependent kinase; cdk; biomarker; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2005012875-A2.
XX
FD 10-FEB-2005.
XX
PF 29-JUL-2004; 2004WO-US024424.
XX
PR 29-JUL-2003; 2003US-0490890P.
XX
PR (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX
WPI; 2005-163068/17.
DR P-PSDB; ADX06357.
DR
PT Biomarkers useful for predicting or determining the response of a mammal
PT to a cancer treatment comprising administration of a modulator of cyclin-
PT dependent kinase activity.
XX
PS Claim 5; SEQ ID NO 921; 141pp; English.
XX
CC This invention describes a novel method of predicting or determining
CC whether a mammal will respond or is responding to an anti-cancer agent
CC that modulates cyclin-dependent kinase (cdk) activity. The method
CC comprises measuring the level of one or more biomarkers selected from
CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the
CC invention is utilized in a kit for determining or predicting whether
CC patient would be susceptible or resistant to treatment by an agent
CC modulating cdk activity. The invention also describes a method for
CC utilizing individualized genetic profiles for treating diseases and
CC disorders based on patient's response and molecular level, specialized
CC microarrays comprising the biomarkers described, antibodies directed
CC against the biomarkers and a cell culture model to identify biomarkers.
CC The cdk modulator is preferably N-5-[(5-(1,1-dimethylethyl)-2-
CC oxazolyl)methyl]thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
CC tartaric acid salt. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This
CC sequence encodes a biomarker used in the method of the invention.
XX
SQ Sequence 1940 BP; 613 A; 330 C; 439 G; 558 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 2.69e-50 Length: 1940
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 14 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x ADX06356 (1-1940)
Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 185 ATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCCGGTGGAGGAGCGCTTGGACGC 244
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 245 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAAC 304
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 305 GATTCCACCACTTCTTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGCATG 364
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 365 TTCTCTCTCAATACCTGGAATATTGATGATTAGATCTAAACAATCTGTTCAGAGAGGCT 424
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 425 CGAGGGGTGTCTCTACTTA 445
RESULT 7
AAI58997
ID AAI58997 standard; cDNA; 1948 BP.
XX
AC AAI58997;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 1200.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR P-PSDB; AAM39841.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Claim 1; SEQ ID NO 1200; 10078pp; English.
XX

CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 CC encoded polypeptides (AAI38642-AAI42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities, such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification

XX SQ Sequence 1948 BP; 614 A; 335 C; 436 G; 563 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,71e-50 Length: 1948
 Score: 448.00 Matches: 87
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AAI58997 (1-1948)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluSerAlaLeuGluArg 20
 DB 198 ATGGAAGGGCTCTGAACCTCTCGAGCCTCCGGTGGAGAGAGCGCTTGGAAACGC 257
 QY 21 ArgProGluThrIleSerGluProIleSerGluProIleSerGluThr 40
 DB 258 CGACCTGAAACCACTCTCGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 317
 QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 318 GATTCACCACTTCTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGCGACATG 377
 QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 378 TTCTCTCTCATTAACCTGGAAATATTGATGGATTAGATCTAAACAATCTGTCTCAGAGAGGCT 437
 QY 81 ArgGlyValCysSerTyrLeu 87
 DB 438 CGAGGGGTGTGTCTTACTTA 458

RESULT 8

ADQ99219

ID ADQ99219 standard; cDNA; 1948 BP.

XX

AC

XX

DT 23-SEP-2004 (first entry)

XX

DE DNA encoding human GPCR-like protein seqid 889.

XX ophthalmological; immunomodulatory; cytostatic; antiatherosclerotic;
 KW antidiabetic; GPCR-like protein; ophthalmic disorder;
 KW neurological disorder; immunological disorder; nephritic disorder;
 KW hormonal dysfunction; cancer; atherosclerosis; diabetes;
 KW molecular weight marker; food supplement; human; ss.

OS Homo sapiens.

XX US6569662-B1.

PN

XX

PD 27-MAY-2003.

XX

PF 19-JUL-2000; 2000US-00620312.

XX

XX 21-JAN-2000; 2000US-00488725.

PR

PR 25-APR-2000; 2000US-00552317.

XX (HYSE-) HYSEQ INC.

PA

XX Tang YT, Zhou P, Drmanac RT;

XX WPI; 2001-442255/47.

DR

XX New G-protein-coupled receptor-like polypeptides and polynucleotides,

XX useful for treating diseases of ophthalmic, neurological, immunological

PT and nephritic systems and hormonal dysfunction, cancer, atherosclerosis

XX and diabetes.

XX

PS Example 2; SEQ ID NO 889; 92pp; English.

XX

CC The invention describes an isolated polynucleotide (I) comprising a fully

CC defined (SI) of 749, 3188, 2484, 1169, 2936, 1467, 5773, 5714, 4041,

CC 1372, 3996, 3945, 1788, 585, 1782, 927, 5714 or 2282 nucleotides as

CC given in the specification, its translated or protein coding portion, its

CC extracellular portion or its active domain. The GPCR-like polypeptides

CC and polynucleotides are useful for the treatment of diseases of

CC ophthalmic, neurological, immunological and nephritic systems. They may

CC also be used to treat hormonal dysfunction, cancer, atherosclerosis and

CC diabetes. The antibodies are useful for detecting or quantitating the

CC polypeptide in tissue. The polypeptides can also be used as molecular

CC weight markers and as a food supplement. This sequence represents a human

CC polynucleotide of the invention.

XX

SQ Sequence 1948 BP; 614 A; 335 C; 436 G; 563 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,71e-50 Length: 1948

Score: 448.00 Matches: 87

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x ADQ99219 (1-1948)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluSerAlaLeuGluArg 20

DB 198 ATGGAAGGGCTCTGAACCTCTCGAGCCTCCGGTGGAGAGAGCGCTTGGAAACGC 257

QY 21 ArgProGluThrIleSerGluProIleSerGluProIleSerGluThr 40

DB 258 CGACCTGAAACCACTCTCGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 317

QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60

DB 318 GATTCACCACTTCTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGCGACATG 377

QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80

DB 378 TTCTCTCTCATTAACCTGGAAATATTGATGGATTAGATCTAAACAATCTGTCTCAGAGAGGCT 437

QY 81 ArgGlyValCysSerTyrLeu 87

DB 438 CGAGGGGTGTGTCTTACTTA 458

RESULT 9

ADQ99219

ID ADQ99219 standard; cDNA; 1948 BP.

XX

AC

XX

DT 04-DEC-2003 (first entry)

XX

DE Novel human cDNA SEQ ID NO 889.

XX

XX ss; cancer; neurodegenerative disease; human.

XX

OS Homo sapiens.

XX US2003104529-A1.
XX 05-JUN-2003.
XX 04-JAN-2002; 2002US-00037270.
XX 21-JAN-2000; 2000US-00488725.
XX 25-APR-2000; 2000US-00552317.
XX 19-JUL-2000; 2000US-00620312.
XX (ZHOU/) ZHOU P.
XX (TANG/) TANG Y T.
XX (LIUC/) LIU C.
XX (ASUN/) ASUNDI V.
XX (DRMA/) DRMANAC R T.
XX Zhou P, Tang YT, Liu C, Asundi V, Drmanac RT;
XX WPI; 2003-678194/64.
XX New polynucleotide, useful for treating diseases e.g., cancer or
XX neurodegenerative diseases.
XX Claim 1; SEQ ID NO 889; 99pp; English.
XX The invention relates to a polynucleotide comprising a sequence given in
XX the specification, or its mature protein-coding portion, or its
XX complement. The polynucleotide is useful for treating diseases e.g.,
XX cancer or neurodegenerative diseases and many others listed in the
XX specification. The present sequence represents a novel human cDNA. Note:
XX The sequence data for this patent did not form part of the printed
XX specification but was obtained in electronic format directly from USPTO
XX at seqdata.uspto.gov/sequence.html?DocID=20030104529.
XX SQ Sequence 1948 BP; 614 A; 335 C; 436 G; 563 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.71e-50 Length: 1948
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x ADB48979 (1-1948)
Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 198 ATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCGGTGGAGAGCGCCTTGGACGC 257
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 258 CGACTGAAACATCTCTGAGCCGACCTATGTTGACCTAACCAATGAGAAACAACT 317
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnAsnGlySerMet 60
Db 318 GATTCACCACTTCTAAATCAGGCCATCTCTGAAGATCTCAGCAAGAAATGGCAGCATG 377
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 378 TTCTCTCTCATCTACTGGAATATTGATGGATTAGATCTAAACAATCTGTCTGAGAGGGCT 437
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 438 CGAGGGGTGTCTTCTACTTAA 458

RESULT 10
AAI60783
ID AAI60783 standard; cDNA; 1958 BP.
XX
AC AAI60783;
XX

DT 22-OCT-2001 (first entry)
XX Human polynucleotide SEQ ID NO 4772.
XX
XX Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia; ss.
XX Homo sapiens.
XX WO200153312-A1.
XX 26-JUL-2001.
XX 26-DEC-2000; 2000WO-US034263.
XX 23-DEC-1999; 99US-00471275.
XX 21-JAN-2000; 2000US-00488725.
XX 25-APR-2000; 2000US-00552317.
XX 20-JUN-2000; 2000US-00598042.
XX 19-JUL-2000; 2000US-00620312.
XX 03-AUG-2000; 2000US-00653450.
XX 14-SEP-2000; 2000US-00662191.
XX 19-OCT-2000; 2000US-00693036.
XX 29-NOV-2000; 2000US-00727344.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
XX Zhou P, Goodrich R, Drmanac RT;
XX WPI; 2001-442253/47.
XX P-PSDB; AAM41627.
XX Novel nucleic acids and polypeptides, useful for treating disorders such
XX as central nervous system injuries.
XX Claim 1; SEQ ID NO 4772; 10078pp; English.
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
XX encoded polypeptides (AAM38642-AAM42213) with neurotropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemias and
XX C.N.S disorders. Note: The sequence data for this patent did not form
XX part of the printed specification
XX SQ Sequence 1958 BP; 613 A; 339 C; 442 G; 564 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.73e-50 Length: 1958
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AAI60783 (1-1958)
Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
|||||

Db 210 ATGGAAAGGCGCTGTAACCTCTTTCGAGCCTCCGGTGGAGGAGCGCCTTGGAAACGC 269
QY 21 ArgProGluThrIleSerGluProLysThrThrValAspLeuThrAsnGluGluThrThr 40
Db 270 CGACCTGAAACCACTCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 329
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 330 GATTCACCACTCTTAAATCAGCCCATCTGAAGATACTCAGCAGAGAAATGGCAGCATG 389
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 390 TTCTCTCTCATTACCTGGAATATTGATGATTAGATCTAAACAATCTGTCTGTCAGAGAGGCT 449
QY 81 ArgGlyValCysSerTyrLeu 87
Db 450 CGAGGGGTGTCTCTACTTA 470
RESULT 11
ID AAX28153 standard; DNA; 2499 BP.
XX
AC AAX28153;
XX
DT 16-JUN-1999 (first entry)
XX
DE Topoisomerase II binding protein 1 coding sequence.
XX
KW Topoisomerase II binding protein; TopBP; anticancer agent; ds.
XX
OS Homo sapiens.
XX
PN JP11075856-A.
XX
PD 23-MAR-1999.
XX
PF 17-SEP-1997; 97JP-00251544.
XX
PR 17-SEP-1997; 97JP-00251544.
XX
PA (TSURU/) TSURUO T.
PA (CHUS) CHUGAI PHARM CO LTD.
XX
XX WPI; 1999-257704/22.
DR P-PSDB; AAY03182.
XX
PT New Topoisomerase II- binding protein - useful as an anticancer agent.
XX
PS Disclosure; Page 18-19; 28pp; Japanese.
XX
CC This sequence encodes the topoisomerase II binding protein (TopBP) of the
CC invention. The TopBP protein is useful as an anticancer agent. TopBP can
CC be used as the target molecule for anticancer agent
XX
SQ Sequence 2499 BP; 720 A; 505 C; 587 G; 687 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 3.77e-50 Length: 2499
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x AAX28153 (1-2499)
QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 641 ATGGAAAGGCGCTGTAACCTCTTTCGAGCCTCCGGTGGAGGAGCGCCTTGGAAACGC 700
QY 21 ArgProGluThrIleSerGluProLysThrThrValAspLeuThrAsnGluGluThrThr 40
Db 701 CGACCTGAAACCACTCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 760

QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 761 GATTCACCACTCTTAAATCAGCCCATCTGAAGATACTCAGCAAGAAATGGCAGCATG 820
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 821 TTCTCTCTCATTACCTGGAATATTGATGATTAGATCTAAACAATCTGTCTGTCAGAGAGGCT 880
QY 81 ArgGlyValCysSerTyrLeu 87
Db 881 CGAGGGGTGTCTCTACTTA 901
RESULT 12
ID ADA10970 standard; cDNA; 3152 BP.
XX
AC ADA10970;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human cDNA differentially expressed in colon cancer #60.
XX
KW ss; differential expression; colon cancer; cancer; human.
XX
OS Homo sapiens.
XX
PN US2002160382-A1.
XX
PD 31-OCT-2002.
XX
PF 11-OCT-2001; 2001US-00981353.
XX
PR 11-OCT-2000; 2000US-0239841P.
XX
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
XX
PI Lasek AW, Jones DA;
XX
XX WPI; 2003-265756/26.
XX
DR New combination comprising cDNAs that are differentially expressed in
PT colon disorder, useful for diagnosing, treating, staging or monitoring
PT treatment for colon cancers.
XX
PS Claim 1; SEQ ID NO 88; 231pp; English.
XX
CC The invention relates to a combination comprising cDNAs that are
CC differentially expressed in colon disorder. The methods and compositions
CC of the present invention are useful for diagnosing, treating, staging or
CC monitoring treatment for colon cancer. They are also useful in high
CC throughput methods for using cDNAs to detect differential expression of
CC nucleic acids in a sample, screening molecules or compounds to identify a
CC ligand which specifically binds a cDNA and using a protein to screen
CC molecules or compounds to identify at least one ligand which specifically
CC binds the protein. The present sequence represents a human cDNA
CC differentially expressed in colon cancer.
XX
SQ Sequence 3152 BP; 875 A; 643 C; 707 G; 926 T; 0 U; 1 Other;
Alignment Scores:
Pred. No.: 5.14e-50 Length: 3152
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x ADA10970 (1-3152)
QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX Claim 8; SEQ ID NO 13209; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention

XX SQ Sequence 1998 BP; 590 A; 327 C; 426 G; 555 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,36e-49 Length: 1898
Score: 439.00 Matches: 86
Percent Similarity: 98.85% Conservative: 0
Best Local Similarity: 98.85% Mismatches: 1
Query Match: 97.99% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AAH15146 (1-1898)

Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 160 ATGGAAAGGCTCTGAACCTCTGCTTCGAGCCCTCCGGTGAGAGAGCCCTTGGAAACG 219
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 220 CGACCTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACT 279
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 280 GATTCCACCACTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAAAATGCCAGCATG 339
Qy 61 PheSerIleuThrTrpAntileAspGlyLeuAspLeuAenSerGluArgAla 80
Db 340 TTCTCTCTATACCTGGGAATATGATGGATTAGATCTAAACATCTGTGAGAGGGCT 399

Qy 81 ArgGlyValCysSerTyrLeu 87

Db 400 CGAGGGGTGTGCTCTCTACTTGA 420

RESULT 15

ADT95307/c

ID ADT95307 standard; cDNA; 391 BP.

XX ADT95307;

XX 16-DEC-2004 (first entry)

XX Colon cancer associated human cDNA sequence #826.

XX Colon cancer; T cell; tumour protein; C634S; C635S; C637S; C640S; C636S;

KW humoral immune response; cellular immune response; cytostatic; immunostimulant; human; ss.

XX Homo sapiens.

XX US2003087818-A1.

XX 08-MAY-2003.

XX 01-FEB-2002; 2002US-00066543.

XX 02-FEB-2001; 2001US-0267400P.

XX 07-FEB-2001; 2001US-0267382P.

XX 11-MAY-2001; 2001US-0290322P.

XX 12-JUL-2001; 2001US-0305265P.

XX 16-AUG-2001; 2001US-0313077P.

XX (CORI-) CORIXA CORP.

XX Jiang Y, Chenault RA, Xu J, Indirias CY, Lodes MJ, Secrist H;

XX Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;

XX WPI; 2003-040540/03.

XX New isolated nucleic acids and polypeptides capable of eliciting a humoral and/or cellular immune response, useful for diagnosing, preventing or treating cancer, particularly colon cancer.

XX Claim 1; SEQ ID NO 826; 87pp; English.

XX The invention relates to polynucleotide and polypeptide sequences associated with cancer, particularly colon cancer. Also disclosed are (i) an expression vector comprising the polynucleotide, (ii) a host cell transformed or transfected with the expression vector, (iii) an isolated antibody, or its antigen-binding fragment, which specifically binds to the polypeptide, (iv) a method of detecting or determining the presence of cancer in a patient, (v) a fusion protein comprising at least one of the polypeptides, (vi) an oligonucleotide that hybridises to the polynucleotide sequence under highly stringent conditions, and (vii) a method of stimulating and/or expanding T cells specific for a tumour protein. The polypeptide specifically comprises the amino acid sequence of C634S, C637S, C640S, C636S or one of the potential open reading frames (ORFs) of C636S. These polypeptides are encoded by the polynucleotide sequences, where both are capable of eliciting a humoral and/or cellular immune response. The polynucleotides, polypeptides, and antibodies are useful for diagnosing, preventing or treating cancer, particularly colon cancer. The polynucleotide and polypeptide sequences are also useful in DNA strand invasion, antisense inhibition, mutational analysis, nucleic acid purification, isolation of transcriptionally active genes, blocking or transcription factor binding, genome cleavage or in situ hybridisation, and as enhancers of transcription or biomarkers. This sequence represents a human colon cancer associated cDNA. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov

XX Sequence 391 BP; 83 A; 100 C; 103 G; 104 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 1.31e-46 Length: 391
Score: 414.00 Matches: 81
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 92.41% Indels: 0
DB: 11 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x ADT95307 (1-391)

Qy 1 MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg 20

Db 286 ATGGAAAGGCTCTGAACCTCTGAGCCCTCCGGTGAGAGAGCCCTTGGAAACG 227

Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40

Db	226	CGACCTGAAACCATCTCTGAGCCCAAGACCATCTATGTTGACCTTAACCAATGAAGAACCACT	167
Qy	41	AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet	60
Db	166	GATTCACCACTTCTAAATCAGCCCATCTGAAGATACTCAGCAAGAAATGGCAGCATG	107
Qy	61	PheSerLeuIleThrTTPAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla	80
Db	106	TTCTCTCTCATTAACCTGGAATATTGATGATTAGATCTAAACAATCTGTGAGAGGGCT	47
Qy	81	Arg 81	
Db	46	CGA 44	
RESULT 16			
ADX41789/c			
ID	ADX41789	standard; cDNA; 391 BP.	
XX	AC	ADX41789;	
XX	XX	21-APR-2005 (first entry)	
DE	DE	Human cDNA encoding colon cancer protein SEQ ID NO 826.	
KW	KW	Cytostatic; Immunostimulant; therapy; diagnosis; colon cancer; neoplasm;	
KW	ss	ss; gene.	
OS	OS	Homo sapiens.	
XX	XX	WO200274156-A2.	
XX	XX	26-SEP-2002.	
XX	XX	01-FEB-2002; 2002WO-US002870.	
XX	XX	02-FEB-2001; 2001US-0267400P.	
PR	PR	07-FEB-2001; 2001US-0267382P.	
PR	PR	11-MAY-2001; 2001US-0290322P.	
PR	PR	12-JUL-2001; 2001US-0305265P.	
PR	PR	16-AUG-2001; 2001US-0313077P.	
XX	XX	(CORI-) CORIXA CORP.	
XX	XX	Jiang Y, Chenault RA, Xu J, Indirias CY, Lodes MJ, Secrhist H;	
PI	PI	Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;	
XX	XX	WPI; 2003-040540/03.	
XX	XX	New isolated nucleic acids and polypeptides capable of eliciting a	
PT	PT	humoral and/or cellular immune response, useful for diagnosing,	
PT	PT	preventing or treating cancer, particularly colon cancer.	
XX	XX	Claim 1; SEQ ID NO 826; 244pp; English.	
XX	XX	The invention relates to a new isolated nucleic acid. The nucleic acids,	
CC	CC	polypeptides, antibodies are useful for diagnosing, preventing or	
CC	CC	treating cancer, particularly colon cancer. The nucleic acid and	
CC	CC	polypeptides are also useful in DNA strand invasion, antisense	
CC	CC	inhibition, mutational analysis, nucleic acid purification, isolation of	
CC	CC	transcriptionally active genes, blocking or transcription factor binding,	
CC	CC	genome cleavage or in situ hybridization, and as enhancers of	
CC	CC	transcription or biomarkers. The kits are useful for detecting antibody	
CC	CC	binding. The present sequence represents a human cDNA encoding a colon	
CC	CC	cancer protein.	
XX	SQ	Sequence 391 BP; 83 A; 100 C; 103 G; 104 T; 0 U; 1 Other;	
Alignment Scores:			
Pred. No.:	1.31e-46	Length:	391
Score:	414.00	Matches:	81
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	92.41%	Indels:	0
DB:	11	Gaps:	0
US-10-757-745-2_COPY_54_140 (1-87) x ADX41789 (1-391)			
Qy	1	MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg	20
Db	286	ATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCCGGTGGAGGAGCGCTTGGACGC	227
Qy	21	ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr	40
Db	226	CGACCTGAAACCATCTCTGAGCCCAAGACCATCTATGTTGACCTTAACCAATGAAGAACCACT	167
Qy	41	AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet	60
Db	166	GATTCACCACTTCTAAATCAGCCCATCTGAAGATACTCAGCAAGAAATGGCAGCATG	107
Qy	61	PheSerLeuIleThrTTPAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla	80
Db	106	TTCTCTCTCATTAACCTGGAATATTGATGATTAGATCTAAACAATCTGTGAGAGGGCT	47
Qy	81	Arg 81	
Db	46	CGA 44	
RESULT 17			
AAS86255			
ID	AAS86255	standard; cDNA; 1227 BP.	
XX	AC	AAS86255;	
XX	XX	13-FEB-2002 (first entry)	
DE	DE	DNA encoding novel human diagnostic protein #22059.	
XX	XX	Human; chromosome mapping; gene mapping; gene therapy; forensic;	
KW	KW	food supplement; medical imaging; diagnostic; genetic disorder; ss.	
XX	OS	Homo sapiens.	
XX	XX	WO200175067-A2.	
XX	XX	11-OCT-2001.	
XX	XX	30-MAR-2001; 2001WO-US008631.	
PR	PR	31-MAR-2000; 2000US-00540217.	
PR	PR	23-AUG-2000; 2000US-00649167.	
XX	XX	(HYSE-) HYSEQ INC.	
XX	XX	Drmanac RT, Liu C, Tang YT;	
XX	XX	WPI; 2001-639362/73.	
DR	DR	P-PSDB; ABG22068.	
XX	XX	New isolated polynucleotide and encoded polypeptides, useful in	
PT	PT	diagnostics, forensics, gene mapping, identification of mutations	
PT	PT	responsible for genetic disorders or other traits and to assess	
PT	PT	biodiversity.	
XX	XX	Claim 1; SEQ ID NO 22059; 103pp; English.	
XX	XX	The invention relates to isolated polynucleotide (I) and polypeptide (II)	
CC	CC	sequences. (I) is useful as hybridisation probes, polymerase chain	
CC	CC	reaction (PCR) primers, oligomers, and for chromosome and gene mapping,	
CC	CC	and in recombinant production of (II). The polynucleotides are also used	
CC	CC	in diagnostics as expressed sequence tags for identifying expressed	
CC	CC	genes. (I) is useful in gene therapy techniques to restore normal	
CC	CC	activity of (II) or to treat disease states involving (II). (II) is	
CC	CC	useful for generating antibodies against it, detecting or quantitating a	
CC	CC	polypeptide in tissue, as molecular weight markers and as a food	
CC	CC	supplement. (II) and its binding partners are useful in medical imaging	
CC	CC	of sites expressing (II). (I) and (II) are useful for treating disorders	

SQ Sequence 725 BP; 318 A; 213 C; 64 G; 130 T; 0 U; 0 Other;
Alignment Scores: 1.56e-05 Length: 725
Pred. No.: 114.00 Matches: 19
Score: 96.55% Conservativeness: 9
Percent Similarity: 65.52% Mismatches: 1
Best Local Similarity: 25.45% Indels: 0
Query Match: 6 Gaps: 0
DB: 6

US-10-757-745-2_COPY_54_140 (1-87) x ABQ34464 (1-725)
QY 2 GluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArgAG 21
DB 571 CAAAAACCTCTAAACTCTTCTCGAACCTCGATATAAAAAACGCTTTAAACGCCGA 630

QY 22 ProGluThrIleSerGluProLysThr 30
DB 631 CCTAAACCATCTCTAAACCCAAACC 657

RESULT 21
ID ABQ34464/C
XX ABQ34464 standard; DNA; 725 BP.
AC ABQ34464;
XX

DT 12-JUL-2002 (first entry)
XX

DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 21055.
XX

KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX

OS Homo sapiens.
XX

FN WO200218632-A2.
XX

PD 07-MAR-2002.
XX

PP 01-SEP-2001; 2001WO-EP010074.
XX

XX 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX

PA (EPIG-) EPIGENOMICS AG.
XX

XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI WPI; 2002-371829/40.
XX

XX Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX

XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX

CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for

CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX

SQ Sequence 725 BP; 130 A; 64 C; 213 G; 318 T; 0 U; 0 Other;
Alignment Scores: 1.56e-05 Length: 725
Pred. No.: 114.00 Matches: 19
Score: 96.55% Conservativeness: 9
Percent Similarity: 65.52% Mismatches: 1
Best Local Similarity: 25.45% Indels: 0
Query Match: 6 Gaps: 0
DB: 6

US-10-757-745-2_COPY_54_140 (1-87) x ABQ34464 (1-725)
QY 2 GluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArgAG 21
DB 155 CAAAAACCTCTAAACTCTTCTCGAACCTCGATATAAAAAACGCTTTAAACGCCGA 96

QY 22 ProGluThrIleSerGluProLysThr 30
DB 95 CCTAAACCATCTCTAAACCCAAACC 69

RESULT 22
AAAX41008
ID AAX41008 standard; cDNA; 258 BP.
XX

AC AAX41008;
XX

DT 18-JUN-1999 (first entry)
XX

DE Human secreted protein 5' EST SEQ ID NO: 220.
XX

XX Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX

OS Homo sapiens.
XX

XX WO9906554-A2.
FN

XX 11-FEB-1999.
PD

XX 31-JUL-1998; 98WO-IB001238.
PP

XX 01-AUG-1997; 97US-00905134.
PR

XX (GEST) GENSET.
XX

XX Dumas Milne Edwards J, Duclert A, Lacroix B;
PI WPI; 1999-153784/13.
XX

XX P-PSDB; AAY12175.
DR

XX New nucleic acids encoding human secreted proteins - obtained from cDNA
XX libraries prepared from kidney, fetal kidney, dystrophic muscle, muscle
XX and heart tissue.
XX

XX Claim 1; Page 319; 622pp; English.
XX

XX AAX40826 to AAX41093 represent 5' expressed sequence tags (ESTs) for
XX human secreted proteins, and encode the proteins given in AAY01602 and
XX AAY11994 to AAY12260, respectively. The proteins given represent the
XX signal peptide and an N-terminal fragment of a secreted protein. The
XX nucleic acid sequences can be used for producing secreted human gene
XX products. They can also be used to develop products for diagnosis and
XX therapy. The proteins obtained may have cytokine activity, cell

CC proliferation/differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell
XX
SQ Sequence 258 BP; 54 A; 54 C; 105 G; 40 T; 0 U; 5 Other;

Alignment Scores:
Pred. No.: 5.38e-06 Length: 258
Score: 113.00 Matches: 22
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 25.22% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AAX41008 (1-258)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaIeuGluArg 20
Db 190 ATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCGGTGGAGAGAGCGCCTTGGAAAGC 249

Qy 21 ArgPro 22
|||||
Db 250 CGACCA 255

RESULT 23
ABN41860
ID ABN41860 standard; DNA; 60 BP.
XX
AC ABN41860;
XX
DT 15-JUL-2002 (first entry)
DE Human spliced transcript detection oligonucleotide SEQ ID NO:14608.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX
FA (COMP-) COMPUGEN INC.
XX
FI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
PS Example 1; SEQ ID NO 14608; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridising selectively to a set of

CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 60 BP; 19 A; 16 C; 11 G; 14 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.27e-05 Length: 60
Score: 101.00 Matches: 19
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 22.54% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x ABN41860 (1-60)

Qy 48 SerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrp 66
|||||
Db 2 AGCCCATCTGAAGATACCTCAGCAAGAAAATGCCAGCATGTTCTCTCATTTACCTGG 58

RESULT 24
AAS87500
ID AAS87500 standard; cDNA; 1589 BP.
XX
AC AAS87500;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #23304.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US0008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG23313.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 23304; 103pp; English.
XX

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1589 BP; 475 A; 331 C; 359 G; 424 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0.447 Length: 1589
 Score: 84.50 Matches: 26
 Percent Similarity: 47.19% Conservative: 16
 Best Local Similarity: 29.21% Mismatches: 26
 Query Match: 18.86% Indels: 21
 DB: Gaps: 5

US-10-757-745-2_COPY_54_140 (1-87) x AAS87500 (1-1589)

QY 10 GluProProValGluSerAlaLeuGluArgProGluThrIleSerGluPro--- 28
 DB 638 GAACCTACTACTAAAGAGTCT-----AGACCACAGGCTATAAAGACCTGTG 685
 QY 29 -----LysThrTyrValAspLeuThrAsnGluGluThrThrAspSerThr 44
 DB 686 AGCCAGTCTGAAAACCGGATGTTTACCTTACTTAATGAGGACACCATCAAGCAACCTACT 745
 QY 45 SerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeu 64
 DB 746 GAATCTGTTAAAGAAACTGAACTCTGCAGAAAGAA-----AGCACAGTT 790
 QY 65 ThrTrpAsnIle---AspGlyLeuAsp-----LeuAsnAsnLeuSer 77
 DB 791 ACAGAGAATTAAAGAGAGGTATCGATGCTGTTTACCCTCATTTGGTAGTACTGCTGAT 850
 QY 78 GluArgAlaArgGlyValCysSerTyr 86
 DB 851 TCTAAAGCAGAGGGTATTAAAGAACTAT 877

RESULT 25

ID AAS87499 standard; cDNA; 2228 BP.

AC AAS87499;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #23303.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX Homo sapiens.

OS WO200175067-A2.

XX 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 XX Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 DR P-P8DB; ABG23312.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 1; SEQ ID NO 23303; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have application in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 2228 BP; 657 A; 468 C; 501 G; 602 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0.702 Length: 2228
 Score: 84.50 Matches: 26
 Percent Similarity: 47.19% Conservative: 16
 Best Local Similarity: 29.21% Mismatches: 26
 Query Match: 18.86% Indels: 21
 DB: Gaps: 5

US-10-757-745-2_COPY_54_140 (1-87) x AAS87499 (1-2228)

QY 10 GluProProValGluSerAlaLeuGluArgProGluThrIleSerGluPro--- 28
 DB 1028 GAACCTACTACTAAAGAGTCT-----AGACCACAGGCTATAAAGACCTGTG 1075
 QY 29 -----LysThrTyrValAspLeuThrAsnGluGluThrThrAspSerThr 44
 DB 1076 AGCCAGTCTGAAAACCGGATGTTTACCTTACTTAATGAGGACACCATCAAGCAACCTACT 1135
 QY 45 SerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeu 64
 DB 1136 GAATCTGTTAAAGAAACTGAACTCTGCAGAAAGAA-----AGCACAGTT 1180
 QY 65 ThrTrpAsnIle---AspGlyLeuAsp-----LeuAsnAsnLeuSer 77
 DB 1181 ACAGAGAATTAAAGAGAGGTATCGATGCTGTTTACCCTCATTTGGTAGTACTGCTGAT 1240
 QY 78 GluArgAlaArgGlyValCysSerTyr 86
 DB 1241 TCTAAAGCAGAGGGTATTAAAGAACTAT 1267

```
RESULT 26
AAS82908/c
ID AAS82908 standard; cDNA; 2717 BP.
XX
AC AAS82908;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #18712.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
FN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Dmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
XX
DR P-PSDB; ABG18721.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 18712; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 2717 BP; 755 A; 606 C; 559 G; 797 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.914 Length: 2717
Score: 84.50 Matches: 26
Percent Similarity: 47.19% Conservative: 16
Best Local Similarity: 29.21% Mismatches: 26
Query Match: 18.86% Indels: 21
DB: 5 Gaps: 5

US-10-757-745-2_COPY_54_140 (1-87) x AAS82908 (1-2717)
QY 10 GluProValGluSerAlaLeuGluArgProGluThrIleSerGluPro--- 28
```

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Db 2109 GAACCTACTACTAAAGAGTCT-----AGACCACAGGCTATAAAGAACCTGTG 2062
QY 29 -----LysThrTyrValAspLeuThrAsnGluThrAspSerThrThr 44
Db 2061 AGCCAGTCTGAAAAACGGGATGTTAACTTACTTAATGAGGACCATCAAGCAACTACT 2002
QY 45 SerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerIleIle 64
Db 2001 GAATCTGTGTTAAAGAACTGAAACTTCGCAAAAGAA-----AGCACAGTT 1957
QY 65 ThrTrpAsnIle---AspGlyLeuAsp-----LeuAsnAsnLeuSer 77
Db 1956 ACAGAAGAAATTAAAGAAAGGTATCGATGCTGTTTACCCCTCATTTGGTAGGTACTGCTGAT 1897
QY 78 GluArgAlaArgGlyValCysSerTyr 86
Db 1896 TCTAAGCAGAGGGTATTAAAGAACTAT 1870

RESULT 27
AAS75995
ID AAS75995 standard; cDNA; 4002 BP.
XX
AC AAS75995;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #11799.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
FN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Dmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
XX
DR P-PSDB; ABG11808.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 11799; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
```

CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 4002 BP; 1159 A; 837 C; 891 G; 1115 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.53 Length: 4002
 Score: 84.50 Matches: 26
 Percent Similarity: 47.19% Conservative: 16
 Best Local Similarity: 29.21% Mismatches: 26
 Query Match: 18.86% Indels: 21
 DB: 5 Gaps: 5

US-10-757-745-2_COPY_54_140 (1-87) x AAS75995 (1-4002)

QY 10 GluProValGluGluSerAlaLeuGluArgArgProGluThrIleSerGluPro--- 28
 DB 1435 GAACCTACTACTAAAGAGTCT-----AGACCACAGGCTATAAAGAACCTGTG 1482

QY 29 -----LysThrTyrValAspLeuThrAsnGluGluThrThrAspSerThrThr 44
 DB 1483 AGCCAGTCTGAAACACGGGATGTTAACTTACTATGAGGACACCATCAAGCAACCTACT 1542

QY 45 SerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIle 64
 DB 1543 GAATCTGTTAAAGAAACTGAAACTTCTGCAAAAGAA-----AGCACAGTT 1587

QY 65 ThrTrpAsnIle---AspGlyLeuAsp-----LeuAsnAsnLeuSer 77
 DB 1588 ACAGAAGAATTAGAGAAGGTATCGATGCTGTTTACCCTCATTTGGTAGTACTGCTGAT 1647

QY 78 GluArgAlaArgGlyValCysSerTyr 86
 DB 1648 TCTAAAGCAGAGGGTATTAAAGAACTAT 1674

RESULT 28
 ID AAS87489/C
 ID AAS87489 standard; cDNA; 4890 BP.
 AC AAS87489;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #23293.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US0008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR P-PSDB; ABG23302.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 1; SEQ ID NO 23293; 103pp; English.
 PS
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 4890 BP; 1388 A; 1100 C; 986 G; 1416 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2 Length: 4890
 Score: 84.50 Matches: 26
 Percent Similarity: 47.19% Conservative: 16
 Best Local Similarity: 29.21% Mismatches: 26
 Query Match: 18.86% Indels: 21
 DB: 5 Gaps: 5

US-10-757-745-2_COPY_54_140 (1-87) x AAS87489 (1-4890)

QY 10 GluProValGluGluSerAlaLeuGluArgArgProGluThrIleSerGluPro--- 28
 DB 2181 GAACCTACTACTAAAGAGTCT-----AGACCACAGGCTATAAAGAACCTGTG 2134

QY 29 -----LysThrTyrValAspLeuThrAsnGluGluThrThrAspSerThrThr 44
 DB 2133 AGCCAGTCTGAAACACGGGATGTTAACTTACTATGAGGACACCATCAAGCAACCTACT 2074

QY 45 SerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIle 64
 DB 2073 GAATCTGTTAAAGAAACTGAAACTTCTGCAAAAGAA-----AGCACAGTT 2029

QY 65 ThrTrpAsnIle---AspGlyLeuAsp-----LeuAsnAsnLeuSer 77
 DB 2028 ACAGAAGAATTAGAGAAGGTATCGATGCTGTTTACCCTCATTTGGTAGTACTGCTGAT 1969

QY 78 GluArgAlaArgGlyValCysSerTyr 86
 DB 1968 TCTAAAGCAGAGGGTATTAAAGAACTAT 1942

RESULT 29
 ID AAS82911
 ID AAS82911 standard; cDNA; 6448 BP.
 XX
 AC AAS82911;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #18715.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.

US-10-757-745-2_COPY_54_140 (1-87) x AAS87485 (1-7197)

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Qy 10 GluProProValGluGluSerAlaLeuGluArgArgProGluThrIleSerGluPro---- 28
Db 5158 GAACCTACTACTAAAGAGTCT-----AGACCACAGGCTATAAAGAACCTGTG 5205
Qy 29 -----LysThrTyrValAspLeuThrAsnGluGluThrThrAspSerThrThr 44
Db 5206 AGCCAGTCTGAAAACGGGATGTTAACTTACTATGAGGACACCATCAAGCAACCTACT 5265
Qy 45 SerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIle 64
Db 5266 GAATCTGTTAAAGAAACTGAAACTCTGCAAAAGAA-----AGCACAGTT 5310
Qy 65 ThrTrpAsnIle---AspGlyLeuAsp-----LeuAsnAsnLeuSer 77
Db 5311 ACAGAAAGATTAAAGAGAGGTATCGATGCTGTTTACCCCTCATTTGGTAGGTACTGCTGAT 5370
Qy 78 GluArgAlaArgGlyValCysSerTyr 86
Db 5371 TCTAAAGCAGAGGGTATTAAAGAACTAT 5397
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Search completed: December 4, 2005, 09:02:49
Job time : 307.055 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 3, 2005, 23:34:21; Search time 2292.36 Seconds
(without alignments)
2157.330 Million cell updates/sec

Title: US-10-757-745-2_COPY_54_140

Perfect score: 448

Sequence: 1 MERALNSFEPVBSALER.....IDGLDLNLSBRARGVCSYL 87

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Command line parameters:

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-UNITS=bits -START=i -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=500
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=30 -MODE=LOCAL
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-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*
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2: gb.in.*
3: gb.env.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pr.*
9: gb.ro.*
10: gb.sts.*
11: gb.sy.*
12: gb.un.*
13: gb.vi.*
14: gb.htg.*
15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	448	100.0	1261	8	AF201687 Homo sapi
3	448	100.0	1920	6	BD205490 CD40-Inte

4	448	100.0	1920	6	AR594294	AR594294 Sequence	
5	448	100.0	1920	6	AX011599	AX011599 Sequence	
6	448	100.0	1921	8	HS269473	AJ269473 Homo sapi	
7	448	100.0	1936	8	AF223469	AF223469 Homo sapi	
8	448	100.0	1948	6	AR333938	AR333938 Sequence	
9	448	100.0	1952	8	BC017553	BC017553 Homo sapi	
10	448	100.0	2499	6	E23195	E23195 Toxoplasma	
11	439	98.0	752	6	BD150065	BD150065 Primer fo	
12	439	98.0	752	6	AX870003	AX870003 Sequence	
13	439	98.0	1898	6	BD157138	BD157138 Primer fo	
14	439	98.0	1898	6	AX878304	AX878304 Sequence	
15	439	98.0	1898	8	AK002168	AK002168 Homo sapi	
16	424	94.6	858	6	CQ726600	CQ726600 Sequence	
c	17	332	74.1	150344	14	AC152027	AC152027 Dasyptus n
18	288.5	64.4	2151	8	HS2420495	HS2420495 Homo sapi	
19	288	64.3	20938	8	AY613922	AY613922 Homo sapi	
20	288	64.3	102200	8	HS30M3	AL031775 Human DNA	
21	288	64.3	167847	8	CR925830	CR925830 Human DNA	
22	288	64.3	176819	8	CR942205	CR942205 Human DNA	
c	23	269	60.0	411	10	HS133N16S	AL110344 H.sapiens
24	211.5	47.2	1312	6	BD205491	BD205491 CD40-Inte	
25	211.5	47.2	1312	6	AR594295	AR594295 Sequence	
26	211.5	47.2	1312	6	AX011601	AX011601 Sequence	
27	211.5	47.2	1943	9	MMU251328	AJ251328 Mus muscu	
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29	173	38.6	1451	5	BC083404	BC083404 Danio rer	
c	30	160.5	35.8	256608	9	AL589699	AL589699 Mouse DNA
31	157.5	35.2	245394	14	AC125756	AC125756 Rattus no	
32	153	34.2	1455	5	BC097117	BC097117 Danio rer	
33	148.5	33.1	200076	5	BX511258	BX511258 Zebrafish	
34	145.5	32.5	198752	5	BX957279	BX957279 Zebrafish	
35	145	32.4	379	6	BD112459	BD112459 EST and e	
36	145	32.4	379	6	AR416906	AR416906 Sequence	
37	145	32.4	379	6	AX977600	AX977600 Sequence	
38	113	25.2	258	6	BD077628	BD077628 5'EST of	
39	113	25.2	258	6	AX939201	AX939201 Sequence	
40	101	22.5	60	6	CQ544973	CQ544973 Sequence	
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42	90	20.1	64027	14	AC018192	AC018192 Drosophil	
43	90	20.1	84549	14	AC006243	AC006243 Drosophil	
44	90	20.1	190616	2	AC007884	AC007884 Drosophil	
45	90	20.1	343833	2	AE003465	AE003465 Drosophil	
46	88	19.6	229070	14	AC157293	AC157293 Bos tauru	
c	47	85	19.0	229070	14	AC157293	AC157293 Bos tauru
48	84	18.8	180129	14	AC074173	AC074173 Mus muscu	
49	84	18.8	184800	14	AC074144	AC074144 Mus muscu	
50	84	18.8	240203	14	CR974423	CR974423 Mus muscu	
51	82.5	18.4	176379	8	AC016751	AC016751 Homo sapi	
52	81.5	18.2	3321	6	BD004082	BD004082 Apoptosis	
53	81.5	18.2	6763	6	BD004101	BD004101 Apoptosis	
54	81.5	18.2	6763	9	AF132726	AF132726 Mus muscu	
55	81.5	18.2	138031	9	AL805973	AL805973 Mouse DNA	
c	56	80	17.9	233372	14	AC109433	AC109433 Rattus no
57	80	17.9	239241	14	AC128484	AC128484 Rattus no	
58	79.5	17.7	110000	1	CP000099	Continuation (48 o	
c	59	79.5	17.7	143171	15	CLBGCGA	X70810 Euglena gra
60	79.5	17.7	214994	14	AC152575	AC152575 Bos tauru	
c	61	79	17.6	479	8	AY228365	AY228365 Homo sapi
62	79	17.6	1006	6	CQ728084	CQ728084 Sequence	
c	63	79	17.6	1093	6	CQ728085	CQ728085 Sequence
64	79	17.6	1473	6	AX571858	AX571858 Sequence	
c	65	79	17.6	1597	8	BC101094	BC101094 Homo sapi
66	79	17.6	1597	8	BC101095	BC101095 Homo sapi	
c	67	79	17.6	1720	8	BC101092	BC101092 Homo sapi
68	79	17.6	1720	8	BC101093	BC101093 Homo sapi	
c	69	79	17.6	2268	8	BC101093	BC101093 Homo sapi
70	79	17.6	2456	6	CQ850796	CQ850796 Sequence	
c	71	79	17.6	2456	6	AK127978	AK127978 Homo sapi
72	79	17.6	3558	6	CQ845983	CQ845983 Sequence	
c	73	79	17.6	3558	6	AK131483	AK131483 Homo sapi
74	78	17.4	3672	8	HUMIGFBP5X	L27560 Homo sapien	
c	75	78	17.4	4001	6	CQ787212	CQ787212 Sequence
76	78	17.4	4750	6	BD194552	BD194552 Human nuc	

77	78	17.4	4750	6	AX015406	AX015406 Sequence	150	73.5	16.4	124394	8	AC087593	AC087593 Homo sapi
c 78	78	17.4	110000	1	CP000099_25	Continuation (26 o	151	73.5	16.4	152651	14	AC015556	AC015556 Homo sapi
79	78	17.4	179859	8	AC007563	AC007563 Homo sapi	c 152	73.5	16.4	202014	14	AC152873	AC152873 Bos tauru
c 80	77.5	17.3	653	10	BV018522	BV018522 S212P6048	c 153	73.5	16.4	209003	14	AC073724	AC073724 Mus muscu
81	77.5	17.3	3349	5	BC085071	BC085071 Xenopus l	c 154	73.5	16.4	240242	14	AC155047	AC155047 Bos tauru
82	77.5	17.3	195917	14	AC164039	AC164039 Bos tauru	c 155	73	16.3	4763	1	AF385683	AF385683 Streptoco
83	77.5	17.3	215975	9	AC113019	AC113019 Mus muscu	156	73	16.3	109043	5	CNS08CA7	AL808032 BAC 30B15
84	77	17.2	861	2	AK174793	AK174793 Ciona int	c 157	73	16.3	173400	9	AC101922	AC101922 Mus muscu
85	77	17.2	110000	15	CR382131_09	Continuation (10 o	c 158	73	16.3	205206	14	AC135913	AC135913 Mus muscu
86	77	17.2	110000	5	AL953852_05	Continuation (6 of	159	73	16.3	209458	14	AC152063	AC152063 Mus muscu
87	77	17.2	200882	5	AL953852	AL953852 Zebrafish	c 160	73	16.3	223920	14	AC156314	AC156314 Bos tauru
c 88	77	17.2	225238	14	AC097825	AC097825 Rattus no	161	73	16.3	224865	14	AC163364	AC163364 Bos tauru
c 89	77	17.2	243360	14	AC127920	AC127920 Rattus no	162	73	16.3	249363	14	AC155158	AC155158 Mus muscu
c 90	77	17.2	262405	14	AC102976	AC102976 Rattus no	c 162	73	16.3	255053	14	AC131844	AC131844 Rattus no
91	77	17.2	265382	14	AC114439	AC114439 Rattus no	164	73	16.3	302162	14	AC156490	AC156490 Bos tauru
92	76.5	17.1	1263	15	AB023787	AB023787 Ipomoea b	165	72.5	16.2	573	6	AR545877	AR545877 Sequence
93	76.5	17.1	16751	5	AB166795	AB166795 Pogona vi	166	72.5	16.2	970	1	SEQ249889	AJ249889 Streptoco
94	76	17.0	163959	9	AC131704	AC131704 Mus muscu	167	72.5	16.2	1420	13	AF138884	AF138884 Newcastle
c 95	76	17.0	207781	14	AC129022	AC129022 Mus muscu	168	72.5	16.2	2281	5	AB128031	AB128031 Xenopus l
c 96	76	17.0	224320	14	AC079435	AC079435 Mus muscu	169	72.5	16.2	2291	5	BC090573	BC090573 Xenopus t
c 97	76	17.0	230796	14	AC098154	AC098154 Rattus no	170	72.5	16.2	2632	2	AK174902	AK174902 Ciona int
98	75.5	16.9	10617	11	AY128691	AY128691 Synthetic	171	72.5	16.2	2839	5	BC044999	BC044999 Xenopus l
99	75.5	16.9	11588	11	AE013213	AE013213 Thermoana	172	72.5	16.2	3542	2	AF319614	AF319614 Caenorhab
100	75.5	16.9	17432	7	AF350004	AF350004 Bacteriop	173	72.5	16.2	15192	13	AY562985	AY562985 Newcastle
c 101	75.5	16.9	100736	14	AC166088	AC166088 Bos tauru	174	72.5	16.2	49131	14	AL731837	AL731837 Smithops
c 102	75.5	16.9	104180	14	CEZK340	Z82091 Caenorhabdi	c 175	72.5	16.2	8395	14	AC165548	AC165548 Bos tauru
c 103	75.5	16.9	110000	15	CR382136_12	Continuation (13 o	c 176	72.5	16.2	89405	14	AC166481	AC166481 Bos tauru
c 104	75.5	16.9	144868	14	AC079508	AC079508 Mus muscu	c 177	72.5	16.2	115904	15	AC144807	AC144807 Medicago
c 105	75.5	16.9	196560	9	AC116856	AC116856 Mus muscu	178	72.5	16.2	152177	5	AL935114	AL935114 Zebrafish
c 106	75.5	16.9	211336	9	AC139886	AC139886 Mus muscu	c 179	72.5	16.2	188273	9	BX936296	BX936296 Mouse DNA
107	75	16.7	1905	2	AK116456	AK116456 Ciona int	180	72.5	16.2	204504	14	AC150645	AC150645 Bos tauru
c 108	75	16.7	2601	2	AK116922	AK116922 Ciona int	c 181	72.5	16.2	219368	9	AC098721	AC098721 Mus muscu
c 109	75	16.7	136358	14	AC141180	AC141180 Rattus no	c 182	72.5	16.2	225388	14	AC162984	AC162984 Bos tauru
c 110	75	16.7	145157	14	CR853298	CR853298 Danio rer	183	72.5	16.2	231912	14	AC087566	AC087566 Mus muscu
c 111	75	16.7	148601	14	AC149650	AC149650 Bos tauru	184	72.5	16.2	233692	14	AC164255	AC164255 Bos tauru
c 112	75	16.7	171265	14	AC158071	AC158071 Bos tauru	c 185	72.5	16.2	234231	9	AC161217	AC161217 Mus muscu
113	75	16.7	224166	14	AC110955	AC110955 Rattus no	186	72.5	16.2	235023	14	AC124170	AC124170 Mus muscu
114	75	16.7	347050	2	PF929351	AL929351 Plasmodiu	187	72.5	16.2	273602	14	AC160667	AC160667 Bos tauru
115	74.5	16.6	13251	2	AF148954	AF148954 Caenorhab	c 188	72.5	16.2	286509	14	AC156646	AC156646 Bos tauru
116	74.5	16.6	13761	2	AF148953	AF148953 Caenorhab	189	72.5	16.2	325334	14	AC155126	AC155126 Bos tauru
c 117	74.5	16.6	39415	2	AC139529	AC139529 Botryllus	190	72	16.1	741	15	AY135641	AY135641 Solanum t
118	74.5	16.6	44699	2	AF040648	AF040648 Caenorhab	191	72	16.1	892	15	AY217354	AY217354 Manihot e
119	74.5	16.6	134075	14	AC124217	AC124217 Medicago	192	72	16.1	1536	9	AF387880	AF387880 Rattus no
c 120	74.5	16.6	151336	8	AC012001	AC012001 Homo sapi	193	72	16.1	1536	9	AF387881	AF387881 Rattus no
c 121	74.5	16.6	159240	14	AC031309	AC031309 Homo sapi	194	72	16.1	1536	9	AF387882	AF387882 Rattus no
c 122	74.5	16.6	164426	14	AC012143	AC012143 Homo sapi	195	72	16.1	1536	9	AF387883	AF387883 Rattus no
123	74.5	16.6	212505	14	AC162978	AC162978 Bos tauru	196	72	16.1	1536	9	AF387884	AF387884 Rattus no
c 124	74.5	16.6	298960	14	AC006896	AC006896 Caenorhab	197	72	16.1	1536	9	AF387885	AF387885 Rattus no
c 125	74	16.5	2182	15	BT000991	BT000991 Arabidops	198	72	16.1	1536	9	AF387886	AF387886 Rattus no
c 126	74	16.5	2522	5	AF191032	AF191032 Myxine gl	199	72	16.1	1536	9	AF387887	AF387887 Rattus no
c 127	74	16.5	2547	15	ATY16327	Y16327 Arabidopsis	200	72	16.1	1536	9	AF387888	AF387888 Rattus no
c 128	74	16.5	2634	15	AF370139	AF370139 Arabidops	201	72	16.1	1536	9	AF387889	AF387889 Rattus no
129	74	16.5	62420	15	AB025622	AB025622 Arabidops	202	72	16.1	2555	6	CQ06503	CQ06503 Sequence
c 130	74	16.5	110000	1	AP006716_24	Continuation (25 o	c 203	72	16.1	3289	2	DR08B97D	DR08B97D Droso
c 131	74	16.5	110000	15	CR382129_11	Continuation (12 o	c 204	72	16.1	3521	2	BT010254	BT010254 Droso
c 132	74	16.5	161153	9	AC122032	AC122032 Mus muscu	c 205	72	16.1	3748	6	CQ585929	CQ585929 Sequence
c 133	74	16.5	173893	9	AC101778	AC101778 Mus muscu	c 206	72	16.1	50701	1	CP000082_26	Continuation (27 o
c 134	74	16.5	179503	8	AL445468	AL445468 Human DNA	207	72	16.1	110000	14	CP000082_04	Continuation (5 of
c 135	74	16.5	184037	9	AC147369	AC147369 Mus muscu	208	72	16.1	110000	14	CT005265_03	Continuation (4 of
136	73.5	16.4	893	1	AF180521	AF180521 Streptoco	209	72	16.1	110000	15	AP008207_237	Continuation (238
c 137	73.5	16.4	893	6	BT266898	BT266898 Streptoco	210	72	16.1	117376	14	AC014838	AC014838 Droso
c 138	73.5	16.4	893	6	AR630985	AR630985 Sequence	211	72	16.1	133606	14	AC147959	AC147959 Medicago
c 139	73.5	16.4	893	6	AX026748	AX026748 Sequence	c 212	72	16.1	134443	14	AC015547	AC015547 Homo sapi
140	73.5	16.4	3143	1	AF180520	AF180520 Streptoco	213	72	16.1	136080	15	CR932957	CR932957 Medicago
141	73.5	16.4	11162	1	AE006505	AE006505 Streptoco	214	72	16.1	144091	15	AP003022	AP003022 Oryza sat
142	73.5	16.4	11165	1	AE009988	AE009988 Streptoco	215	72	16.1	163671	15	AP003330	AP003330 Rattus no
143	73.5	16.4	53523	1	AE014143	AE014143 Streptoco	216	72	16.1	170356	2	AC009981	AC009981 Droso
144	73.5	16.4	78657	14	AC164682	AC164682 Bos tauru	217	72	16.1	171361	14	CR936317	CR936317 Danio rer
c 145	73.5	16.4	93684	8	AC109513	AC109513 Homo sapi	c 218	72	16.1	199200	8	AL359633	AL359633 Human DNA
c 146	73.5	16.4	110000	1	BA000034_15	Continuation (16 o	219	72	16.1	209003	14	AC073724	AC073724 Mus muscu
147	73.5	16.4	110000	1	CP000003_03	Continuation (4 of	c 220	72	16.1	216884	14	AC096834	AC096834 Rattus no
148	73.5	16.4	110000	1	CP000017_03	Continuation (4 of	221	72	16.1	228635	2	AE003758	AE003758 Droso
149	73.5	16.4	110000	1	CP000056_03	Continuation (4 of	222	72	16.1	228870	9	AL808119	AL808119 Mouse DNA

223	72	16.1	233149	14	AC125916	AC125916 Rattus no	71	15.8	217779	14	AC121655	AC121655 Rattus no	
224	72	16.1	240594	14	AC095388	AC095388 Rattus no	c 224	71	15.8	218320	14	AC128946	AC128946 Rattus no
c 225	72	16.1	243726	14	AC111753	AC111753 Rattus no	c 225	71	15.8	230184	9	AC138679	AC138679 Bos tauru
c 226	72	16.1	246581	14	AC156042	AC156042 Bos tauru	c 226	71	15.8	231738	14	AC152784	AC152784 Bos tauru
c 227	72	16.1	249187	14	AC109848	AC109848 Rattus no	c 227	71	15.8	233181	14	AC111558	AC111558 Rattus no
c 228	72	16.1	249187	14	AC109848	AC109848 Rattus no	c 228	71	15.8	238646	14	AC099463	AC099463 Rattus no
c 229	72	16.1	275941	14	AC102982	AC102982 Rattus no	c 229	71	15.8	246979	14	AC094480	AC094480 Rattus no
c 230	72	16.1	280585	14	AC128381	AC128381 Rattus no	c 230	71	15.8	261992	14	AC119481	AC119481 Rattus no
c 231	71.5	16.0	349391	1	BS572095	BS572095 Prochloro	c 231	71	15.8	270050	1	AL591977	AL591977 Listeria
c 232	71.5	16.0	608	10	BV371149	BV371149 S231P672R	c 232	71	15.8	305431	1	AE017325	AE017325 Listeria
c 233	71.5	16.0	822	6	CQ646220	CQ646220 Sequence	c 233	71	15.8	349980	6	AX641667	AX641667 Sequence
c 234	71.5	16.0	904	10	CNS06HY2	AL399600 T7 end of	c 234	70.5	15.7	2710	8	HS808357	HS808357 Sequence
c 235	71.5	16.0	921	6	AX477495	AX477495 Sequence	c 235	70.5	15.7	6012	6	CQ897489	CQ897489 Sequence
c 236	71.5	16.0	933	6	AX954017	AX954017 Sequence	c 236	70.5	15.7	6012	6	CQ897489	CQ897489 Sequence
c 237	71.5	16.0	999	6	AR557033	AR557033 Sequence	c 237	70.5	15.7	6015	6	CQ965350	CQ965350 Sequence
c 238	71.5	16.0	2328	2	AK112480	AK112480 Ciona int	c 238	70.5	15.7	10253	6	AE007416	AE007416 Streptoco
c 239	71.5	16.0	2443	15	ANU63416	U63416 Aspergillus	c 239	70.5	15.7	10253	6	CQ788935	CQ788935 Sequence
c 240	71.5	16.0	2874	9	BC057561	BC057561 Mus muscu	c 240	70.5	15.7	15213	6	AR218794	AR218794 Sequence
c 241	71.5	16.0	3088	9	BC096467	BC096467 Mus muscu	c 241	70.5	15.7	15213	6	AR218794	AR218794 Sequence
c 242	71.5	16.0	3175	9	BC037641	BC037641 Mus muscu	c 242	70.5	15.7	15213	6	AR218794	AR218794 Sequence
c 243	71.5	16.0	3509	9	RATHISHIR	D12800 Rattus norv	c 243	70.5	15.7	110000	1	BA000019_59	BA000019_59
c 244	71.5	16.0	4320	6	CQ579315	CQ579315 Sequence	c 244	70.5	15.7	110000	1	BA000019_60	BA000019_60
c 245	71.5	16.0	7530	9	AF051357	AF051357 Mus muscu	c 245	70.5	15.7	110000	1	BA000019_60	BA000019_60
c 246	71.5	16.0	9023	13	AY445885	AY445885 Small rum	c 246	70.5	15.7	110000	1	BA000019_60	BA000019_60
c 247	71.5	16.0	9473	15	AC149210	AC149210 Medicago	c 247	70.5	15.7	110000	1	BA000019_60	BA000019_60
c 248	71.5	16.0	71088	15	NCB7F18	AL389891 Neurospor	c 248	70.5	15.7	112863	8	AC011309	AC011309 Homo sapi
c 249	71.5	16.0	74723	15	BX842633	BX842633 Neurospor	c 249	70.5	15.7	123143	14	AC162140	AC162140 Loxodonta
c 250	71.5	16.0	76004	15	BX842625	BX842625 Neurospor	c 250	70.5	15.7	124906	14	AC138526	AC138526 Medicago
c 251	71.5	16.0	94838	14	AC164745	AC164745 Bos tauru	c 251	70.5	15.7	125215	14	AC124609	AC124609 Medicago
c 252	71.5	16.0	103274	14	AC166465	AC166465 Bos tauru	c 252	70.5	15.7	139418	14	AC162757	AC162757 Loxodonta
c 253	71.5	16.0	110000	1	AE005174_04	Continuation (5 of	c 253	70.5	15.7	144147	8	AC145394	AC145394 Pan trogl
c 254	71.5	16.0	110000	1	AP006840_19	Continuation (20 o	c 254	70.5	15.7	153774	14	AC021009	AC021009 Homo sapi
c 255	71.5	16.0	110000	1	BA000007_04	Continuation (5 of	c 255	70.5	15.7	153774	14	AC021009	AC021009 Homo sapi
c 256	71.5	16.0	113689	15	CR382132_29	Continuation (30 o	c 256	70.5	15.7	157286	2	AC154041	AC154041 Drosophil
c 257	71.5	16.0	131867	2	AY449460	AY449460 Oikopleur	c 257	70.5	15.7	159317	9	AC124478	AC124478 Mus muscu
c 258	71.5	16.0	139613	6	CQ869695	CQ869695 Sequence	c 258	70.5	15.7	163874	9	AC115006	AC115006 Mus muscu
c 259	71.5	16.0	179537	14	AC158710	AC158710 Sus scrof	c 259	70.5	15.7	169755	14	AC163479	AC163479 Bos tauru
c 260	71.5	16.0	184366	9	AC121783	AC121783 Mus muscu	c 260	70.5	15.7	172401	2	AC010575	AC010575 Drosophil
c 261	71.5	16.0	186453	14	AC126165	AC126165 Rattus no	c 261	70.5	15.7	174149	14	AC009688	AC009688 Homo sapi
c 262	71.5	16.0	193109	14	AC119927	AC119927 Mus muscu	c 262	70.5	15.7	174424	14	AC166342	AC166342 Mus muscu
c 263	71.5	16.0	198536	14	AC155032	AC155032 Bos tauru	c 263	70.5	15.7	176129	8	AP003061	AP003061 Homo sapi
c 264	71.5	16.0	205813	14	CR385054	CR385054 Danilo rer	c 264	70.5	15.7	184759	14	AC163424	AC163424 Bos tauru
c 265	71.5	16.0	208725	14	AC156420	AC156420 Bos tauru	c 265	70.5	15.7	184805	9	AC158917	AC158917 Mus muscu
c 266	71.5	16.0	218723	14	AC156235	AC156235 Mus muscu	c 266	70.5	15.7	193540	14	AC162637	AC162637 Bos tauru
c 267	71.5	16.0	233825	14	AC129679	AC129679 Rattus no	c 267	70.5	15.7	198388	9	AC100506	AC100506 Mus muscu
c 268	71.5	16.0	240016	14	AC157297	AC157297 Bos tauru	c 268	70.5	15.7	199474	9	AC122873	AC122873 Mus muscu
c 269	71.5	16.0	288587	14	AC160252	AC160252 Bos tauru	c 269	70.5	15.7	200711	14	AC156188	AC156188 Bos tauru
c 270	71	15.8	770	5	XLU22395	U22395 Xenopus lae	c 270	70.5	15.7	201964	14	AC150756	AC150756 Bos tauru
c 271	71	15.8	1259	5	BC043990	BC043990 Xenopus l	c 271	70.5	15.7	202128	14	AC162531	AC162531 Bos tauru
c 272	71	15.8	1357	2	CEU18781	U18781 Caenorhabdi	c 272	70.5	15.7	202128	14	AC162531	AC162531 Bos tauru
c 273	71	15.8	2177	5	BC076729	BC076729 Xenopus l	c 273	70.5	15.7	227099	14	AC147619	AC147619 Mus muscu
c 274	71	15.8	3551	5	AB100355	AB100355 Mus muscu	c 274	70.5	15.7	227099	14	AC147619	AC147619 Mus muscu
c 275	71	15.8	5057	2	AF037042	AF037042 Dictyoste	c 275	70.5	15.7	229451	14	AC160505	AC160505 Bos tauru
c 276	71	15.8	24459	6	AR623603	AR623603 Sequence	c 276	70.5	15.7	234856	14	AC157006	AC157006 Bos tauru
c 277	71	15.8	32241	6	AR619852	AR619852 Sequence	c 277	70.5	15.7	235510	14	AC161381	AC161381 Mus muscu
c 278	71	15.8	93177	8	AC098678	AC098678 Homo sapi	c 278	70.5	15.7	239893	14	AC156958	AC156958 Bos tauru
c 279	71	15.8	110000	14	TANN11_12	Continuation (13 o	c 279	70.5	15.7	249153	14	AC162990	AC162990 Bos tauru
c 280	71	15.8	110000	15	AP008215_094	Continuation (95 o	c 280	70.5	15.7	254147	14	AC161524	AC161524 Bos tauru
c 281	71	15.8	128674	14	AC098368	AC098368 Rattus no	c 281	70.5	15.7	254147	14	AC161524	AC161524 Bos tauru
c 282	71	15.8	136519	14	AC166490	AC166490 Mus muscu	c 282	70.5	15.7	270524	14	AC151173	AC151173 Bos tauru
c 283	71	15.8	141544	15	AP005593	AP005593 Oryza sat	c 283	70.5	15.7	270524	14	AC151173	AC151173 Bos tauru
c 284	71	15.8	149622	14	AC074082	AC074082 Homo sapi	c 284	70.5	15.7	271456	14	AC162950	AC162950 Bos tauru
c 285	71	15.8	151143	8	AC108714	AC108714 Homo sapi	c 285	70.5	15.7	278521	14	AC156118	AC156118 Bos tauru
c 286	71	15.8	156707	8	AL359764	AL359764 Human DNA	c 286	70.5	15.7	280577	14	AC160659	AC160659 Bos tauru
c 287	71	15.8	166883	9	AC122541	AC122541 Mus muscu	c 287	70.5	15.7	280577	14	AC160659	AC160659 Bos tauru
c 288	71	15.8	167677	14	AC121510	AC121510 Mus muscu	c 288	70.5	15.7	285314	14	AC151194	AC151194 Bos tauru
c 289	71	15.8	181678	14	AC119610	AC119610 Rattus no	c 289	70.5	15.7	290683	1	AE017329	AE017329 Listeria
c 290	71	15.8	201805	9	AL608466	AL608466 Mouse DNA	c 290	70.5	15.7	294850	1	EX294148	EX294148 Pirellula
c 291	71	15.8	205990	14	AC114161	AC114161 Rattus no	c 291	70.5	15.7	315988	2	AE003481	AE003481 Drosophil
c 292	71	15.8	206494	9	AC138766	AC138766 Mus muscu	c 292	70.5	15.7	349980	6	AX571763	AX571763 Sequence
c 293	71	15.8	210533	9	AL773580	AL773580 Mouse DNA	c 293	70	15.6	578	2	AY292616	AY292616 Oikopleur
c 294	71	15.8	212299	9	AC144908	AC144908 Mus muscu	c 294	70	15.6	835	6	AR120284	AR120284 Sequence
c 295	71	15.8	214180	14	AC127209	AC127209 Rattus no	c 295	70	15.6	835	6	BD063293	BD063293 Streptoco

369	70	15.6	835	6	AR340975	Sequence	442	69.5	15.5	486	6	AR558783	Sequence
370	70	15.6	835	6	AR653238	Sequence	443	69.5	15.5	756	2	SILPH4G	XI6019 S. lemae hi
371	70	15.6	854	9	MMU48615	Mastomys na	444	69.5	15.5	1443	13	NDVPP	M20302 Newcastle d
372	70	15.6	1514	9	AF387892	Mus muscu	445	69.5	15.5	1759	2	AF510209	AF510209 Uroleptus
373	70	15.6	1536	9	AF387891	Mus muscu	446	69.5	15.5	2288	15	YSAPOX	M16193 Candida tro
374	70	15.6	1536	9	AF387893	Mus muscu	447	69.5	15.5	2845	15	YSAPOX4	M1260 Yeast (C.tr
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376	70	15.6	1536	9	AF387895	Mus muscu	449	69.5	15.5	3768	15	AK069523	AK069523 Oryza sat
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379	70	15.6	1536	9	AF388053	Mus muscu	452	69.5	15.5	11096	15	SCYNL054W	Z71330 S. crevisia
380	70	15.6	1536	9	AF388054	Mus muscu	453	69.5	15.5	28278	2	CEFO9B12	Z83104 Caenorhabd
381	70	15.6	1536	9	AF388055	Mus muscu	454	69.5	15.5	44465	15	SCU12141	U12141 Saccharomyc
382	70	15.6	1536	9	AF388056	Mus muscu	455	69.5	15.5	67378	14	AC120190	AC120190 Mus muscu
383	70	15.6	1536	9	AF388057	Mus muscu	456	69.5	15.5	68088	14	AC165738	AC165738 Bos tauru
384	70	15.6	1714	6	AR120239	Sequence	457	69.5	15.5	79509	14	AC166134	AC166134 Bos tauru
385	70	15.6	1714	6	BD063248	Streptoco	458	69.5	15.5	83719	15	AC165739	AC165739 Bos tauru
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387	70	15.6	1714	6	AR653193	Sequence	460	69.5	15.5	96413	9	AL831779	AL831779 Mouse DNA
388	70	15.6	2173	2	BT023409	Drosophil	461	69.5	15.5	103282	9	AL929311	AL929311 Mouse DNA
389	70	15.6	2303	15	SBY14274	Yi14274 Sorghum bic	462	69.5	15.5	108908	5	EX547993	EX547993 Zebrafish
390	70	15.6	2450	6	CQ614448	Sequence	463	69.5	15.5	110000	1	BA000012	Continuation (9 of
391	70	15.6	2694	6	CQ719899	Sequence	464	69.5	15.5	110000	1	BA000012	Continuation (10 of
392	70	15.6	2769	8	AB169176	Macaca fa	465	69.5	15.5	110000	15	CR380956	Continuation (4 of
393	70	15.6	3591	8	AY531390	Homo sapi	466	69.5	15.5	110000	15	AE016819	Continuation (2 of
394	70	15.6	3640	6	AR448205	Sequence	467	69.5	15.5	110000	15	AP008207	Continuation (35 o
395	70	15.6	3640	6	AX301218	Sequence	468	69.5	15.5	115109	9	AL731827	AL731827 Mouse DNA
396	70	15.6	3875	8	AB020710	Homo sapi	469	69.5	15.5	130127	4	AC153760	AC153760 Loxodonta
397	70	15.6	4061	6	AR3338872	Sequence	470	69.5	15.5	13482	14	AC109786	AC109786 Bos tauru
398	70	15.6	4818	8	BC067215	Homo sapi	471	69.5	15.5	139139	14	AC153340	AC153340 Loxodonta
399	70	15.6	4911	8	AX027388	Sequence	472	69.5	15.5	140791	15	AP002912	AP002912 Oryza sat
400	70	15.6	5077	8	AX331186	Homo sapi	473	69.5	15.5	141009	14	AC109915	AC109915 Bos tauru
401	70	15.6	5218	9	AF115970	Sequence	474	69.5	15.5	147688	4	AC153764	AC153764 Loxodonta
402	70	15.6	7832	2	AF366567	Sequence	475	69.5	15.5	156687	14	AC158133	AC158133 Mus muscu
403	70	15.6	8039	2	AY248889	Plasmodiu	476	69.5	15.5	159930	15	AJ627251	AJ627251 Nymphaea
404	70	15.6	10170	7	B4PORFSX	L35061 Bacterioph	477	69.5	15.5	164083	14	AC109297	AC109297 Mus muscu
405	70	15.6	14273	15	AC144717	Zea mays	478	69.5	15.5	164277	14	AC154625	AC154625 Mus muscu
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407	70	15.6	36400	2	AF067622	Sequence	480	69.5	15.5	167127	8	CNS01RHR	AL162311 Human chr
408	70	15.6	41278	2	CBRG30E10	Sequence	481	69.5	15.5	168323	9	AC127223	AC127223 Mus muscu
409	70	15.6	100367	8	AL357137	Human DNA	482	69.5	15.5	172161	15	AP003301	AP003301 Oryza sat
410	70	15.6	110000	1	BA000019	Continuation (5 of	483	69.5	15.5	175174	15	AP003339	AP003339 Oryza sat
411	70	15.6	110000	1	BA000019	Continuation (64 o	484	69.5	15.5	175315	15	AC161135	AC161135 Bos tauru
412	70	15.6	110000	1	BA000023	Continuation (21 o	485	69.5	15.5	176388	14	AC162494	AC162494 Bos tauru
413	70	15.6	110000	14	CT005270	Continuation (13 o	486	69.5	15.5	177889	14	AC164139	AC164139 Bos tauru
414	70	15.6	110000	15	CR382136	Continuation (10 o	487	69.5	15.5	178616	9	AC102420	AC102420 Mus muscu
415	70	15.6	159734	9	AC122533	Mus muscu	488	69.5	15.5	181850	14	AC153167	AC153167 Bos tauru
416	70	15.6	160961	14	AL345794	AL345794 Xenopus t	489	69.5	15.5	188215	14	AC025725	AC025725 Caenorhab
417	70	15.6	161513	14	AL365262	AL365262 Homo sapi	490	69.5	15.5	188616	2	AC084158	AC084158 Caenorhab
418	70	15.6	163489	14	AC035078	AC025078 Homo sapi	491	69.5	15.5	189920	8	AC092682	AC092682 Homo sapi
419	70	15.6	163972	8	AC103987	AC103987 Homo sapi	492	69.5	15.5	190051	14	AC118044	AC118044 Mus muscu
420	70	15.6	164013	14	AC140446	AC140446 Mus muscu	493	69.5	15.5	195185	14	AC163104	AC163104 Mus muscu
421	70	15.6	176757	14	AC163537	AC163537 Bos tauru	494	69.5	15.5	196583	9	AC151472	AC151472 Mus muscu
422	70	15.6	179909	9	AL671741	AL671741 Mouse DNA	495	69.5	15.5	202729	14	AC163560	AC163560 Bos tauru
423	70	15.6	181413	14	AP001352	AP001352 Homo sapi	496	69.5	15.5	204144	14	AC152787	AC152787 Bos tauru
424	70	15.6	184090	9	AC123304	AC123304 Mus muscu	497	69.5	15.5	205650	9	AC154362	AC154362 Mus muscu
425	70	15.6	186867	14	AC164420	AC164420 Mus muscu	498	69.5	15.5	206954	14	AC162701	AC162701 Bos tauru
426	70	15.6	189616	14	AC119603	AC119603 Rattus no	499	69.5	15.5	212931	14	AC156482	AC156482 Bos tauru
427	70	15.6	190298	9	AC121294	AC121294 Mus muscu	500	69.5	15.5	212149	14	AC163930	AC163930 Bos tauru
428	70	15.6	195349	14	AC006705	AC006705 Caenorhab							
429	70	15.6	195644	9	AC102784	AC102784 Mus muscu							
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432	70	15.6	226810	14	AC125804	AC125804 Rattus no							
433	70	15.6	227462	14	AC164099	AC164099 Mus muscu							
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435	70	15.6	234156	14	AC163295	AC163295 Mus muscu							
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437	70	15.6	242832	9	AC117584	AC117584 Mus muscu							
438	70	15.6	246551	14	AC096478	AC096478 Rattus no							
439	70	15.6	252470	14	AC095986	AC095986 Rattus no							
440	70	15.6	266811	14	AC162633	AC162633 Bos tauru							
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ALIGNMENTS

RESULT 1	LOCUS	BD076937	5' EST of secretory protein expressed in prostate.	483 bp	DNA	linear	PAT 27-AUG-2002
BD076937	DEFINITION	BD076937					
	ACCESSION	BD076937					
	VERSION	BD076937.1	GI:22622540				
	KEYWORDS	JP 2001512013-A/184					
	SOURCE	Homo sapiens (human)					
	ORGANISM	Homo sapiens					
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 483)
Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
5' EST of secretory protein expressed in prostate
Patent: JP 2001512013-A 184 21-AUG-2001;
GENSET

OS Homo sapiens (human)
PN JP 2001512013-A/184
PD 31-AUG-2001
PF 31-JUL-1998 JP 2000505291
PR 01-AUG-1997 US 08/905144
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO PI
LACROIX

PC C12N15/09,C07K14/47,C12P21/02,C12Q1/02,C12Q1/68,C12N15/00 CC
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CC identity 99
CC region 1. .310
CC id T26956
CC est
CC blastn
CC identity 98
CC region 1. .315
CC id T31666
CC est
CC blastn
CC identity 100
CC region 137. .267
CC id R14990
CC est
CC blastn
CC identity 100
CC region 63. .137
CC id R14990
CC est
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CC identity 100
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CC Von Heijne matrix
CC score 5.2
CC seq LCVEFASVASCDA/AV

PH Key Location/Qualifiers
FT misc_feature 105. .414
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FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 8.23e-46 Length: 483
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BD076937 (1-483)

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Db 160 ATGGAAGGGCTCTGAATCTCCTACTCGAGCTCCGGTGAGGAGCGCTTGGACGC 219
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Db 220 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAACACT 279

Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
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280 GATTCACCACTTCTAAATCAGCCATCTGAAGATACTCAGCAAGAAAATGGCAGCATG 339
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Qy 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
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340 TTCTCTCTCATTCCTGGAATATTGATGATTAGATCTAAACAAATCTCTGAGAGAGGGCT 399
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Qy 81 ArgGlyValCysSerTyrLeu 87
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Db 400 CGAGGGGTGTGTTCTACTTTA 420

RESULT 2
AF201687 1261 bp mRNA linear PRI 16-MAY-2003
LOCUS Homo sapiens ETS1-associated protein 2 (EAP2) mRNA, complete cds.
DEFINITION AF201687
ACCESSION AF201687
VERSION AF201687.1 GI:11493668
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1261)
AUTHORS Pei,H., Yordy,J.S., Leng,Q., Zhao,Q., Watson,D.K. and Li,R.
TITLE EAP11 interacts with ETS1 and modulates its transcriptional
function
JOURNAL Oncogene 22 (18), 2699-2709 (2003)
PUBMED 12743594
REFERENCE 2 (bases 1 to 1261)
AUTHORS Li,R., Pei,H. and Papas,T.S.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-1999) Center for Molecular and Structural
Biology, Department of Medicine, and Hollings Cancer Center,
Medical University of South Carolina, 86 Jonathan Lucas St.,
Charleston, SC 29425, USA
FEATURES
Location/Qualifiers
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LKKRSNVIITGHEEGYFTALMLKSRVKLSQELI PPSTKMNENLCLVHVNVSGL
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ORIGIN
Alignment Scores:
Pred. No.: 2.42e-45 Length: 1261
Score: 448.00 Matches: 87
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AF201687 (1-1261)

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Db 185 ATGGAAGGGCTCTGAACCTCTACTTCGAGCTCCGGTGGAGGAGCGCTTGGAAAGC 244
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db 245 CGACCTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAAC 304
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 305 GATTCCACCACTCTTAAATCAGCCCACTCTGAAGATACCTCAGCAAGAAAATGGCAGCATG 364
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 365 TTCTCTCTCATTTACCTGGAATATTGATGATTAGATCTTAAACAATCTGTCTCAGAGGGCT 424
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 425 CGAGGGGTGTCTCTACTTAA 445

RESULT 3
LOCUS BD205490 1920 bp DNA linear PAT 17-JUL-2003
DEFINITION CD40-Interacting and TRAF-interacting protein.
ACCESSION BD205490
VERSION BD205490.1 GI:33015260
KEYWORDS JP 2002512796-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1920)
AUTHORS Pype,S.M.C., Ghislain,J.E.F.J., Remacle and Huylebroeck,D.F.E.
TITLE CD40-Interacting and TRAF-interacting protein
JOURNAL Patent: JP 2002512796-A 1 08-MAY-2002;
VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE VZW
COMMENT OS Homo sapiens (human)
PN JP 2002512796-A/1
PD 08-MAY-2002
PF 28-APR-1999 JP 2000546003
PI STEFAN MARIA CHRISTIAN PYPE,
PI JACQUES EMILE FERNAND JOSIANE GHISLAIN REMACLE, PI DANNY
FRANCOIS EVELINE HUYLEBROECK
PC C12N15/09,A61K38/00,A61P9/10,A61P19/02,A61P25/00,A61P35/00,PC
A61P37/02,
PC A61P37/06,A61P43/00,C07K14/47,C07K16/18,G01N33/15,G01N33/50,
PC G01N33/566,
PC C12N15/00,A61K37/02
CC CD40-Interacting and TRAF-interacting protein. FH Key
FT CDS
Location/Qualifiers
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ORIGIN
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Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-757-745-2_COPY_54_140 (1-87) x BD205490 (1-1920)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 179 ATGGAAGGGCTCTGAACCTCTACTTCGAGCTCCGGTGGAGGAGCGCTTGGAAAGC 238
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db 239 CGACCTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAAC 298
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 299 GATTCCACCACTCTTAAATCAGCCCACTCTGAAGATACCTCAGCAAGAAAATGGCAGCATG 358
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 359 TTCTCTCTCATTTACCTGGAATATTGATGATTAGATCTTAAACAATCTGTCTCAGAGGGCT 418
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 419 CGAGGGGTGTCTCTACTTAA 439

RESULT 4
LOCUS AR594294 1920 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 1 from patent US 6812203.
ACCESSION AR594294
VERSION AR594294.1 GI:56643900
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1920)
AUTHORS Pype,S.M.C., Remacle,J.E.F. and Huylebroeck,D.F.E.
TITLE CD40-Interacting and TRAF-interacting proteins
JOURNAL Patent: US 6812203-A 1 02-NOV-2004;
Vlaams Interuniversitair Instituut voor Biotechnologie VZW;
Zwijnaarde;
WOX;
Location/Qualifiers
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ORIGIN
Alignment Scores: 3.88e-45 Length: 1920
Pred. No.: 448.00 Matches: 87
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-757-745-2_COPY_54_140 (1-87) x AR594294 (1-1920)

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Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 299 GATTCCACCACTCTTAAATCAGCCCACTCTGAAGATACCTCAGCAAGAAAATGGCAGCATG 358
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 359 TTCTCTCTCATTTACCTGGAATATTGATGATTAGATCTTAAACAATCTGTCTCAGAGGGCT 418
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 419 CGAGGGGTGTCTCTACTTAA 439

RESULT 5
AX011599
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LOCUS AX011599 1920 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 1 from Patent WO9955859.
ACCESSION AX011599
VERSION AX011599.1 GI:9998123
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE Remacle,J.B., Huylebroeck,D.F. and Pype,S.M.
AUTHORS Cd40-interacting and traf-interacting proteins
TITLE Patent: WO 9955859-A 1 04-NOV-1999;
JOURNAL REMACLE JACQUES EMILE FERNAND (BE); VLAAMS INTERUNIV INST BIOTECH
(BE); HUYLEBROECK DANNY FRANCOIS EVE (BE); PYPE STEFAN MARIA
CHRISTIAAN (BE)
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CDS
ORIGIN
Alignment Scores: 3.88e-45 Length: 1920
Pred. No.: 448.00 Matches: 87
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
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Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAenGluThrThr 40
Db 239 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACA 298
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAenGlySerMet 60
Db 299 GATTCACCACTTCTAAATCAGCCCATCTGAGATACCTCAGCAAGAAATGCGCAGATG 358
Qy 61 PheSerLeuIleThrTyrAenIleAspGlyLeuAspLeuAenLeuSerGluArgAla 80
Db 359 TTCTCTCTCAATACCTGGAATATGATGATTAGATCTAAACAATCTGTGAGAGGGCT 418
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 419 CGAGGGGTGTTCCTACTTA 439
RESULT 6
HSA269473 1921 bp mRNA linear PRI 27-MAY-2000
LOCUS HSA269473
DEFINITION Homo sapiens mRNA for TRAF and TNF receptor associated protein
(ctrap gene).
ACCESSION AJ269473
VERSION AJ269473.1 GI:8247253

KEYWORDS TRAF and TNF receptor associated protein; trtap gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE Pype,S., Declercq,W., Ibrahim,A., Michiels,A., Van
AUTHORS Rietschoten,J.G., Dewulf,N., de Boer,M., Vandenabeele,P.,
Huylebroeck,D. and Remacle,J.B.
TITLE TTRAP, a novel protein that associates with CD40, tumor necrosis
factor (TNF) receptor-75 and TNF receptor-associated factors
(TRAFs), and that inhibits nuclear factor-kappa B activation
J. Biol. Chem. 275 (24), 18586-18593 (2000)
JOURNAL 10764746
PUBMED
REFERENCE 2 (bases 1 to 1921)
AUTHORS Pype,S.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-1999) Pype S., VIB07, Dept. Cell Growth,
Differentiation and Development, Flanders Interuniversity Institute
for Biotechnology, CELGEN, K.U. Leuven, Gasthuisberg Campus,
Herestraat 49, B-3000 Leuven, BELGIUM
COMMENT Related sequence: AL031775.
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ORIGIN
Alignment Scores: 3.88e-45 Length: 1921
Pred. No.: 448.00 Matches: 87
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
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US-10-757-745-2_COPY_54_140 (1-87) x HSA269473 (1-1921)
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Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAenGluThrThr 40
Db 241 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACA 300
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAenGlySerMet 60

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Db 301 GATTCCACACTTCTAAATCAGCCACTCGAGACTCTGAGAGAAATGGCAGCATG 360
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Db 361 TTCTCTCTCATACCTGGAATATTGATGATTAGATCTAAACAATCTGTCTCAGAGGGCT 420
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Qy 81 ArgGlyValCysSerTyrLeu 87
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Db 421 CGAGGGGTGTCTCTACTTA 441
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RESULT 7
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LOCUS Homo sapiens AD022 protein (AD022) mRNA, complete cds.
DEFINITION AF223469
VERSION AF223469.1 GI:7578788
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1936)
AUTHORS Song,H., Gao,G., Peng,Y., Ren,S., Chen,Z. and Han,Z.
TITLE A novel gene expressed in human adrenal gland
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1936)
AUTHORS Song,H., Gao,G., Peng,Y., Ren,S., Chen,Z. and Han,Z.
TITLE Direct Submision
JOURNAL Submitted (12-JAN-2000) Chinese National Human Genome Center at
Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
Shanghai 201203, China
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ORIGIN
Alignment Scores:
Pred. No.: 3.92e-45 Length: 1936
Score: 448.00 Matches: 87
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Db 176 ATGGAAGGGCTCTGAATCTCTACTTCGAGCCTCGGTGGAGGAGCGCTTGGAAAGC 235
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Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
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LOCUS Homo sapiens TRAF and TNF receptor associated protein, mRNA (cDNA
clone MGC:9099 IMAGE:3920790), complete cds.
DEFINITION BC017553
VERSION BC017553.2 GI:34782842
KEYWORDS MGC.
SOURCE Homo sapiens (human)
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Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
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Db 416 CGAGGGGTGTCTCTACTTA 436
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AR339398 1948 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 889 from patent US 6569662.
DEFINITION AR339398
ACCESSION AR339398
VERSION AR339398.1 GI:33726255
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1948)
AUTHORS Tang,Y.T., Zhou,P. and Dmanac,R.T.
TITLE Nucleic acids and polypeptides
JOURNAL Patent: US 6569662-A 889 27-MAY-2003;
Hyseq, Inc.; Sunnyvale, CA
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Pred. No.: 3.95e-45 Length: 1948
Score: 448.00 Matches: 87
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db 258 CGACTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAACACT 317
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Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
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Db 318 GATTCCACCACTTCTAAATCAGCCCACTCTGAAGATACTCAGCAAGAAAATGGCAGCATG 377
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Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
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Qy 81 ArgGlyValCysSerTyrLeu 87
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Db 438 CGAGGGGTGTCTCTACTTA 458
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RESULT 9
BC017553 1952 bp mRNA linear PRI 29-JUN-2004
LOCUS Homo sapiens TRAF and TNF receptor associated protein, mRNA (cDNA
clone MGC:9099 IMAGE:3920790), complete cds.
DEFINITION BC017553
VERSION BC017553.2 GI:34782842
KEYWORDS MGC.
SOURCE Homo sapiens (human)
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ORGANISM	Homo sapiens	CDS	38..1126
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AUTHORS	1 (bases 1 to 1952)		/codon_start=1
	Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenman, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.		/product="TRAF and TNF receptor-associated protein"
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		/db_xref="GI:17028465"
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		/db_xref="WIM:605764"
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REFERENCE	2 (bases 1 to 1952)		
AUTHORS	Strauberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	On Sep 16, 2003 this sequence version replaced gi:17028464. Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC/DC/DT/PTP CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Anara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Telka Olson, Diana Palmquist, Anca Petrescu, Anna Lilea Prabh, Parvaneh Saeedi, JR Santos, Angeliq Schnerch, Ursula Skalska, Duane Smallos, Jeff Stott, Miranda Tsai, George Yang, Jacque Schein, Asim Siddiqui, Rob Holt, Marco Marra.		
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	DB 257 CGACCTGAAACATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 316		
	QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60		
	DB 317 GATTCACCACTTCTAAATCAGCCATCTGAAGATCTCAGCAAGAAATGSCAGCATG 376		
	QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80		
	DB 377 TTCTCTCTCATTCCTGGAATATTGATGATTAGATCTAAACAATCTGTGAGAGGGCT 436		
	QY 81 ArgGlyValCysSerTyrLeu 87		
	DB 437 CGAGGGGTGTGTCTCTACTTA 457		
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	ACCESSION	E23195	
	VERSION	E23195.1 GI:13024277	
	KEYWORDS	JP 1999075856-A/1.	
	SOURCE	unidentified	
	ORGANISM	unclassified.	
	REFERENCE	1 (bases 1 to 2499)	
	AUTHORS	Takashi, T. and Kazuhiko, Y.	
	TITLE	Topoisomerase binding protein	
	JOURNAL	Patent: JP 1999075856-A 1 23-MAR-1999;	
	COMMENT	TAKASHI TSURUO, CHUGAI PHARMACEUT CO LTD	
		OS Unidentified	
		PN JP 1999075856-A/1	
		PD 23-MAR-1999	
		PF 17-SEP-1997 JP 1997251544	
		PR	
		PI TAKASHI TSURUO, KAZUHIKO YAMANE	
		PC C12N15/09, C07K14/47, C12N9/90, C12N15/00	
		CC Strandedness: Double;	
		CC Topology: Linear;	
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		FT Location/Qualifiers	
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FEATURES	FT	Location/Qualifiers		/organism='Unidentified'.	
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Alignment Scores:	Pred. No.:	5.22e-45	Length:	2499	
	Score:	448.00	Matches:	87	
	Percent Similarity:	100.00%	Conservative:	0	
Query Match:	Best Local Similarity:	100.00%	Mismatches:	0	
	Indels:	0			
	Gaps:	0			
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	Db	701	CGACTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAACACT	760	
	Qy	41	AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAenGlySerMet	60	
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	Qy	61	PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAenLeuSerGluArgAla	80	
	Db	821	TTCTCTCTCATTTACCTGGAATATTGATGGATTAGATCTAAACAATCTGTCTCAGAGGGCT	880	
US-10-757-745-2_COPY_54_140 (1-87) x BD150065 (1-752)	Qy	81	ArgGlyValCysSerTyrLeu	87	
	Db	881	CGAGGGGTGTGTTCTTACTTA	901	
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	LOCUS	Sequence 4908 from Patent EP1074617.			
	DEFINITION	Primer for synthesizing full-length cDNA and use thereof.			
US-10-757-745-2_COPY_54_140 (1-87) x AX870003 (1-752)	ACCESSION	AX870003			
	VERSION	AX870003.1 GI:27855823			
	KEYWORDS	JP 2002191363-A/4908.			
US-10-757-745-2_COPY_54_140 (1-87) x AX870003 (1-752)	SOURCE	Homo sapiens (human)			
	ORGANISM	Homo sapiens			
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			
US-10-757-745-2_COPY_54_140 (1-87) x AX870003 (1-752)	AUTHORS	Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.			
	TITLE	Primer for synthesizing full-length cDNA and use thereof			
	JOURNAL	Patent: JP 2002191363-A 4908 09-JUL-2002;			
US-10-757-745-2_COPY_54_140 (1-87) x AX870003 (1-752)	COMMENT	HELIOS RESEARCH INSTITUTE			
	OS	Homo sapiens (human)			
	PN	JP 2002191363-A/4908			
US-10-757-745-2_COPY_54_140 (1-87) x AX870003 (1-752)	PD	09-JUL-2002			
	PF	28-JUL-2000 JP 2000280990			
	PI	TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SAITO,			
US-10-757-745-2_COPY_54_140 (1-87) x AX870003 (1-752)	PI	JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,			
	PI	KEIICHI NAGAI, TETSUJI OTSUKI			
	PC	C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/68, C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC			
US-10-757-745-2_COPY_54_140 (1-87) x AX870003 (1-752)	Primer for synthesizing full-length cDNA and use thereof	FH			
	Location/Qualifiers	1..752			
	FT	source			
US-10-757-745-2_COPY_54_140 (1-87) x AX870003 (1-752)	FT	/organism='Homo sapiens (human)'.			
	FEATURES	Location/Qualifiers			

FEATURES	FT	Location/Qualifiers		/organism='Unidentified'.	
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		/db_xref="taxon:9606"		/db_xref="taxon:9606"	
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	Qy	1	MetGluArgAlaLeuAenSerTyrPheGluProValGluGluSerAlaLeuGluArg	20	
	Db	160	ATGGAAGGGCTCTGAACCTCTCTGAGCCTCCGGTGGAGGAGCGCTTGGAAACGC	219	
Alignment Scores:	Pred. No.:	1.74e-44	Length:	752	
	Score:	439.00	Matches:	86	
	Percent Similarity:	98.85%	Conservative:	0	
Query Match:	Best Local Similarity:	98.85%	Mismatches:	1	
	Indels:	0			
	Gaps:	0			
US-10-757-745-2_COPY_54_140 (1-87) x BD150065 (1-752)	Qy	21	ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr	40	
	Db	220	CGACCTGGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAACAACACT	279	
	Qy	41	AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAenGlySerMet	60	
US-10-757-745-2_COPY_54_140 (1-87) x AX870003 (1-752)	Db	280	GATTCCACCATCTTAAAAATCAGCCCATCTGAAGTACTCAGCAAGAAATGGCAGCATG	339	
	Qy	61	PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAenLeuSerGluArgAla	80	
	Db	340	TTCTCTCTCATTTACCTGGAATATTGATGGATTAGATCTAAACAATCTGTCTCAGAGGGCT	399	
US-10-757-745-2_COPY_54_140 (1-87) x BD150065 (1-752)	Qy	81	ArgGlyValCysSerTyrLeu	87	
	Db	400	CGAGGGGTGTGTTCTTACTTA	420	
RESULT 12	AX870003	752 bp DNA linear		PAT 17-DEC-2003	
	LOCUS	Sequence 4908 from Patent EP1074617.			
	DEFINITION	Primer for synthesizing full-length cDNA and their use			
US-10-757-745-2_COPY_54_140 (1-87) x AX870003 (1-752)	ACCESSION	AX870003			
	VERSION	AX870003.1 GI:40024866			
	KEYWORDS	Homo sapiens (human)			
US-10-757-745-2_COPY_54_140 (1-87) x AX870003 (1-752)	SOURCE	Homo sapiens			
	ORGANISM	Homo sapiens			
	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			
US-10-757-745-2_COPY_54_140 (1-87) x AX870003 (1-752)	AUTHORS	Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.			
	TITLE	Primers for synthesizing full-length cDNA and their use			
	JOURNAL	Patent: EP 1074617-A 4908 07-FEB-2001;			
US-10-757-745-2_COPY_54_140 (1-87) x AX870003 (1-752)	FEATURES	Research Association for Biotechnology (JP)			
	source	Location/Qualifiers			
		1..752			
US-10-757-745-2_COPY_54_140 (1-87) x AX870003 (1-752)	COMMENT	/organism="Homo sapiens"			
	OS	/mol_type="unassigned DNA"			
	PN	/db_xref="taxon:9606"			
US-10-757-745-2_COPY_54_140 (1-87) x AX870003 (1-752)	PD	1.74e-44			
	PF	439.00			
	PI	98.85%			
US-10-757-745-2_COPY_54_140 (1-87) x AX870003 (1-752)	PI	98.85%			
	PI	98.85%			
	PI	98.85%			
US-10-757-745-2_COPY_54_140 (1-87) x AX870003 (1-752)	PC	98.85%			
	PC	98.85%			
	PC	98.85%			
US-10-757-745-2_COPY_54_140 (1-87) x AX870003 (1-752)	Primer for synthesizing full-length cDNA and use thereof	FH			
	Location/Qualifiers	1..752			
	FT	source			
US-10-757-745-2_COPY_54_140 (1-87) x AX870003 (1-752)	FT	/organism="Homo sapiens"			
	FEATURES	Location/Qualifiers			

Db 160 ATGAAAGGCGCTGAACCTCTGCTTCCGAGCCTCCGGTGGAGAGAGCGCTTGAACGC 219

Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40

Db 220 CGACCTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 279

Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60

Db 280 GATTCACCACTCTTAATAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGCATG 339

Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80

Db 340 TTCTCTCTCATTAACCTGGAATATTGATGATTAGATCTAAACAATCTGTGCAGAGGGCT 399

Qy 81 ArgGlyValCysSerTyrLeu 87

Db 400 CGAGGGGTGTGCTCTACTTA 420

RESULT 13

LOCUS BD157138 1898 bp DNA linear PAT 17-JAN-2003

DEFINITION Primer for synthesizing full-length cDNA and use thereof.

ACCESSION BD157138

VERSION BD157138.1 GI:27862896

KEYWORDS JP 2002191363-A/11981.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1898)

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

TITLE Primer for synthesizing full-length cDNA and use thereof

JOURNAL Patent: JP 2002191363-A 11981 09-JUL-2002;

COMMENT OS Homo sapiens (human)

PN JP 2002191363-A/11981

PD 09-JUL-2002

PF 28-JUL-2000 JP 2000280990

PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU

PI SAITO,

PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,

PI KEIICHI NAGAI,TETSUUI OTSUKI

PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC 10,

PC C12P21/02,C12Q1/68/C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC

Primer for synthesizing full-length cDNA and use thereof FH Key

Location/Qualifiers (1)..(1086).

FEATURES

source

1..1898

/organism="Homo sapiens"

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ORIGIN

Alignment Scores:

Pred. No.: 4,94e-44 Length: 1898

Score: 439.00 Matches: 86

Percent Similarity: 98.85% Conservative: 0

Best Local Similarity: 98.85% Mismatches: 1

Query Match: 97.99% Indels: 0

DB: 6 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BD157138 (1-1898)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20

Db 160 ATGAAAGGCGCTGAACCTCTGCTTCCGAGCCTCCGGTGGAGAGAGCGCTTGAACGC 219

Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40

Db 220 CGACCTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 279

Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60

Db 280 GATTCACCACTCTTAATAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGCATG 339

Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80

Db 340 TTCTCTCTCATTAACCTGGAATATTGATGATTAGATCTAAACAATCTGTGCAGAGGGCT 399

Qy 81 ArgGlyValCysSerTyrLeu 87

Db 400 CGAGGGGTGTGCTCTACTTA 420

RESULT 14

LOCUS AX878304 1898 bp DNA linear PAT 17-DEC-2003

DEFINITION Sequence 13209 from Patent EP1074617.

ACCESSION AX878304

VERSION AX878304.1 GI:40033040

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

TITLE Primers for synthesizing full-length cDNA and their use

JOURNAL Patent: EP 1074617-A 13209 07-FEB-2001;

FEATURES

source

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/organism="Homo sapiens"

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1..1089

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ELCLMTSHLESTRGHAARMNQLKMLKKMQEAPESATVIFAGDTNLRDREVTCCGL

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CDS

ORIGIN

Alignment Scores:

Pred. No.: 4,94e-44 Length: 1898

Score: 439.00 Matches: 86

Percent Similarity: 98.85% Conservative: 0

Best Local Similarity: 98.85% Mismatches: 1

Query Match: 97.99% Indels: 0

DB: 6 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AX878304 (1-1898)

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Db 160 ATGAAAGGCGCTGAACCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 219

Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluThrThr 40

Db 220 CGACCTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAAC 279

Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60

Db 280 GATTCACCACTCTTAATAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGCATG 339

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Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAnAsnLeuSerGluArgala 80
Db 340 TTCTCTCTCAATACCTGGAATATTGATGGATTAGATCTAAACAATCTGTCTCAGAGAGGCT 399

Qy 81 ArgGlyValCysSerTyrLeu 87
Db 400 CGAGGGGTGTCTCTCTACTTA 420

RESULT 15
AK002168
LOCUS Homo sapiens cDNA FLJ11306 fis, clone PLAC1010031.
DEFINITION AK002168
ACCESSION AK002168
VERSION AK002168.1 GI:7023882
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1
Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,
Sekine, M., Ohayashi, M., Nishi, T., Shibahara, T., Tanaka, T.,
Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,
Nagahara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M.,
Shiratori, A., Sudo, H., Hosiiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T.,
Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuno, N., Sato, K.,
Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yanashita, H.,
Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M.,
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Yosida, M., Hotsuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A.,
Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R.,
Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A.,
Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T.,
Shohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S.,
Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H.,
Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T.,
Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K.,
Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M.,
Tachiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yanada, K., Fujii, Y.,
Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N.,
Inagaki, H., Ikemura, Y., Okamoto, S., Okitani, R., Kawakami, T.,
Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K.,
Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T.,
Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J.,
Sato, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,
Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R.,
Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.
Complete sequencing and characterization of 21,243 full-length
human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
14702039
2
Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H.,
Wakamatsu, M., Hosiiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K.,
Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K.,
Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A.,
Nakamura, Y., Nagahara, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T.
NEDO human cDNA sequencing project
Unpublished
3 (bases 1 to 1898)
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
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sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

FEATURES

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CDS

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LKRSSNYEIIITGHEGYFTAILMKSRVKLQSEIIPFSTKMRLNLLCVHNVSGN
ELCLMTSHLESTRGHAARNQMLKWLKQEAPEASATVIFAGDTNLRDREVTCCGL
PNNIVDWELGPKHCKOYTDWTQMNSNLGITAAKLRFPRIFFRAAESEGHIIIPRL
DLGLEKLDGCRFPDSHGLNLDIIL"

ORIGIN

Alignment Scores:
Pred. No.: 4,94e-44 Length: 1898
Score: 439.00 Matches: 86
Percent Similarity: 98.85% Conservative: 0
Best Local Similarity: 98.85% Mismatches: 1
Query Match: 97.99% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AK002168 (1-1898)

Qy 1 MetGluArgalaLeuAnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 160 ATGGAAGAGGCTCTGAACTCTCTGCTCGAGCCTCGGTGGAGGAGCGCTTGGAAACGC 219
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Db 220 CGACCTGAACACCTCTCTGAGCCCAACACCTATGTTGACCTAACCAATGAGAACAACACT 279
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 280 GATTCCACCACTTCTAAATCAGCCCATCTGAAGATACTCAGCAAGAAATGGCAGCATG 339
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAnLeuSerGluArgala 80
Db 340 TTCTCTCTCAATACCTGGAATATTGATGGATTAGATCTAAACAATCTGTCTCAGAGAGGCT 399
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 400 CGAGGGGTGTCTCTCTACTTA 420

RESULT 16

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

COMMENT

1

Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.

Kits, such as nucleic acid arrays, comprising a majority of

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominoidea; Homo.

1

Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.

Kits, such as nucleic acid arrays, comprising a majority of

humanexons or transcripts, for detecting expression and other uses thereof

JOURNAL
Patent: WO 02068579-A 12534 06-SEP-2002;
PE Corporation (NY) (US)

FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"

ORIGIN

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Score: 424.00 Matches: 83
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.64% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CQ726600 (1-858)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
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Db 160 ATGGAAGGGCTCTGAACCTCTTCTGAGCCTCCGCTGGAGAGAGCGCTTGGAAACG 219
|||||

QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
|||||
Db 220 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTGTGACCTAACCAATGAAGAAACAACT 279
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QY 41 AspSerThrThrSerIlylleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
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Db 280 GATTCCACCACCTCTTAATAATCACCCATCTGAAGATACCTCAGCAAGAAATGCGACATG 339
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QY 61 PheSerLeuIleThrIrpAenIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
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Db 340 TTCTCTCTATTAACCTGGATATGTGATGATTAGATCTTAACAACTGTGCAGAGAGGGCT 399
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QY 81 ArgGlyVal 83
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Db 400 CGAGGGGGT 408
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RESULT 17
AC152027/c
LOCUS
DEFINITION
AC152027 150344 bp DNA linear HTG 11-NOV-2004
Dasyapus novemcinctus clone VMRC5-12D21, WORKING DRAFT SEQUENCE, 5
ordered pieces.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AC152027.2 GI:55700150
HTG; HTGS_PHASE2; HTGS DRAFT.
Dasyapus novemcinctus (nine-banded armadillo)
Dasyapus novemcinctus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Xenarthra; Dasypodidae; Dasyapus.
1 (bases 1 to 150344)
Antonellis,A., Ayelle,K., Benjamin,B., Blakesley,R.W., Boakye,A.,
Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,H.,
Engle,J., Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N.,
Ho,S.-L., Hu,P., Hurl,B., Idol,J.R., Jones,C., Kwong,P., Laric,P.,
Larson,S., Lee-Lin,S.-Q., Legaspi,R., Madden,M., Maduro,Q.L.,
Maduro,V.B., Margulies,E.H., Masiello,C., Maskeri,B., McDowell,J.,
Mullikin,J.C., Oestreicher,J.S., Park,M., Portnoy,M.E., Prasad,A.,
Puri,O., Reddi-Dugue,N., Rosas,B., Schandler,K., Schueler,M.G.,
Shah,K., Sison,C., Stantrilop,S., Stephen,E., Thomas,J.W.,
Thomas,P.J., Tsipouri,V., Vogt,J.L., Wetherby,K.D., Young,A. and
Green,E.D.

TITLE
JOURNAL
REFERENCE
AUTHORS

NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 150344)
Green,E.D.
Direct Submission
Submitted (21-OCT-2004) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 150344)

AUTHORS
TITLE
JOURNAL
COMMENT

Green,E.D.
Direct Submission
Submitted (11-NOV-2004) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
On Nov 11, 2004 this sequence version replaced gi:54312159.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
----- Project Information
Center project name: ifi
Center clone name: 012D21

The sequence data in this record represents an 'enhanced'
version of a Phase 2 submission. Specifically, the indicated
order and orientation of each sequence contig has been
established using one or more of the following: read-pair
data from individual subclones, overlaps with neighboring
clones, alignment with available reference sequence (e.g.,
human), and/or confirmation by PCR testing. In addition,
the sequence assembly is based on at least 8X average
coverage in Q20 bases and has been reviewed to rule out
gross misassemblies, the low-quality ends of sequence
contigs have been trimmed away, and each base is associated
with a Phrap-derived Quality score.

----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 149480 bases at least Q40
Consensus quality: 149754 bases at least Q30
Consensus quality: 149909 bases at least Q20
Insert size: 155000; agarose-fp
Insert coverage: 149944; sum-of-contigs
Quality coverage: 9.52x in Q20 bases; agarose-fp
Quality coverage: 9.84x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

1 36273: contig of 36273 bp in length
* 36274 36373: gap of unknown length
* 36374 55049: contig of 18676 bp in length
* 55050 55149: gap of unknown length
* 55150 101939: contig of 46790 bp in length
* 101940 102039: gap of unknown length
* 102040 114806: contig of 12767 bp in length
* 114807 114906: gap of unknown length
* 114907 150344: contig of 35438 bp in length.

Location/Qualifiers
1..150344
/organism="Dasyapus novemcinctus"
/mol_type="genomic DNA"
/db_xref="taxon:9361"
/clone="VMRC5-12D21"
/clone_lib="VMRC5"
/notes="BAC resource: http://bacpac.chori.org/"
1..36273
/notes="assembly_fragment
clone end:SP6
vector_side:left"
1..23436
/notes="clone overlaps with GenBank Accession Number
AC150209 clone VMRC5-168B11 (center project name ifj)"
36274..36373
/estimated_length=unknown

misc_feature
1..36273
misc_feature
1..23436
gap

FEATURES
source

```

misc_feature 36374..55049
              /note="assembly_fragment"
gap          55050..55149
              /estimated_length=unknown
misc_feature 55150..101939
              /note="assembly_fragment"
gap          101940..102039
              /estimated_length=unknown
misc_feature 102040..114806
              /note="assembly_fragment"
gap          114807..114906
              /estimated_length=unknown
misc_feature 114907..1150344
              /note="assembly_fragment"
              clone_end:17
              vector_side:right"

ORIGIN
Alignment Scores:
Pred. No.: 1.06e-28 Length: 150344
Score: 332.00 Matches: 66
Percent Similarity: 83.91% Conservative: 7
Best Local Similarity: 75.86% Mismatches: 14
Query Match: 74.11% Indels: 0
DB: 14 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AC152027 (1-150344)
Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
Db 53438 ATGGAAGAGCGCAGAACTCTACTTTGAGCGGTGGTGGAGGAGCGCCCGGAGAGC 53379
Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
Db 53378 CGGCCTCGGAGCCCTCGCGCCGAGCGCTGTGTGACCTTAAGCAACGAAGATACGACT 53319
Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnAsnGlySerMet 60
Db 53318 GATTCCAATGTTCTTAAATCACCCTCATCTGAAATATTTCAGCAAGAGATGGCAGTATG 53259
Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 53258 TTCTCTTAAATACCTCGAATATTGATGATTCATGATTCATAACACCTTCAAGAGAGGCT 53199
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 53198 CGAGGGGTGTGTTCTTACTTA 53178

RESULT 18
HSA420495 HSA420495 2151 bp mRNA linear PRI 23-NOV-2001
LOCUS Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1761756.
DEFINITION
ACCESSION AJ420495
VERSION AJ420495.1 GI:17066359
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1
AUTHORS Auffray,C., Ansorge,W., Ballabio,A., Estivill,X., Gibson,K.,
          Lehrach,H., Pouscka,A. and Lundeberg,J.
TITLE The European IMAGE consortium for integrated Molecular analysis of
          human gene transcripts
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2151)
AUTHORS Persson,A.
TITLE Direct Submission
JOURNAL Submitted (02-OCT-2001) Persson A., Center for Molecular
          Biotechnology, KTH, SCFAB, Institute of Biotechnology, Roslagsvagen
          30B, 106 91 Stockholm, SWEDEN
COMMENT This clone is available royalty-free through IMAGE Consortium

```

Distributors. IMPORTANT: This sequence represents the full insert of this IMAGE cDNA clone. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived.

FEATURES

```

Location/Qualifiers
source      1..2151
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /chromosome="6"
            /clone="EUROIMAGE 1761756"
            /clone_lib="NCI_CGAP_Kid3"
polyA_signal 2105..2110
ORIGIN

```

```

Alignment Scores:
Pred. No.: 2.07e-25 Length: 2151
Score: 288.50 Matches: 76
Percent Similarity: 35.51% Conservative: 0
Best Local Similarity: 35.51% Mismatches: 2
Query Match: 64.40% Indels: 137
DB: 8 Gaps: 1

```

US-10-757-745-2_COPY_54_140 (1-87) x HSA420495 (1-2151)

```

Qy 10 GluProValGluGluSerAlaLeuGluArgProGluThrIleSerGluProLys 29
Db 6 GAGGCTCCGTGGAGGAGCGCCCTTGAACGCCGACCTGAAACCATCTCTGAGCCCAAG 65
Qy 29 -----
Db 66 ACCTAGTAGTGATGATGGGGGAGCGGAGCCAGTCCGCGAGGAGGAGCTTTGATACCAAGT 125
Qy 29 -----
Db 126 AGCCCTCGGCTCCTGGGAGCTGCGGTGGAGTGGCGGACGATGCTGAGCGAGATCTCC 185
Qy 29 -----
Db 186 AAGTCGTGATGCCAGAGGAGGAGGCGTTCGCTGCTGCTGCGCGGAGTTGGCGGCCCA 245
Qy 29 -----
Db 246 GCAGCGGATCTAACACTGCACACAGCTGCTCGCTTCGAACGCTGATTGGGGTCCAGGGAG 305
Qy 29 -----
Db 306 AAAAGATGGAATGTAATGTTTAACTCAAATGAAAGGAATAAGTAAGCGGAGGTTTGA 365
Qy 29 -----
Db 366 AACAAATGAACGAAGGCTAAACCTTCTATCGAAAAATGGCAACTTGGAAAGTCTCCTTGCT 425
Qy 30 -----
Db 426 TCCTGTATTGTTATTATTCTAGCCCTAGGCTGACCGCCAGACAATAACAGT-GTTGAC 484
Qy 34 LeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSerProSerGluAspThr 53
Db 485 CTAACCAATGAAGAAACAACACTGATTCCACCACCTTCTAAAAATCAGCCCATCTGAAGATACT 544
Qy 54 GlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeu 73
Db 545 CAGCAAGAAATGGCAGCATGTTCTCTCTATACCTGGAAATATTGATGATTAGATCTA 604
Qy 74 AsnAsnLeuSerGluArgAlaAatGlyValCysSerTyrLeu 87
Db 605 AACAACTCTGCAGAGAGGCTCGAGGGGTGTGTTCTTACTTACTTA 646

```

RESULT 19

```

AY613922 AY613922 20938 bp DNA linear PRI 11-MAY-2004
LOCUS Homo sapiens TRAF and TNF receptor associated protein (TRAF) gene,
DEFINITION

```

complete cds.	
ACCESSION	AY613922
VERSION	AY613922.1 GI:47060296
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 20938)
AUTHORS	Rieder,M.J., Daniels,R.L., da Ponte,S.H., Hastings,N.C., Ahearn,M.O.; Rajkumar,N., Yi,Q. and Nickerson,D.A.
TITLE	Direct Submission
JOURNAL	Submitted (30-APR-2004) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA
COMMENT	To cite this work please use: SeattlesNP. NHLBI HL66682 Program for Genomic Applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu). Location/Qualifiers
FEATURES	1..20938
source	/organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
repeat_region	1..32 /rpt_family="ERV1" /rpt_type=dispersed
variation	81 /frequency="0.67" /replace=""
repeat_region	87..368 /rpt_family="ERV1" /rpt_type=dispersed
repeat_region	369..673 /rpt_family="Alu" /rpt_type=dispersed
variation	449 /frequency="0.96" /replace=""
variation	540 /frequency="0.01" /replace=""
variation	586 /frequency="0.01" /replace=""
variation	650 /frequency="0.03" /replace=""
variation	658..660 /frequency="0.01" /replace=""
repeat_region	683..989 /rpt_family="Alu" /rpt_type=dispersed
variation	695 /frequency="0.18" /replace=""
variation	922 /frequency="0.02" /replace=""
variation	1319 /frequency="0.15" /replace=""
variation	1456 /frequency="0.19" /replace=""
variation	1532 /frequency="0.01" /replace=""
variation	1711..1713 /frequency="0.04" /replace=""
variation	1795 /frequency="0.10"
variation	1821 /replace=""
variation	1830..1862 /frequency="0.04" /replace=""
variation	1913..1914 /frequency="0.13" /replace=""
gene	<2005..18938 /gene="TTRAP"
mRNA	join(<2005..2194,2281..2366,10172..10345,11003..11094, 14376..14494,15753..15923,17846..18938) /gene="TTRAP"
CDS	/product="TNF and TNF receptor associated protein" join(2030..2194,2281..2366,10172..10345,11003..11094, 14376..14494,15753..15923,17846..18127) /gene="TTRAP"
	/codon_start=1 /product="TNF and TNF receptor associated protein" /protein_id="AA09764.1" /db_xref="GI:47060297"
variation	/translation="NELGSCLEGGREAREBEVEKRRLLCVEPASFASCDAAVAQ CFLAENDWEMERALNSYFPPEVESALERPETISEPTYVDLTNEETSTTSKIS SEDTQENGSMFLITWNIDGLNNLSERAGVCSYLAIYSPDVIPLQEVIPPIYSI LKKRSNYEIIITGHEEGYFTAILMKSRVKLKSQEIIFFPTSKMRNLLCVHNVSNG ELCLMTSHLESTRGHAEARMNLKWLKMOPESATVIPAGDNLRDRVTTCGGI PNNIIVDMFEILGPKHQCYTDWTOMNSNLGITACKLRFDRIFFRAAAEEGHITPRSI DLLEGKLDCCRFPSDHGILLCNLDIL"
variation	2381 /gene="TTRAP" /frequency="0.08" /replace=""
variation	2767 /gene="TTRAP" /frequency="0.08" /replace=""
variation	2800 /gene="TTRAP" /frequency="0.79" /replace=""
repeat_region	2919..3323 /rpt_family="L2" /rpt_type=dispersed
variation	2927 /gene="TTRAP" /frequency="0.13" /replace=""
variation	3004 /gene="TTRAP" /frequency="0.04" /replace=""
variation	3061 /gene="TTRAP" /frequency="0.13" /replace=""
variation	3062 /gene="TTRAP" /frequency="0.13" /replace=""
variation	3114 /gene="TTRAP" /frequency="0.21" /replace=""
variation	3418 /gene="TTRAP" /frequency="0.03" /replace=""
variation	3781 /gene="TTRAP" /frequency="0.15" /replace=""

variation 3988 /gene="TTRAP"
/frequency="0.01"
/replace="a"
4191 /gene="TTRAP"
/frequency="0.01"
/replace="c"
4393 /gene="TTRAP"
/frequency="0.97"
/replace=""
4414 /gene="TTRAP"
/frequency="0.03"
/replace="c"
4437 /gene="TTRAP"
/frequency="0.07"
/replace="g"
4446 4530 /rpt_family="MER1_type"
/rpt_type="dispersed"
4559..4609 /rpt_family="MER1_type"
/rpt_type="dispersed"
4565 /gene="TTRAP"
/frequency="0.52"
/replace=""
4625..4760 /rpt_family="MER1_type"
/rpt_type="dispersed"
4658 /gene="TTRAP"
/frequency="0.01"
/replace="a"
4861 /gene="TTRAP"
/frequency="0.02"
/replace="a"
4941 /gene="TTRAP"
/frequency="0.07"
/replace="g"
4983 /gene="TTRAP"
/frequency="0.07"
/replace="c"
5024 /gene="TTRAP"
/frequency="0.07"

Alignment Scores:
Pred. No.: 3,08e-24 Length: 20938
Score: 288.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 64.29% Indels: 0
DB: 8 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AV613922 (1-20938)

Qy 32 ValAspLeuThrAsnGluThrThrAspSerThrThrSerLysLeSerProSerGlu 51
Db 10173 GTTGACCTAAACCAATGAAGAAACAACTGATTCACCACTTCTAAATCAGCCCATCTGAA 10232
Qy 52 AspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeu 71
Db 10233 GATACCTAGCAAGAAATGGCAGCATGTTCTCTCATCTACTGGAATATTGATGGATTA 10292
Qy 72 AspLeuAsnAsnLeuSerGluArgAlaahrgGlyValCysSerTyrLeu 87

Db 10293 GATCTAAACAATCTGTCTCAGAGAGGGCTCGAGGGGTGTGTCTCTACTTTA 10340
RESULT 20
HS30M3
LOCUS
DEFINITION
HS30M3 102200 bp DNA linear PRI 18-MAY-2005
Human DNA sequence from clone RPI-30M3 on chromosome 6p22.1-22.3
Contains the 5' end of gene KIAA0319, the gene for TRAF and TNF
receptor-associated protein (TTRAP) (EAP2, AD022, MGC9099), gene
FLJ20501, the 3' end of gene FLJ12619 (DKFZP564G182) and two Cpg
islands, complete sequence.
ACCESSION
AL031775
VERSION
AL031775.1 GI:4071041
KEYWORDS
HTG; AD022; Cpg island; DKFZP564G182; FLJ12619; FLJ20501; KIAA0319;
TNF; TTRAP; TTRAP.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 102200)
Phillips, S.
Direct Submission
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
On Dec 29, 1998 this sequence version replaced gi:4007165.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
RPI-30M3 is from the library RPCI-1 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vegas@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone, and the assembly was confirmed by restriction digest,
except on the rare occasion of the clone being a YAC.

FEATURES
source

1..102200
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="RZPD:RPCI1P704M0330"
/db_xref="taxon:9606"
/chromosome="6"
/map="p22.1-22.3"
/clone="RPI-30M3"
/clone_lib="RPCI-1"
join(complement(AL133264.10:4611..6907),
complement(AL133264.10:2219..2395),
complement(AL133264.10:389..511),5119..5253,7768..9169)
/gene="C6orf62"
/locus_tag="RPI-30M3.4-001"
join(complement(AL133264.10:4611..6907),
complement(AL133264.10:2219..2395),
complement(AL133264.10:389..511),5119..5253,7768..9169)
/gene="C6orf62"
/locus_tag="RPI-30M3.4-001"
/product="chromosome 6 open reading frame 62"

gene

mRNA

Qy 52 AspThrGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeu 71
|||||
Db 55357 GATACCTACGACAGAAATGGCAGCATGTTCTCTCATTAATGGAATATTGATGGATTA 55416
|||||
Qy 72 AspLeuAenLeuSerGluArgAlaArgGlyValCysSerTyrLeu 87
|||||
Db 55417 GATCTAAACAATCTGTCTACAGAGGGCTCGAGGGGTGTGTTCTTACTTA 55464
|||||

RESULT 21
CR925830 167847 bp DNA linear PRI 08-JAN-2005
LOCUS Human DNA sequence from clone RP11-195J19 on chromosome 6, complete
DEFINITION
sequence.
ACCESSION CR925830
VERSION CR925830.3 GI:56798018
KEYWORDS HTG.
SOURCE
ORGANISM Homo sapiens (human)
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 167847)
AUTHORS Palmer, S.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Dec 24, 2004 this sequence version replaced gi:56542150.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information
on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr6>
RP11-195J19 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6.

FEATURES
source
Location/Qualifiers
1..167847
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/clone="RP11-195J19"
/clone_lib="RPCI-11.1"

ORIGIN

Alignment Scores: 3.2e-23 Length: 167847
Pred. No.:

Score: 288.00 Matches: 56
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 64.29% Indels: 0
DB: 8 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x CR925830 (1-167847)
Qy 32 ValAspLeuThrAenGluThrThrAppSerThrThrSerIleSerProSerGlu 51
|||||
Db 35540 GTTGACCTAACCAATGAAGAAACAACACTGATCCACCACTTCTTAAATCAGCCCCATCTGAA 35599
|||||
Qy 52 AspThrGlnGluAsnGlySerMetPheSerLeuIleThrTrpAsnIleAspGlyLeu 71
|||||
Db 35600 GATACCTACGACAGAAATGGCAGCATGTTCTCTCATTAATGGAATATTGATGGATTA 35659
|||||
Qy 72 AspLeuAenLeuSerGluArgAlaArgGlyValCysSerTyrLeu 87
|||||
Db 35660 GATCTAAACAATCTGTCTACAGAGGGCTCGAGGGGTGTGTTCTTACTTA 35707
|||||

RESULT 22
CR942205 176819 bp DNA linear PRI 29-APR-2005
LOCUS Human DNA sequence from clone RP11-948M1 on chromosome 6, complete
DEFINITION
sequence.
ACCESSION CR942205
VERSION CR942205.4 GI:62989869
KEYWORDS HTG.
SOURCE
ORGANISM Homo sapiens (human)
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 176819)
AUTHORS Almeida, J.
TITLE Direct Submission
JOURNAL Submitted (29-APR-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 30, 2005 this sequence version replaced gi:62551221.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information
on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr6>
RP11-948M1 is from the library RPCI-11.4 constructed by the group
of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6.

Pyte, S., Declercq, W., Ibrahim, A., Michiels, C., Van Rietschoten, J.G., Dewulf, N., de Boer, M., Vandenabeele, P., Huybrebeck, D. and Remacle, J.E.	CR761829	1236 bp	mrna	linear	VRT 15-SEP-2004
TTRAP, a novel protein that associates with CD40, tumor necrosis factor (TNF) receptor-75 and TNF receptor-associated factors (TRAFs), and that inhibits nuclear factor-kappa B activation	Xenopus tropicalis finished cDNA, clone TGas102g02.				
J. Biol. Chem. 275 (24), 18586-18593 (2000)	CR761829.1	GI:51967738			
10764746	Xenopus tropicalis (Silurana tropicalis)				
2 (bases 1 to 1943)	Xenopus tropicalis				
Pyte, S.M.C.	Xenopus tropicalis				
Direct Submission	Xenopus tropicalis				
Submitted (25-NOV-1999)	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus; Silurana.				
Differentiation and Developme, Flanders Interuniversity Institute for Biotechnology, K.U.Leuven, Campus Gasthuisberg, Herestraat 49, 3000 Leuven, BELGIUM	1 (bases 1 to 1236)				
Related sequence: AJ269473.	Amaya, E., Ashurst, J.L., Bonfield, J.K., Croning, M.D.R., Davies, R.M., Francis, M.D., Garrett, N., Gilchrist, M.J., Grafham, D.V., McLaren, S.R., Papalopulu, N., Rogers, J., Smith, J.C., Taylor, R.G., Voigt, J. and Zorn, A.M.				
Location/Qualifiers	Direct Submission				
1..1943	Submitted (15-SEP-2004)				
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/mol_type="mRNA"	Sanger Xenopus tropicalis EST/cDNA project.				
/db_xref="taxon:10090"	This sequence is from a Xenopus Gene Collection (XGC) library, from a library constructed by Aaron M. Zorn. cDNA was prepared from RNA extracted from gastrula embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.				
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Alignment Scores:	Alignment Scores:				
Pred. No.:	Pred. No.:				
Score:	Score:				
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DB:	DB:				
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Clone requests: clonerequest@eanger.ac.uk
On Apr 26, 2001 this sequence version replaced gi.13751568.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP database can be found at http://www.eanger.ac.uk/Projects/C_elegans/wormpep -----
Genome Center
Center: UK Medical Research Council
Center code: UK-MRC
Web site: <http://mrcseq.har.mrc.ac.uk>
Contact: mouseq@har.mrc.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun map has been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.
RP23-92G13 is from the RPCI-23 Mouse BAC Library constructed by the group of Pieter de Jong.
For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBACe3.6.

FEATURES
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 17:47:31 ; Search time 172.349 Seconds
(without alignments)
2773.640 Million cell updates/sec

Title: US-10-757-745-5

Perfect score: 1536

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3289935 seqs, 155610033 residues

Total number of hits satisfying chosen parameters: 6579870

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

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- 6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 5	43.2	2.8	165883	7	US-11-112-908-18
C 6	41.6	2.7	2257	6	US-10-750-185-53428
C 7	40.8	2.7	3275	6	US-10-750-185-40388
C 8	40.6	2.6	1348	6	US-10-750-185-36740
C 9	39.8	2.6	4132	6	US-10-750-185-31076
C 10	39.6	2.6	876	6	US-10-750-185-50175
C 11	39.6	2.6	1742	6	US-10-750-185-31254
C 12	39	2.5	4114	6	US-10-793-626-3572
C 13	39	2.5	5109	6	US-10-714-781A-56
C 14	38.6	2.5	1483	6	US-10-750-185-39052
C 15	38.6	2.5	150450	7	US-11-112-908-54
C 16	38.6	2.5	172147	7	US-11-112-908-22
C 17	38.6	2.5	188682	7	US-11-112-908-23
C 18	38.6	2.5	191343	7	US-11-112-908-53
C 19	38.4	2.5	1628	6	US-10-689-742-217
C 20	38.4	2.5	2796	6	US-10-793-626-4335
C 21	38.2	2.5	1952	6	US-10-750-185-62955
C 22	38.2	2.5	5772	6	US-10-750-185-53415
C 23	38	2.5	2051	6	US-10-750-185-45321
C 24	38	2.5	2051	6	US-10-750-185-45321

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27	2637	2.5	2637	9	US-11-077-550-142	Sequence 142, App
28	2661	2.5	2661	9	US-11-077-550-146	Sequence 146, App
C 29	3469	2.5	3469	6	US-10-750-185-55403	Sequence 55403, A
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C 31	37.8	2.5	255	6	US-10-909-125-1935	Sequence 1935, Ap
C 32	37.6	2.4	3864	6	US-10-793-626-3727	Sequence 3727, Ap
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C 35	37.2	2.4	4290	6	US-10-793-626-3960	Sequence 3960, Ap
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C 37	37	2.4	1057	6	US-10-750-185-45881	Sequence 45881, A
C 38	37	2.4	1260	7	US-11-113-908-220	Sequence 220, App
C 39	37	2.4	2424	6	US-10-750-185-58282	Sequence 58282, A
C 40	37	2.4	150437	7	US-11-112-908-44	Sequence 44, Appl
C 41	37	2.4	150491	7	US-11-112-908-46	Sequence 46, Appl
C 42	37	2.4	182314	7	US-11-112-908-45	Sequence 45, Appl
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C 44	36.8	2.4	1663	6	US-10-750-185-41629	Sequence 41629, A
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C 77	36	2.3	2123	6	US-10-750-185-61021	Sequence 61021, A
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C 86	35.8	2.3	3328	6	US-10-793-626-3446	Sequence 3446, Ap
C 87	35.8	2.3	3427	6	US-10-750-185-38475	Sequence 38475, A
C 88	35.8	2.3	3570	6	US-10-750-185-44897	Sequence 44897, A
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C 90	35.8	2.3	173115	7	US-11-112-908-65	Sequence 65, Appl
C 91	35.6	2.3	339	7	US-11-074-176-333	Sequence 333, App
C 92	35.6	2.3	348	7	US-11-074-176-123	Sequence 123, App
C 93	35.6	2.3	627	6	US-10-793-626-693	Sequence 693, App
C 94	35.6	2.3	627	6	US-10-793-626-1325	Sequence 1325, App
C 95	35.6	2.3	864	6	US-10-750-185-50142	Sequence 50142, A
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101	35.6	2.3	1388	6	US-10-793-626-959	Sequence 959, App	174	34.6	2.3	2307	7	US-11-055-557-7	Sequence 7, Appli
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104	35.6	2.3	1863	6	US-10-750-185-37517	Sequence 37517, A	177	34.6	2.3	3369	7	US-11-191-375-5	Sequence 5, Appli
105	35.6	2.3	2389	6	US-10-793-626-4438	Sequence 4438, Ap	c 177	34.6	2.3	3369	6	US-10-793-626-4313	Sequence 4313, Ap
106	35.6	2.3	2472	6	US-10-750-185-49173	Sequence 49173, A	179	34.6	2.3	3750	7	US-11-191-374-1	Sequence 1, Appli
c 107	35.6	2.3	2999	6	US-10-793-626-4039	Sequence 4039, Ap	180	34.6	2.3	3750	7	US-11-191-375-1	Sequence 1, Appli
108	35.6	2.3	3097	6	US-10-750-185-49888	Sequence 49888, A	181	34.4	2.2	339	6	US-10-793-626-2089	Sequence 2089, Ap
109	35.6	2.3	3450	6	US-10-793-626-3951	Sequence 3951, Ap	182	34.4	2.2	1316	6	US-10-750-185-30943	Sequence 30943, A
c 110	35.6	2.3	3691	6	US-10-793-626-3338	Sequence 3338, Ap	c 183	34.4	2.2	1451	6	US-10-750-185-39708	Sequence 39708, A
c 111	35.6	2.3	3792	6	US-10-793-626-3396	Sequence 3396, Ap	184	34.4	2.2	1500	6	US-10-793-626-1557	Sequence 1557, Ap
112	35.6	2.3	4039	6	US-10-793-626-3361	Sequence 3361, Ap	c 185	34.4	2.2	1592	6	US-10-750-185-57463	Sequence 57463, A
c 113	35.6	2.3	150450	7	US-11-112-908-54	Sequence 54, Appl	c 186	34.4	2.2	1825	6	US-10-750-185-29098	Sequence 29098, A
c 114	35.6	2.3	172781	7	US-11-112-908-25	Sequence 25, Appl	c 187	34.4	2.2	2107	6	US-10-750-185-28511	Sequence 28511, A
c 115	35.6	2.3	191343	7	US-11-112-908-53	Sequence 53, Appl	c 188	34.4	2.2	2580	6	US-10-793-626-4323	Sequence 4323, Ap
c 116	35.6	2.3	207600	7	US-11-112-908-31	Sequence 31, Appl	c 189	34.4	2.2	2747	6	US-10-750-185-50264	Sequence 50264, A
117	35.4	2.3	453	6	US-10-793-626-327	Sequence 327, App	c 190	34.4	2.2	2856	6	US-10-793-626-3440	Sequence 3440, Ap
c 118	35.4	2.3	1590	6	US-10-750-185-45972	Sequence 45972, A	c 191	34.4	2.2	2982	6	US-10-793-626-3555	Sequence 3555, Ap
c 119	35.4	2.3	2355	6	US-10-793-626-4464	Sequence 4464, Ap	c 192	34.4	2.2	3117	6	US-10-793-626-3875	Sequence 3875, Ap
c 120	35.4	2.3	2792	6	US-10-485-517-32	Sequence 92, Appl	c 193	34.4	2.2	3170	6	US-10-793-626-3849	Sequence 3849, Ap
c 121	35.4	2.3	3657	6	US-10-793-626-4187	Sequence 4187, Ap	c 194	34.4	2.2	3227	6	US-10-793-626-3874	Sequence 3874, Ap
c 122	35.2	2.3	600	6	US-10-750-185-1632	Sequence 1632, Ap	c 195	34.4	2.2	3253	6	US-10-793-626-3887	Sequence 3887, Ap
c 123	35.2	2.3	851	6	US-10-750-185-49172	Sequence 49172, A	c 196	34.4	2.2	3328	6	US-10-793-626-4195	Sequence 4195, Ap
c 124	35.2	2.3	1028	7	US-11-015-546A-91	Sequence 91, Appli	c 197	34.4	2.2	4269	6	US-10-750-185-25308	Sequence 25308, A
c 125	35.2	2.3	1028	7	US-11-015-546A-21	Sequence 21, Appl	c 198	34.4	2.2	6189	6	US-10-909-125-825	Sequence 825, App
c 126	35.2	2.3	1373	6	US-10-750-185-37992	Sequence 37992, A	c 199	34.4	2.2	21784	7	US-11-182-752-3	Sequence 3, Appli
c 127	35.2	2.3	1533	6	US-10-793-626-2859	Sequence 2859, Ap	c 200	34.4	2.2	319608	7	US-11-145-703-1	Sequence 1, Appli
c 128	35.2	2.3	1716	7	US-11-021-441-25	Sequence 25, Appl	c 201	34.2	2.2	405	6	US-10-793-626-437	Sequence 437, App
c 129	35.2	2.3	2095	6	US-10-750-185-63644	Sequence 63644, A	c 202	34.2	2.2	486	6	US-10-793-626-2929	Sequence 2929, App
c 130	35.2	2.3	2512	6	US-10-750-185-40273	Sequence 40273, A	c 203	34.2	2.2	600	6	US-10-750-185-20371	Sequence 20371, A
c 131	35.2	2.3	2625	6	US-10-750-185-40655	Sequence 40655, A	c 204	34.2	2.2	1315	6	US-10-750-185-32805	Sequence 32805, A
c 132	35.2	2.3	2993	6	US-10-793-626-4074	Sequence 4074, Ap	c 205	34.2	2.2	1318	6	US-10-750-185-39940	Sequence 39940, A
c 133	35.2	2.3	3024	6	US-10-793-626-3426	Sequence 3426, Ap	c 206	34.2	2.2	1388	6	US-10-750-185-33072	Sequence 33072, A
c 134	35.2	2.3	3187	6	US-10-793-626-4381	Sequence 4381, Ap	c 207	34.2	2.2	1413	6	US-10-750-185-35863	Sequence 35863, A
c 135	35.2	2.3	3404	6	US-10-793-626-4346	Sequence 4346, Ap	c 208	34.2	2.2	1475	6	US-10-750-185-64554	Sequence 64554, A
c 136	35.2	2.3	4202	6	US-10-750-185-27210	Sequence 27210, A	c 209	34.2	2.2	1766	6	US-10-750-185-64570	Sequence 64570, A
c 137	35	2.3	1275	6	US-10-750-185-55720	Sequence 55720, A	c 210	34.2	2.2	1960	6	US-10-750-185-36468	Sequence 36468, A
c 138	35	2.3	1806	6	US-10-750-185-40897	Sequence 40897, A	c 211	34.2	2.2	2407	6	US-10-485-517-42	Sequence 42, Appl
c 139	35	2.3	2380	6	US-10-750-185-39277	Sequence 39277, A	c 212	34.2	2.2	2476	6	US-10-131-826A-489	Sequence 489, App
c 140	35	2.3	2436	6	US-10-750-185-40043	Sequence 40043, A	c 213	34.2	2.2	2596	6	US-10-750-185-43030	Sequence 43030, A
c 141	35	2.3	2475	6	US-10-750-185-57905	Sequence 57905, A	c 214	34.2	2.2	2962	6	US-10-793-626-3511	Sequence 3511, Ap
c 142	35	2.3	4035	6	US-10-750-185-58283	Sequence 58283, A	c 215	34.2	2.2	3221	6	US-10-793-626-4119	Sequence 4119, Ap
c 143	34.8	2.3	577	6	US-10-750-185-20231	Sequence 20231, A	c 216	34.2	2.2	3345	6	US-10-793-626-3368	Sequence 3368, Ap
c 144	34.8	2.3	1329	6	US-10-750-185-12421	Sequence 12421, Ap	c 217	34.2	2.2	3994	6	US-10-793-626-3496	Sequence 3496, Ap
c 145	34.8	2.3	600	6	US-10-750-185-2629	Sequence 2629, Ap	c 218	34.2	2.2	4035	6	US-10-750-185-58283	Sequence 58283, A
c 146	34.8	2.3	1035	6	US-10-750-185-40819	Sequence 40819, A	c 219	34.2	2.2	4138	6	US-10-793-626-3995	Sequence 3995, Ap
c 147	34.8	2.3	1213	6	US-10-750-185-45328	Sequence 45328, A	c 220	34.2	2.2	48000	7	US-11-159-597-20	Sequence 20, Appl
c 148	34.8	2.3	1233	6	US-10-750-185-51369	Sequence 51369, A	c 221	34.2	2.2	180862	7	US-11-112-908-40	Sequence 40, Appl
c 149	34.8	2.3	1329	6	US-10-793-626-3041	Sequence 3041, Ap	c 222	34	2.2	975	7	US-11-074-176-369	Sequence 369, App
c 150	34.8	2.3	2049	6	US-10-750-185-40699	Sequence 40699, A	c 223	34	2.2	1419	6	US-10-750-185-59740	Sequence 59740, A
c 151	34.8	2.3	2224	6	US-10-750-185-53492	Sequence 53492, A	c 224	34	2.2	2130	6	US-10-467-657-4291	Sequence 4291, Ap
c 152	34.8	2.3	2982	6	US-10-131-826A-381	Sequence 381, App	c 225	34	2.2	2848	6	US-10-750-185-56373	Sequence 56373, A
c 153	34.8	2.3	3236	6	US-10-793-626-4062	Sequence 4062, Ap	c 226	34	2.2	3343	6	US-10-485-517-31	Sequence 31, Appl
c 154	34.8	2.3	3041	6	US-10-793-626-4193	Sequence 4193, Ap	c 227	34	2.2	3528	6	US-10-793-626-3791	Sequence 3791, Ap
c 155	34.8	2.3	3349	6	US-10-793-626-3507	Sequence 3507, Ap	c 228	34	2.2	3699	6	US-10-793-626-4450	Sequence 4450, Ap
c 156	34.8	2.3	207908	7	US-11-112-908-21	Sequence 21, Appl	c 229	34	2.2	3723	6	US-10-750-185-32384	Sequence 32384, A
c 157	34.6	2.3	1179	6	US-10-750-185-49165	Sequence 49165, A	c 230	34	2.2	3827	6	US-10-793-626-3598	Sequence 3598, Ap
c 158	34.6	2.3	1215	6	US-10-750-185-44381	Sequence 44381, A	c 231	34	2.2	5076	9	US-11-077-550-135	Sequence 135, App
c 159	34.6	2.3	1236	6	US-10-750-185-59374	Sequence 59374, A	c 232	34	2.2	125594	6	US-10-658-986-5	Sequence 5, Appli
c 160	34.6	2.3	1423	6	US-10-750-185-61132	Sequence 61132, A	c 233	33.8	2.2	600	6	US-10-750-185-21113	Sequence 21113, A
c 161	34.6	2.3	1642	6	US-10-750-185-64770	Sequence 64770, A	c 234	33.8	2.2	727	6	US-10-750-185-55108	Sequence 55108, A
c 162	34.6	2.3	1877	6	US-10-750-185-59415	Sequence 59415, A	c 235	33.8	2.2	753	6	US-10-750-185-45346	Sequence 45346, A
c 163	34.6	2.3	2007	6	US-10-750-185-61205	Sequence 61205, A	c 236	33.8	2.2	899	6	US-10-750-185-58950	Sequence 58950, A
c 164	34.6	2.3	2234	6	US-10-750-185-33327	Sequence 33327, A	c 237	33.8	2.2	1041	6	US-10-750-185-63611	Sequence 63611, A
c 165	34.6	2.3	2234	6	US-10-750-185-49606	Sequence 49606, A	c 238	33.8	2.2	1257	6	US-10-750-185-50606	Sequence 50606, A
c 166	34.6	2.3	2295	7	US-11-055-557-11	Sequence 11, Appl	c 239	33.8	2.2	1679	6	US-10-750-185-37611	Sequence 37611, A
c 167	34.6	2.3	2295	7	US-11-055-557-15	Sequence 15, Appl	c 240	33.8	2.2	1859	6	US-10-750-185-34655	Sequence 34655, A
c 168	34.6	2.3	2295	7	US-11-055-557-19	Sequence 19, Appl	c 241	33.8	2.2	2256	6	US-10-750-185-60277	Sequence 60277, A
c 169	34.6	2.3	2304	7	US-11-055-557-1	Sequence 1, Appli	c 242	33.8	2.2	2929	6	US-10-793-626-4120	Sequence 4120, Ap

C 243	33.8	2.2	3052	6	US-10-485-517-65	Sequence 65, Appl	C 316	33.2	2.2	1813	6	US-10-750-185-41650	Sequence 41650, A
C 244	33.8	2.2	3052	6	US-10-485-517-74	Sequence 74, Appl	C 317	33.2	2.2	1880	6	US-10-793-626-4426	Sequence 4426, Ap
C 245	33.8	2.2	3058	6	US-10-750-185-41957	Sequence 41957, A	C 318	33.2	2.2	1935	6	US-10-750-185-25718	Sequence 25718, A
C 246	33.8	2.2	3339	6	US-10-793-626-3938	Sequence 3938, Ap	C 319	33.2	2.2	1944	6	US-10-750-185-35847	Sequence 35847, A
C 247	33.8	2.2	3397	6	US-10-793-626-4220	Sequence 4220, Ap	C 320	33.2	2.2	2418	6	US-10-750-185-58756	Sequence 58756, A
C 248	33.8	2.2	4130	6	US-10-793-626-4126	Sequence 4126, Ap	C 321	33.2	2.2	2500	7	US-11-088-686-43	Sequence 43, Appl
C 249	33.6	2.2	600	6	US-10-750-185-21652	Sequence 21652, A	C 322	33.2	2.2	2028	6	US-10-793-626-4247	Sequence 4247, Ap
C 250	33.6	2.2	704	6	US-10-750-185-62381	Sequence 62381, A	C 323	33.2	2.2	3044	6	US-10-793-626-4290	Sequence 4290, Ap
C 251	33.6	2.2	875	6	US-10-750-185-33620	Sequence 33620, A	C 324	33.2	2.2	3108	6	US-10-793-626-3427	Sequence 3427, Ap
C 252	33.6	2.2	1083	6	US-10-750-185-34852	Sequence 34852, A	C 325	33.2	2.2	3350	6	US-10-793-626-4018	Sequence 4018, Ap
C 253	33.6	2.2	1126	6	US-10-750-185-25696	Sequence 25696, A	C 326	33.2	2.2	3361	6	US-10-793-626-3722	Sequence 3722, Ap
C 254	33.6	2.2	1148	6	US-10-750-185-44837	Sequence 44837, A	C 327	33.2	2.2	3598	6	US-10-793-626-4216	Sequence 4216, Ap
C 255	33.6	2.2	1163	6	US-10-750-185-54773	Sequence 54773, A	C 328	33.2	2.2	3598	6	US-10-793-626-4216	Sequence 4216, Ap
C 256	33.6	2.2	1222	6	US-10-750-185-49538	Sequence 49538, A	C 329	33.2	2.2	4339	6	US-10-909-125-801	Sequence 801, App
C 257	33.6	2.2	1285	6	US-10-750-185-44743	Sequence 44743, A	C 330	33	2.1	597	6	US-10-793-626-989	Sequence 989, App
C 258	33.6	2.2	1351	6	US-10-750-185-62515	Sequence 62515, A	C 331	33	2.1	600	6	US-10-750-185-3810	Sequence 3810, Ap
C 259	33.6	2.2	1703	6	US-10-750-185-45699	Sequence 45699, A	C 332	33	2.1	688	6	US-10-793-626-3241	Sequence 3241, Ap
C 260	33.6	2.2	1848	6	US-10-750-185-26377	Sequence 26377, A	C 333	33	2.1	816	6	US-10-793-626-677	Sequence 677, App
C 261	33.6	2.2	1860	6	US-10-750-185-33976	Sequence 33976, A	C 334	33	2.1	847	6	US-10-750-185-48286	Sequence 48286, A
C 262	33.6	2.2	3000	6	US-10-750-185-38020	Sequence 38020, A	C 335	33	2.1	884	6	US-10-750-185-26249	Sequence 26249, A
C 263	33.6	2.2	3222	6	US-10-750-185-33976	Sequence 33976, A	C 336	33	2.1	1032	6	US-10-793-626-1625	Sequence 1625, Ap
C 264	33.6	2.2	3376	6	US-10-793-626-4055	Sequence 4055, Ap	C 337	33	2.1	1032	6	US-10-793-626-1963	Sequence 1963, Ap
C 265	33.6	2.2	4200	6	US-10-750-185-53206	Sequence 53206, A	C 338	33	2.1	1047	6	US-10-750-185-35834	Sequence 35834, A
C 266	33.4	2.2	600	6	US-10-750-1732	Sequence 21732, A	C 339	33	2.1	1098	6	US-10-750-185-60508	Sequence 60508, A
C 267	33.4	2.2	730	6	US-10-750-185-57769	Sequence 57769, A	C 340	33	2.1	1190	6	US-10-750-185-25765	Sequence 25765, A
C 268	33.4	2.2	756	6	US-10-750-185-30870	Sequence 30870, A	C 341	33	2.1	1210	6	US-10-793-626-397	Sequence 397, App
C 269	33.4	2.2	759	6	US-10-793-626-497	Sequence 497, App	C 342	33	2.1	1275	6	US-10-750-185-55720	Sequence 55720, A
C 270	33.4	2.2	759	6	US-10-793-626-1367	Sequence 1367, App	C 343	33	2.1	1306	6	US-10-750-185-28394	Sequence 28394, A
C 271	33.4	2.2	921	6	US-10-750-185-51623	Sequence 51623, A	C 344	33	2.1	1336	6	US-10-750-185-25507	Sequence 25507, A
C 272	33.4	2.2	966	6	US-10-793-626-141	Sequence 141, App	C 345	33	2.1	1336	6	US-10-750-185-29807	Sequence 29807, A
C 273	33.4	2.2	1077	6	US-10-750-185-52374	Sequence 52374, A	C 346	33	2.1	1492	6	US-10-793-626-3677	Sequence 3677, Ap
C 274	33.4	2.2	1094	6	US-10-750-185-42704	Sequence 42704, A	C 347	33	2.1	1560	6	US-10-750-185-30742	Sequence 30742, A
C 275	33.4	2.2	1124	6	US-10-750-185-27308	Sequence 27308, A	C 348	33	2.1	1598	6	US-10-750-185-46742	Sequence 46742, A
C 276	33.4	2.2	1418	6	US-10-750-185-59732	Sequence 59732, A	C 349	33	2.1	1604	6	US-10-750-185-32408	Sequence 32408, A
C 277	33.4	2.2	1542	6	US-10-750-185-36659	Sequence 36659, A	C 350	33	2.1	1726	6	US-10-750-185-36454	Sequence 36454, A
C 278	33.4	2.2	1586	6	US-10-750-185-38949	Sequence 38949, A	C 351	33	2.1	1791	6	US-10-750-185-43115	Sequence 43115, A
C 279	33.4	2.2	1642	6	US-10-750-185-47826	Sequence 47826, A	C 352	33	2.1	1839	6	US-10-750-185-25838	Sequence 25838, A
C 280	33.4	2.2	1661	6	US-10-750-185-56735	Sequence 56735, A	C 353	33	2.1	1942	6	US-10-750-185-59697	Sequence 59697, A
C 281	33.4	2.2	1691	6	US-10-750-185-58132	Sequence 58132, A	C 354	33	2.1	2216	6	US-10-750-185-31847	Sequence 31847, A
C 282	33.4	2.2	1738	6	US-10-750-185-38977	Sequence 38977, A	C 355	33	2.1	2220	6	US-10-750-185-41287	Sequence 41287, A
C 283	33.4	2.2	1917	6	US-10-793-626-1467	Sequence 1467, App	C 356	33	2.1	2367	6	US-10-750-185-58552	Sequence 58552, A
C 284	33.4	2.2	2001	6	US-10-485-517-90	Sequence 90, Appl	C 357	33	2.1	2477	6	US-10-750-185-31684	Sequence 31684, A
C 285	33.4	2.2	2278	6	US-10-793-626-4286	Sequence 4286, Ap	C 358	33	2.1	2596	6	US-10-750-185-43030	Sequence 43030, A
C 286	33.4	2.2	2292	6	US-10-793-626-3385	Sequence 3385, Ap	C 359	33	2.1	2713	6	US-10-750-185-32766	Sequence 32766, A
C 287	33.4	2.2	3005	6	US-10-793-626-4096	Sequence 4096, Ap	C 360	33	2.1	2806	6	US-10-485-517-30	Sequence 30, Appl
C 288	33.4	2.2	3068	6	US-10-793-626-3824	Sequence 3824, Ap	C 361	33	2.1	2902	6	US-10-793-626-4170	Sequence 4170, Ap
C 289	33.4	2.2	3076	6	US-10-793-626-4043	Sequence 4043, Ap	C 362	33	2.1	3001	7	US-11-145-703-183	Sequence 183, App
C 290	33.4	2.2	3276	6	US-10-793-626-4240	Sequence 4240, Ap	C 363	33	2.1	3069	6	US-10-793-626-4068	Sequence 4068, Ap
C 291	33.4	2.2	3344	6	US-10-793-626-3504	Sequence 3504, Ap	C 364	33	2.1	3095	6	US-10-793-626-4038	Sequence 4038, Ap
C 292	33.4	2.2	3615	6	US-10-793-626-3565	Sequence 3565, Ap	C 365	33	2.1	3206	6	US-10-750-185-34773	Sequence 34773, A
C 293	33.4	2.2	3867	6	US-10-793-626-3769	Sequence 3769, Ap	C 366	33	2.1	3227	6	US-10-793-626-3688	Sequence 3688, Ap
C 294	33.4	2.2	4042	6	US-10-793-626-3701	Sequence 3701, Ap	C 367	33	2.1	3381	6	US-10-750-185-24749	Sequence 24749, A
C 295	33.4	2.2	4158	6	US-10-793-626-3879	Sequence 3879, Ap	C 368	33	2.1	3423	6	US-10-793-626-3474	Sequence 3474, Ap
C 296	33.4	2.2	4665	6	US-10-750-185-54341	Sequence 54341, A	C 369	33	2.1	3555	6	US-10-793-626-3396	Sequence 3396, Ap
C 297	33.4	2.2	5921	6	US-10-750-185-41152	Sequence 41152, A	C 370	33	2.1	3618	6	US-10-793-626-3387	Sequence 3387, Ap
C 298	33.4	2.2	15071	6	US-10-793-626-2963	Sequence 2963, Ap	C 371	33	2.1	3745	6	US-10-793-626-4045	Sequence 4045, Ap
C 299	33.4	2.2	150468	7	US-11-112-908-56	Sequence 56, Appl	C 372	33	2.1	3825	6	US-10-793-626-3794	Sequence 3794, Ap
C 300	33.4	2.2	193789	7	US-11-112-908-55	Sequence 55, Appl	C 373	33	2.1	3965	6	US-10-750-185-56162	Sequence 56162, A
C 301	33.2	2.2	646	6	US-10-750-185-1522	Sequence 1522, Ap	C 374	33	2.1	4396	6	US-10-485-517-43	Sequence 43, Appl
C 302	33.2	2.2	779	6	US-10-750-185-51034	Sequence 51034, A	C 375	33	2.1	6450	7	US-11-091-668-3	Sequence 3, Appl
C 303	33.2	2.2	909	6	US-10-750-185-64789	Sequence 64789, A	C 376	33	2.1	26000	6	US-10-949-720-391	Sequence 20, Appl
C 304	33.2	2.2	920	6	US-10-750-185-24602	Sequence 24602, A	C 377	33	2.1	191331	7	US-11-112-908-20	Sequence 1296, Ap
C 305	33.2	2.2	924	6	US-10-508-263-112	Sequence 112, App	C 378	32.8	2.1	578	6	US-10-750-185-4229	Sequence 4229, Ap
C 306	33.2	2.2	1200	6	US-10-793-626-2575	Sequence 2575, Ap	C 379	32.8	2.1	600	6	US-10-750-185-4429	Sequence 4429, Ap
C 307	33.2	2.2	1312	6	US-10-750-185-63105	Sequence 63105, A	C 380	32.8	2.1	755	6	US-10-750-185-47742	Sequence 47742, A
C 308	33.2	2.2	1498	6	US-10-750-185-64093	Sequence 64093, A	C 381	32.8	2.1	779	6	US-10-750-185-33001	Sequence 33001, A
C 309	33.2	2.2	1515	6	US-10-750-185-51381	Sequence 51381, A	C 382	32.8	2.1	814	6	US-10-750-185-53436	Sequence 53436, A
C 310	33.2	2.2	1577	6	US-10-750-185-53847	Sequence 53847, A	C 383	32.8	2.1	974	6	US-10-750-185-27417	Sequence 27417, A
C 311	33.2	2.2	1618	6	US-10-750-185-57879	Sequence 57879, A	C 384	32.8	2.1	1088	6	US-10-750-185-60209	Sequence 60209, A
C 312	33.2	2.2	1659	6	US-10-750-185-53431	Sequence 53431, A	C 385	32.8	2.1	1158	6	US-10-750-185-42790	Sequence 42790, A
C 313	33.2	2.2	1696	6	US-10-750-185-56574	Sequence 56574, A	C 386	32.8	2.1	1185	7	US-11-074-176-187	Sequence 187, App
C 314	33.2	2.2	1737	6	US-10-750-185-54366	Sequence 54366, A	C 387	32.8	2.1	1222	6	US-10-750-185-29627	Sequence 29627, A
C 315	33.2	2.2	1797	6	US-10-750-185-54366	Sequence 54366, A	C 388	32.8	2.1	1228	6	US-10-518-753-8	Sequence 8, Appl

Db 31 AAAGAATTAAATCTAAAGAGTAAGAGATTTATAGATGATTTAAAAAGATGATGAATGTTGAA 90
Qy 704 GCAGTTCGGCATTTGGGATCGAAAGCAGAAAGCATGTCATGTGTCGAAGGATGATTT 763
Db 91 GTGTCAATCATATGCAAGCTTTAGAAAGAGAAACAATCAAAGCATTAGATAAAAAATTT 150
Qy 764 GCATATTTAGTAACCCCTAATGGCAGTAAATAAACTACTAGGCAAGCTTCTCTAGAAAA 823
Db 151 AAAGCTCTCAAGCGAAGACACTATATAACAAATACTCAAAATATCACCAAAATCT 210
Qy 824 AAAATTAGGGAACATGATGTTTCTAAAGCCCATGTTAAATTCAGGATTTGTTAAAGAA 883
Db 211 AATAATAACAAAATTTCTAACGATAAGAAAAACAACAAGTAAGATAATAGTAAACCA 270
Qy 884 TCACTAATGATTCATTTGTTAATTTAGTGATAAACAATAATATAAAATTTATGATGCT 943
Db 271 ACAGAGAAAAAGAAACAACAACAAGGAAAAACAGCAAAATAAAAAACAATAAACTAAT 330
Qy 944 ACTGTAAAGTTTCAATACTGTTTACAGTTTGTAGTAAACATAACAGACCTTTTATCTGAT 1003
Db 331 AAGATCAAAAAACAATAAATAAAGATATAATAATAATAAATCAAACTCAAAATGAG 390
Qy 1004 ATTGAGGGGCAAGAGATTACAGAAAAAATGAGAGGTAATTTGTTTAAATACAGT 1063
Db 391 GTAGCAGAAAAACAAGAAATGCCCTCTAAATCACTTATCAAGAGGCATAACTGTCGT 450
Qy 1064 TACAGTGCACAGAAATAGCAGAACATATTGCAAAAGAAATGAAGATGAAGATATTAAAG 1123
Db 451 GAGTTAGCTGAAAGCTAAATGTAGATCAAGTGTGTTATTTAAAAAATTTGTTCTACTA 510
Qy 1124 AATATTATAG 1133
Db 511 GGTATTATGG 520

RESULT 2

US-10-793-626-3962/c
; Sequence 3962, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3962
; LENGTH: 3898
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3962

Query Match 3.0%; Score 46.8; DB 6; Length 3898;
Best Local Similarity 43.5%; Pred. No. 0.31;
Matches 213; Conservative 0; Mismatches 277; Indels 0; Gaps 0;
Qy 644 ACAGAACATAAATGGCTTGAATAAAGAGGTAATTAAGGATGTAAGATTTGTTCA 703
Db 915 AAAGAAATTAATCTAAAGAGTAAGAGATTATAGATGAGTTAAAAAGTATGAATGTTGAA 856
Qy 704 GCAGTTCCGCAATTTGGATCGAAAGCAGAAAGCATGTCATGTGTCGAAGGATGATTT 763
Db 855 GTGTCAATCATATGCAAGCTTTAGAAAGAGAAACAATAAAGCATTAGATAAAAAATTT 796
Qy 764 GCATATTTAGTAACCCCTAATGGCAGTAATAAACTACTAGGCAAGCTTCTCTACGAAA 823
Db 795 AAAGCTCTCAAGCGAAGACACTATAAACAATACTCAAAATAATCAACCAAAATCT 736

Qy 824 AAAATTAGGGAACATGATGTTTCTAAAGCCCATGTTAAAAATTCAGGATTTGTTAAAGGAA 883
Db 735 AATAATAAACAATTTCTAAGGATAAGAAAAACAACAAGTAAAGATAATAGTAAACCA 676
Qy 884 TCACTAATGATTCATTTGTTAATTTAGTGATAAACAATAATATAAAATTTATGATGCT 943
Db 675 ACAGAGAAAAAGAAACAACAACAAGGAAAAACAGCAAAATAAAAAACAATAAACTAAT 616
Qy 944 ACTGTAAAGTTTCAATACTGTTTACAGTTTGTAGTAAACATAACAGACCTTTTATCTGAT 1003
Db 615 AAGATCAAAAAACAATAAATAAAGATATAATAATAAATCAAACTCAAAATGAG 556
Qy 1004 ATTGAGGGGCAAGAGAAATTAACAGAAAAAATGGAGAGGTAATTTGTTTAAATACAGT 1063
Db 555 GTAGCAGAAAAACAAGAAATGCCCTCTAAATCACTTATCAAGAGGCATAACTGTCGT 496
Qy 1064 TACAGTGCACAGAAATAGCAGAACATATTGCAAAAGAAATGAAGATGAAGATATTAAAG 1123
Db 495 GAGTTAGCTGAAAGCTAAATGTAGATCAAGTGTGTTATTTAAAAAATTTGTTCTACTA 436
Qy 1124 AATATTATAG 1133
Db 435 GGTATTATGG 426

RESULT 3

US-10-793-626-4149/c
; Sequence 4149, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4149
; LENGTH: 3543
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4149

Query Match 3.0%; Score 45.4; DB 6; Length 3543;
Best Local Similarity 44.9%; Pred. No. 0.61;
Matches 172; Conservative 0; Mismatches 211; Indels 0; Gaps 0;
Qy 826 AATTAGGGAACATGATGTTTCTAAAGCCCATGTTAAAAATTCAGGATTTGTTAAAGGAATC 885
Db 3542 AATTAGTAAGATTGATAATGCTACAAACGAATAATCAAAATTCATGTTGTTGAGTGAGG 3483
Qy 886 AACTAATGATTCATTTGTTAATTTAGTGCATAAACAATAATAAAATATTGATGCTAC 945
Db 3482 TAGACAAAGCATAAATGCAATTTACACCTGATACATCAATTAAGAGAAATGCTAAAAATGA 3423
Qy 946 TGTAAGAAGTTTCAATACTGTTTACAGTTTGTAGTAAACAATAACAGACCTTTTATCTGATAT 1005
Db 3422 TATTGATATTAAAGCAGCTGATAGAAATAAATAAATTCAGAAATTAATGATGCTACAGA 3363
Qy 1006 TGAGGGGCAAGAGAAATTAACAGAAAAAATGGAGAGGTAATTTGTTTAAATACAGTTA 1065
Db 3362 TGAAGAAATTCAGAAAGCGAAATCGTAAATTTGAAGAAGCTAAGATTGAAGCAAAAGATAA 3303
Qy 1066 CAGTGCACAGAAATAGCAGAACATATTGCAAAAGAAATGAAGATGAAGATATTAAAGAA 1125
Db 3302 TATTCAAGCAATAGTACTAGAGATCAAGTAATGAAGCGAAAACTAATGGGAATAATAA 3243

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Qy 1126 TATTATAGACAGAAATGCCAAATCTGTATCATTAATGTGATGAGGCATCTACAGTTTCAAA 1185
Db 3242 AATAGAAATATAACACCCAGCACTACTGTGAAATCTGAAGCTAGACAAAGCAGTACAGAA 3183
Qy 1186 GAAAACCAACCCTAGTGTATTC 1208
Db 3182 TAAAGCAATGAACAGATTATC 3160

RESULT 4
US-11-102-978-3
; Sequence 3, Application US/11102978
; Publication No. US20050250142A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Technology Transfer Office
; APPLICANT: University of Utah Research Foundation
; TITLE OF INVENTION: Diagnosis and Treatment of Herpes Simplex Virus Disease
; FILE REFERENCE: 0274-5537.1US
; CURRENT APPLICATION NUMBER: US/11/102,978
; CURRENT FILING DATE: 2005-04-11
; PRIOR APPLICATION NUMBER: PCT/US2003/033152
; PRIOR FILING DATE: 2003-10-18
; PRIOR APPLICATION NUMBER: 60/419,576
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 340000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (56948)..(57115)
; OTHER INFORMATION: C21orf34 exon
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (80066)..(81089)
; OTHER INFORMATION: Gene VDACP2; voltage-dependent anion channel isoform 2 pseudogene
; FEATURE:
; NAME/KEY: exon
; LOCATION: (167308)..(167438)
; OTHER INFORMATION: C21orf34 exon
; FEATURE:
; NAME/KEY: exon
; LOCATION: (216732)..(216833)
; OTHER INFORMATION: C21orf34 exon
US-11-102-978-3

Query Match 2.8%; Score 43.6; DB 7; Length 340000;
Best Local Similarity 56.4%; Pred. No. 15;
Matches 102; Conservative 0; Mismatches 75; Indels 4; Gaps 1;

Qy 1341 AATATTGAAAGCAAAATTAATTCATTTCTCTGATGGTGCTAAATACAAACCTGGAA 1400
Db 17050 AATATTGCAATAAAATCTTAGATATATTTTCATGATGTTGTGTTACAAAATCTGAAG 17109
Qy 1401 GAAAGTCGGAGTAGTACAAAATTTGTAGAAAATTTTCTCGAAATCATCATTTTGGAACT 1460
Db 17110 GACAGTTGGAGTTTAGCTAACTGTCATAAAGTTTTCGATATTTTATTAGTACC 17169
Qy 1461 GTTTAAATCATGATTACAAATGTCATGATGATCTATATCCGAATAAAACAAATTA 1520
Db 17170 ----ACATTGTTATATTCATTTCTCGGTGAGGTGATAGAAGATGTAATAATAATTA 17225
Qy 1521 A 1521
Db 17226 A 17226

RESULT 5
US-11-112-908-18
; Sequence 18, Application US/11112908
; Publication No. US20050260659A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 165883
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-18

Query Match 2.8%; Score 43.2; DB 7; Length 165883;
Best Local Similarity 48.0%; Pred. No. 13;
Matches 123; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

Qy 438 ATTTTAAATATCAAGAAGTGAATAACAGACACAGAAAATAATGAAGTGAGCAAAAATC 497
Db 164333 ATATATTAGCCAAAAGTTTATAGAGATAAAGAAAACATTATATATTAATAAAG 164392
Qy 498 ACTGCAGATTGCTAAGGCAAGAACCAATTTTCGAGTATATAGAACCAACCAATCATG 557
Db 164393 AATATATTATATATAATTAATAACAATAATATGAATAATTTTAAACATTTTACACAT 164452
Qy 558 AAGAAAGCCATCATTTCATCAAGAAAGAAAGAAATAGATAATCTTGCTCTCCAGATTGTT 617
Db 164453 ACACACACCATCAAAATACAAAGCAAAACCTAATGGAATTAAGGGGAATCAATA 164512
Qy 618 GGAATGAAAAACAAGCATTTTATGTTTACAGAACAAATACAAATGGCTTTGAAATAAAGAAG 677
Db 164513 GTTGTTTAAAAATAGTTGAAATCTCAATACTCCCTCTCAATGATAGAACACACAGACA 164572
Qy 678 GTAAATTAGGATGAA 693
Db 164573 GAAGATTAGTAGTAA 164588

RESULT 6
US-10-750-185-53428/c
; Sequence 53428, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53428
; LENGTH: 2257
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-53428
```

Query Match 2.7%; Score 41.6; DB 6; Length 2257;
Best Local Similarity 51.0%; Pred. No. 3.5; Mismatches 0; Gaps 0;
Matches 98; Conservative 0; Indels 94; Length 2257;
QY 512 AAGGCAAGGCAACCAATTTGAGTATATAGAACCAACCAATCATTTGAAGAAAGCCATCA 571
DB 899 AAAGAAAAAGTCTGCTTACTTACCTTTTAAAGAAATTCATAGTTGAAATGCCCTTA 840
QY 572 CTTTCATCAAGAAGAATAAGATATCTTGTGCTTCAGATTTGGAATGAAAGAAACAA 631
DB 839 CTTTAAAGAAAGAGATGGTGAATTTTACAGATATATAAATTTGTTGAAGCTTCAGACA 780
QY 632 GCATTTATGTTTACAGACAATACAAATGGCTTGAATTAAGAAAGGTAATTTAGGATGT 691
DB 779 GCATTTATGTTTAAACAGATATCTATCTAAATTTAGTATTAACAATTTTATGTCAGGAATT 720
QY 692 AAGGATTTGTTCA 703
DB 719 ATGAAATATCA 708

RESULT 7

US-10-750-185-40388/c
; Sequence 40388, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 40388
; LENGTH: 3275
; TYPE: DNA
; ORGANISM: Bovine 19866881198799
US-10-750-185-40388

Query Match 2.7%; Score 40.8; DB 6; Length 3275;
Best Local Similarity 48.6%; Pred. No. 6.4; Mismatches 147; Indels 1; Gaps 1;
Matches 140; Conservative 0; Indels 147; Length 3275;
QY 1014 CAAGAGAATTACAGGAAAAAATGGAGAGTAAATTTTAAATACACGTTACAGTGCAA 1073
DB 1167 CAACAGAGTTAATGGAATTAATCTAAACAGCAATGAAATAATAAACTGTAATTTGATA 1108
QY 1074 CAAGATACAGAACATATTTGAAAGAAATGAAGATGAAGATATTTAGATATATATAG 1133
DB 1107 AAGGTAAGCCATCCACATTTTCAAGAAAAATGTATATAACGATATAACCAAAATGATAG 1048
QY 1134 AAGAGAATCCAAAATCTGTATCATATTAATGATGAGGC-ATCTACAGTTTCAAGAAAGACC 1192
DB 1047 ATGTATCGTTTACTCTTAAGCTTTTACTTAAAGACTATCTACATCTCAAAAAAANA 988
QY 1193 ACCCTAGTATTTATCTCCAGTGCAAAATTCAGTCAGCTCTCGACCTGTATGTTATTT 1252
DB 987 TCATCTTTAGATATATACTATATCTTTCTGAAAGAACTTTTCTCCACTGATTACTAAGAT 928
QY 1253 GTGGCTTTAAAGAAATGGTGTCAACTATAGCAGAGTGTATGTCAT 1300
DB 927 GAGCTCTTACATTTGTTAGTTGAGAGCAATTTGCAATTTGCAATGAAACCTTTTATT 880

RESULT 8

US-10-750-185-36740
; Sequence 36740, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 36740
; LENGTH: 1348
; TYPE: DNA
; ORGANISM: Bovine 19866880869275
US-10-750-185-36740

Query Match 2.6%; Score 40.6; DB 6; Length 1348;
Best Local Similarity 54.9%; Pred. No. 4.6; Mismatches 79; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 1263 AAGAAATTGGTCTCAACTATAGCAGAGTGATTTGCAATACATATTGCAATACATTTAAATG 1322
DB 778 AATRAAGCAAGTCATCCACAGATAACCTCTTCTCAATATTTTCTTAACATAATTTTCATG 837
QY 1323 ATTGTGTTTTACAAATCAATTTTGAAGCAAAATTTAATGCAATTTGTTCTGATGGTG 1382
DB 838 ATTTGGGGGAAATTTATGAATATATATATGAATTTATAGACTCTTGTACCTGATCTT 897
QY 1383 CTAATACAANCTGGGAAGAAAGT 1406
DB 898 GCCATGGAATGCAGAAATGAAGT 921

RESULT 9

US-10-750-185-31076/c
; Sequence 31076, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 31076
; LENGTH: 4132
; TYPE: DNA
; ORGANISM: Bovine 19866881042046
US-10-750-185-31076

Query Match 2.6%; Score 39.8; DB 6; Length 4132;
Best Local Similarity 51.4%; Pred. No. 12; Mismatches 92; Conservative 0; Gaps 0;
Matches 92; Conservative 0; Mismatches 87; Indels 0; Gaps 0;


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Qy 832 GGAACATGATGTTCTTAAAGCCCATGGTAAATTCAGGATTTGTTAAAGGAATCAACTAA 891
Db 161 TGATGATGCTACAATGAAGAGAGAGAGTGCAGAAATTAATTTAGTTAATGCATCACAGCA 102
Qy 892 TGATTCATTTGTAATTTAGTGCATAAACAAAAATAAATAATTTGATGCTACTGTAAA 951
Db 101 AAATGTAATTAAGATTGATAATGTACAAACGAATAATCAAAATTCGATGGTATTGTGAG 42
Qy 952 AGTT 955
Db 41 TGAT 38

RESULT 21
US-10-750-185-62955
; Sequence 62955, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 62955
; LENGTH: 1952
; TYPE: DNA
; ORGANISM: Bovine 19866880381074
US-10-750-185-62955

Query Match 2.5%; Score 38.2; DB 6; Length 1952;
Best Local Similarity 59.3%; Pred. No. 19;
Matches 64; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 1299 ATACATTTGACTACTTTAAATGATGCTGTTTACAAATGAATTTGAAACCAATT 1358
Db 534 ATAATATATTTAATAGCATAAATAATTTGTTATGCACTTTAAAAATATTCTAAATCAAGTA 593
Qy 1359 TAATTGCAATTTGTTCTGATGCTAATAACAACCTGGGAAGAAAGT 1406
Db 594 TATAAGTTTCAATGTTCTCTGAGCTGAAACAGACCTGAGAAAAAGT 641

RESULT 22
US-10-750-185-53415
; Sequence 53415, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 53415
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; LENGTH: 5772
; TYPE: DNA
; ORGANISM: Bovine 19866880706942
US-10-750-185-53415

Query Match 2.5%; Score 38.2; DB 6; Length 5772;
Best Local Similarity 48.4%; Pred. No. 33;
Matches 138; Conservative 0; Mismatches 143; Indels 4; Gaps 1;

Qy 848 AAAGCCCATGGTAAAAATTCAGGATTTGTTAAAGGAATCAACTAATGATTCAAATTTGTAAT 907
Db 1293 AAATTTGATTTTAAAGCTTACATTTTGTATTAGTGACAATAATAGATGCAATAATAATA 1352
Qy 908 TTAGTGCATAAACAAAAATAAATAATTTGATGCTACTGTAAGAGTTTTCAATACACTGTT 967
Db 1353 TATTTTATTTACAAAATGATGAAGATTTTTCATAGTATT---TAAATTTAAATTTCTCT 1408
Qy 968 TACAGTTTGTAGTAAACATAACAGACCTTTATCTGTATTTGAGGGGCAAGAGAATTACAG 1027
Db 1409 TCTCTCTCATAAATAACATCTTTTACCTTTTGTATTTCATGTTTACATATTTTAG 1468
Qy 1028 GAAAAAATGGAGAGGTAAATTTGTTTAAATACACGTTACAGTGCACAAGAAATAGCAGAA 1087
Db 1469 TACACAAATTTCTCTTCAGATTTTTCAGAGGCTGTTTCCAGAGCAAAAAAAGAAAAA 1528
Qy 1088 CATATTGCCAAAGAAATGAAGATGAAGATATTTTAAAGATATTATA 1132
Db 1529 TTGAGCTCATAGGTAACTCTTGTGCATTTTATTAGGTATGAAA 1573

RESULT 23
US-10-750-185-45321
; Sequence 45321, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 45321
; LENGTH: 2051
; TYPE: DNA
; ORGANISM: Bovine 19866881033980
US-10-750-185-45321

Query Match 2.5%; Score 38; DB 6; Length 2051;
Best Local Similarity 48.6%; Pred. No. 22;
Matches 104; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

Qy 904 TAATTTAGTGCATAAACAAAAATAAATAATTTGATGCTACTGTAAGAGTTTTCAATAC 963
Db 1792 TAGTGTATGCTAATAATAGTAATTAATTTACATGTTTTCACATAGTTAGTTAATATCAATAC 1851
Qy 964 TGTTTACAGTTTAGTAAAAACATAACAGACCTTTTATCTGATATTGAGGGGCAAGAGAATT 1023
Db 1852 ATATTAGTGTATGTTAAACATACACTAACCAAAACCTTTTTCATTTGAAAAAGGAAGATG 1911
Qy 1024 ACAGGAAAAAATGGAGAGGTAAATTTGTTTAAATACACGTTACAGTGCACAAGAAATAGC 1083
Db 1912 AAAAGCAAGAAGTTAAATGAAAATTTCTGCAATTTCTAAATTTAAAGTTAAAAATCAATTAT 1971
Qy 1084 AGACATATTTCGCAAAAGAAATGAAGATGAAGATA 1117
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Db 1972 ACTTGATTTTAAACATACACTTAAGAGAGAAAAGA 2005

RESULT 24

US-10-750-185-38972

; Sequence 38972, Application US/10750185

; Publication No. US20050260603A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM1100-2

; CURRENT APPLICATION NUMBER: US/10/750,185

; CURRENT FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 38972

; LENGTH: 2455

; TYPE: DNA

; ORGANISM: Bovine 19866880903525

US-10-750-185-38972

Query Match 2.5%; Score 38; DB 6; Length 2455;

Best Local Similarity 46.0%; Pred. No. 24;

Matches 172; Conservative 0; Mismatches 195; Indels 7; Gaps 1;

QY 820 AAAAAAATTAGGACATGATGTTTCTAAAGCCCATGGTAAATTCAGGATTTGTTAAA 879

Db 168 AAAAAAATTAAACATAAATTTAGTAACCCAACTTAACTGAATTAACCTATAAGAAA 227

QY 880 GGAATCACTAATGATTCATTTGTAATTTAGTGCATAACAAAATAATAAAATATTGA 939

Db 228 TACCAATTTCAATTAATTAATATCTTTTATTACTAGAAATTTATGAAATGAAATTTG 287

QY 940 TGCTACTGTAAAGTTTCAATPACTGTTTACAGTTTGTAGTAAACATACAGACCTTTATC 999

Db 288 CACTGCAAGAGATGAATCAAAATTTAAACCTGTTTACGAAAAACAGGAAAAACATAATA 347

QY 1000 TG-----ATATTGAGGGGCAAGAGAAATTTACAGAAAAAATGGAGAGTAAATGTT 1052

Db 348 AGGATAAAATTAATGAAGACCATTTGAATGAAAAATTTGAAACAAATTTGAAAAACCTG 407

QY 1053 TAAATACCTTTACATGTCACAAAGATAGCAGACATATTGCAAAAGAAATGAAGATGA 1112

Db 408 TAAGTACATTTGAAATTAAGAGAAAAAGTTAAATGAAAGAACAGGATTTAGGCTT 467

QY 1113 AGATATTTAAGATATTATAGAAGAGAAATGCCAAATCTGTATCATTAATGATGAGCAT 1172

Db 468 ATATGTAAACAAAGATACATGTAATCAATTAATTTCTTAAATTTAAACAAAGCAT 527

QY 1173 CTACAGTTTCAAAG 1186

Db 528 CTATACCATGACAG 541

RESULT 25

US-10-750-185-25482

; Sequence 25482, Application US/10750185

; Publication No. US20050260603A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

Db 2559 ACTT 2562

RESULT 29

US-10-750-185-55403/c
; Sequence 55403, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55403
; LENGTH: 3469
; TYPE: DNA
; ORGANISM: Bovine 19866808074635
US-10-750-185-55403

Query Match 2.5%; Score 38; DB 6; Length 3469;
Best Local Similarity 50.5%; Pred. No. 29;
Matches 92; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 775 AACCCCTAATGCGAGTAATAAACTACTAGGCAAGCTTCTTACGAAAAAAATTAGGGA 834
Db 2039 AACAAATCTTGGGAAGAATAAAACATTTATGTCAATTAAACAATCCAGAAATTTAGAA 1980
QY 835 ACATGATGTTTCTAAAGCCCATGGTAAATTCAGGATTTGTTAAAGGATCACTAATGA 894
Db 1979 CTATAATATTTGTGATGTTTATTAGTAAATAGGAGAGCGTGGGAGAAACCCATATTCA 1920
QY 895 TTCAATTTGTAATTTAGTGCATAAACAATAATAAAATATTGATGCTACTGTAAAGT 954
Db 1919 AAATATTTGCGATAAACCAACCAAAAAAAGAGAGAGGAGATATTTAAAGAAATATCATATT 1860
QY 955 TT 956
Db 1859 TT 1858

RESULT 30

US-11-077-550-140
; Sequence 140, Application US/11077550
; Publication No. US2005024435A1
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford Charles
; APPLICANT: Quinn, Conrad Padraig
; APPLICANT: Foster, Keith Alan
; APPLICANT: Chaddock, John
; APPLICANT: Marks, Philip
; APPLICANT: Sutton, J. Mark
; APPLICANT: Stancombe, Patrick
; APPLICANT: Wayne, Jonathan
; TITLE OF INVENTION: Recombinant Toxin Fragments
; FILE REFERENCE: 1581.0130004
; CURRENT APPLICATION NUMBER: US/11/077,550
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 10/241,596
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 09/255,829
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/GB97/02273

; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/782,893
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: GB9625996.5
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: GB9617671.4
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 140
; LENGTH: 3948
; TYPE: DNA
; ORGANISM: Clostridium tetani
US-11-077-550-140

Query Match 2.5%; Score 38; DB 9; Length 3948;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 122; Conservative 0; Mismatches 120; Indels 2; Gaps 1;

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Db 2321 AAATTAATAATCTGAAAAACAACCTTGAAGAAAAAGGCTAATAAAGCAATGATAAACATAA 2380
QY 937 TGATGCTACTGTAAAAAGTTTTCAAATCTGTTACAGTTTAGTAAACACATACAGACCTTT 996
Db 2381 ATATATTTATGAGGGAAGTTCTAGATCATTTTTTAGTTAATCAATGATTAAACGAAGCTA 2440
QY 997 ATCTGATATTGAGGGGCAAGAGAAATTACAGGAAAAAAATGGAGAGGTAAATTTGTTAAA 1056
Db 2441 AAAAGCAGTTATTAGAGTTTGTATCTCAAGCAAAAAATATTTTATGCGAG--TATATAAA 2498
QY 1057 TACAGTTTACAGTGCACAACAAGAAATAGCAGAAACATATTGCAAAAAAAATGAAGATGAAGAT 1116
Db 2499 AGCAAAATTTCTAAATTTATAGGTATACTGAACCTAAAAAAATTTAGAAATCAAAAAATAACAA 2558
QY 1117 ATTT 1120
Db 2559 AGTT 2562

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 11:01:36 ; Search time 1294.71 Seconds
(without alignments)
9810.499 Million cell updates/sec

Title: US-10-757-745-5

Perfect score: 1536

Sequence: 1 agagaagaggctcgggga.....attaatcatttaantataa 1536

Scoring table: IDENTITY_NUC

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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	329	21.4	352	7	US-10-242-535A-52672
4	329	21.4	352	7	US-10-085-783A-52672
5	317.6	20.7	4999	7	US-10-362-463-1
6	317.6	20.7	4999	7	US-10-362-463-2
7	317.6	20.7	5144	7	US-10-362-463-3
8	317.6	20.7	5144	7	US-10-362-463-4
9	308	20.1	448	3	US-09-918-995-28032
10	301.4	19.6	3363	8	US-10-450-763-17121
11	208.2	13.6	4961	8	US-10-775-169-139
12	170	11.1	2039	9	US-10-450-763-17122
13	165.2	10.8	3042	7	US-10-362-463-5
14	165.2	10.8	3042	7	US-10-362-463-6
15	165.2	10.8	3183	7	US-10-362-463-9
16	165.2	10.8	3183	7	US-10-362-463-10
17	164.8	10.7	394	9	US-10-450-763-15209
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19	67.8	4.4	12237	6	US-10-311-455-2331
20	66	4.3	921	8	US-10-425-115-38710
21	65	4.2	202802	6	US-10-085-117-286
22	63.6	4.1	1081	8	US-10-425-115-16756
23	62.8	4.1	6292	7	US-10-221-714A-461

62.8	4.1	7442	7	US-10-221-714A-409	Sequence 409, App
62.6	4.1	3683	8	US-10-473-126-339	Sequence 339, App
62.4	4.1	6668	6	US-10-311-455-1670	Sequence 1670, App
59.6	3.9	12142	6	US-10-311-455-1646	Sequence 1646, App
59.2	3.9	8056	8	US-10-473-126-386	Sequence 386, App
59	3.8	577	4	US-09-925-065A-316174	Sequence 316174, App
59	3.8	6419	6	US-10-311-455-240	Sequence 240, App
59	3.8	7597	6	US-10-311-455-386	Sequence 386, App
58.8	3.8	7814	7	US-10-221-714A-252	Sequence 252, App
58.2	3.8	3683	8	US-10-473-126-193	Sequence 193, App
58	3.8	461	3	US-09-814-353-17724	Sequence 17724, App
58	3.8	1300	6	US-10-668-749A-1	Sequence 1, Appli
57.8	3.8	3057	6	US-10-349-680-148	Sequence 148, App
57.6	3.8	6109	6	US-10-311-455-299	Sequence 299, App
57.6	3.8	6109	7	US-10-221-613-33	Sequence 33, Appl
57.6	3.8	6286	7	US-10-221-714A-313	Sequence 313, App
57.6	3.8	17674	6	US-10-311-455-1317	Sequence 1317, App
57.4	3.7	6048	7	US-10-433-793-32	Sequence 32, Appl
57.2	3.7	996	8	US-10-425-115-151933	Sequence 151933, App
56.6	3.7	1243	8	US-10-425-115-172717	Sequence 172717, App
56.6	3.7	50000	8	US-10-706-635-25	Sequence 25, Appl
56.2	3.7	393	3	US-09-960-352-4582	Sequence 4582, App
56.2	3.7	396	3	US-09-825-234-53	Sequence 53, Appl
56.2	3.7	396	3	US-09-970-966-53	Sequence 53, Appl
56.2	3.7	396	6	US-10-212-677-53	Sequence 53, Appl
56.2	3.7	396	6	US-10-361-811-53	Sequence 53, Appl
56.2	3.7	396	6	US-10-369-186-53	Sequence 53, Appl
56.2	3.7	1004	8	US-10-425-115-81106	Sequence 81106, App
55.8	3.6	74665	8	US-10-713-993-6854	Sequence 6854, App
55.4	3.6	1297	8	US-10-425-115-67687	Sequence 67687, App
55.4	3.6	8222	9	US-10-486-319A-43	Sequence 43, Appl
55.4	3.6	8222	9	US-10-486-319A-65	Sequence 65, Appl
55.4	3.6	13784	7	US-10-257-166-144	Sequence 144, App
54.8	3.6	1204	7	US-10-437-963-77858	Sequence 77858, App
54.8	3.6	14006	6	US-10-311-455-1931	Sequence 1931, App
54.8	3.5	5989	7	US-10-221-714A-258	Sequence 258, Appl
54.2	3.5	9539	5	US-10-239-676-52	Sequence 52, Appl
54.2	3.5	14066	6	US-10-240-453-54	Sequence 54, Appl
54.2	3.5	14066	6	US-10-349-680-149	Sequence 149, App
54.2	3.5	14067	7	US-10-282-122A-40681	Sequence 40681, App
53.8	3.5	969	8	US-10-363-345A-26081	Sequence 26081, App
53.8	3.5	969	8	US-10-363-345A-26082	Sequence 26082, App
53.8	3.5	969	9	US-10-363-483A-26081	Sequence 26081, App
53.8	3.5	969	9	US-10-363-483A-26082	Sequence 26082, App
53.8	3.5	1062	8	US-10-425-115-120013	Sequence 120013, App
53.8	3.5	6254	6	US-10-311-455-1593	Sequence 1593, App
53.4	3.5	88445	7	US-10-322-281-724	Sequence 724, App
53.4	3.5	121434	9	US-10-303-165-11	Sequence 11, Appl
53.4	3.5	121434	9	US-10-983-197-4	Sequence 4, Appl
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53.2	3.5	975	8	US-10-363-345A-16099	Sequence 16099, App
53.2	3.5	975	8	US-10-363-345A-16100	Sequence 16100, App
53.2	3.5	975	9	US-10-363-483A-16099	Sequence 16099, App
53.2	3.5	975	9	US-10-363-483A-16100	Sequence 16100, App
53.2	3.5	15548	6	US-10-311-455-2128	Sequence 2128, App
52.6	3.4	8056	8	US-10-473-126-386	Sequence 386, App
52.4	3.4	18734	6	US-10-311-455-1906	Sequence 1906, App
52.4	3.4	158001	7	US-10-211-179-11	GENERAL INFORMATI
52.4	3.4	9964	6	US-10-311-455-71	Sequence 71, Appl
51.8	3.4	13321	7	US-10-221-714A-143	Sequence 143, App
51.8	3.4	3673778	6	US-10-312-841-1	Sequence 1, Appli
51.6	3.4	5930	6	US-10-311-455-490	Sequence 490, App
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51	3.3	520	7	US-10-021-323-7699	Sequence 7699, App
51	3.3	1413	6	US-10-349-680-4	Sequence 4, Appli
51	3.3	1413	7	US-10-282-122A-40501	Sequence 40501, App
51	3.3	5689	5	US-10-239-676-90	Sequence 90, Appl
51	3.3	5689	6	US-10-240-453-100	Sequence 100, App
51	3.3	5689	7	US-10-221-714A-148	Sequence 148, App
51	3.3	8056	8	US-10-473-126-240	Sequence 240, App

c 97	51	3.3	11036	5	US-10-239-676-118	Sequence 118, App	170	48.4	3.2	16750	7	US-10-221-714A-35	Sequence 35, Appl
c 98	51	3.3	11036	6	US-10-240-453-138	Sequence 138, App	c 171	48.4	3.2	17869	6	US-10-311-455-78	Sequence 78, Appl
c 99	51	3.3	20579	7	US-10-433-793-103	Sequence 103, App	c 172	48.4	3.2	17869	7	US-10-257-166-2	Sequence 2, Appl
c 100	50.8	3.3	1121	8	US-10-425-115-115706	Sequence 115706,	c 173	48.2	3.1	478	7	US-10-021-323-6774	Sequence 6774, App
c 101	101	3.3	1214	7	US-10-424-599-102083	Sequence 102083,	c 174	48.2	3.1	12507	6	US-10-311-455-271	Sequence 271, App
c 102	50.6	3.3	616	4	US-09-925-065A-173328	Sequence 173328,	c 175	48.2	3.1	17538	6	US-10-311-455-1130	Sequence 1130, App
c 103	50.6	3.3	5981	6	US-10-311-455-1735	Sequence 1735, App	c 176	48	3.1	473	7	US-10-424-599-128928	Sequence 128928,
c 104	50.6	3.3	6154	7	US-10-221-613-69	Sequence 69, Appl	c 177	48	3.1	556	8	US-10-363-345A-23587	Sequence 23587, A
c 105	50.6	3.3	6191	6	US-10-311-455-1189	Sequence 1189, App	c 178	48	3.1	556	8	US-10-363-345A-23588	Sequence 23588, A
c 106	50.4	3.3	500	3	US-09-991-936-774	Sequence 774, App	c 179	48	3.1	556	9	US-10-363-483A-23587	Sequence 23587, A
c 107	50.4	3.3	500	9	US-10-978-245-774	Sequence 774, App	c 180	48	3.1	556	9	US-10-363-483A-23588	Sequence 23588, A
c 108	50.4	3.3	778	8	US-10-363-345A-2179	Sequence 2179, App	c 181	48	3.1	1105	8	US-10-425-115-173590	Sequence 173590,
c 109	50.4	3.3	778	8	US-10-363-345A-2180	Sequence 2180, App	c 182	48	3.1	5795	6	US-10-311-455-1742	Sequence 1742, App
c 110	50.4	3.3	778	9	US-10-363-483A-2179	Sequence 2179, App	c 183	48	3.1	6155	6	US-10-240-453-235	Sequence 235, App
c 111	50.4	3.3	778	9	US-10-363-483A-2180	Sequence 2180, App	c 184	48	3.1	6668	6	US-10-311-455-1669	Sequence 1669, App
c 112	50.4	3.3	871	8	US-10-767-795-1710	Sequence 1710, App	c 185	48	3.1	12393	6	US-10-311-455-1235	Sequence 1235, App
c 113	50.4	3.3	9539	5	US-10-239-676-51	Sequence 51, Appl	c 186	47.8	3.1	5750	6	US-10-311-455-1981	Sequence 1981, App
c 114	50.4	3.3	9539	6	US-10-240-453-53	Sequence 53, Appl	c 187	47.8	3.1	5750	7	US-10-221-714A-433	Sequence 433, App
c 115	50.2	3.3	548	7	US-10-021-323-16019	Sequence 16019, A	c 188	47.8	3.1	13326	6	US-10-311-455-1686	Sequence 1686, App
c 116	50.2	3.3	7011	6	US-10-311-455-519	Sequence 519, App	c 189	47.6	3.1	574	5	US-10-198-846-1032	Sequence 1032, App
c 117	50.2	3.3	7011	7	US-10-257-166-21	Sequence 21, Appl	c 190	47.6	3.1	628	8	US-10-363-345A-3323	Sequence 3323, App
c 118	50.2	3.3	9741	6	US-10-311-455-1296	Sequence 1296, App	c 191	47.6	3.1	628	8	US-10-363-345A-3324	Sequence 3324, App
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c 120	50	3.3	3450	10	US-11-097-143-26219	Sequence 26219, A	c 193	47.6	3.1	628	9	US-10-363-483A-3324	Sequence 3324, App
c 121	50	3.3	11076	7	US-10-282-122A-35051	Sequence 35051, A	c 194	47.6	3.1	803	7	US-10-437-963-72176	Sequence 72176, A
c 122	50	3.3	11091	7	US-10-724-972A-2170	Sequence 2170, App	c 195	47.6	3.1	1533	7	US-10-282-122A-16542	Sequence 16542, A
c 123	50	3.3	11143	10	US-11-097-143-16492	Sequence 16492, A	c 196	47.6	3.1	6145	6	US-10-311-455-945	Sequence 945, App
c 124	49.8	3.2	525	5	US-10-198-846-1483	Sequence 1483, App	c 197	47.6	3.1	6337	6	US-10-311-455-1283	Sequence 1283, App
c 125	49.8	3.2	6352	5	US-10-172-086-24	Sequence 24, Appl	c 198	47.6	3.1	6337	7	US-10-221-714A-171	Sequence 171, App
c 126	49.8	3.2	6352	6	US-10-311-455-878	Sequence 878, App	c 199	47.6	3.1	6729	7	US-10-433-793-184	Sequence 184, App
c 127	49.8	3.2	6352	8	US-10-480-846-24	Sequence 24, Appl	c 200	47.6	3.1	11155	6	US-10-311-455-577	Sequence 577, App
c 128	49.8	3.2	7348	7	US-10-221-714A-58	Sequence 58, Appl	c 201	47.6	3.1	11691	6	US-10-311-455-2213	Sequence 2213, App
c 129	49.6	3.2	431	3	US-09-960-352-5558	Sequence 5558, App	c 202	47.6	3.1	13420	6	US-10-311-455-890	Sequence 890, App
c 130	49.4	3.2	1029	8	US-10-425-115-123086	Sequence 123086,	c 203	47.6	3.1	13511	6	US-10-311-455-253	Sequence 253, App
c 131	49.4	3.2	1035	9	US-10-779-543-8023	Sequence 8023, App	c 204	47.6	3.1	16914	7	US-10-221-613-213	Sequence 213, App
c 132	49.4	3.2	3996	5	US-10-087-464-42	Sequence 42, Appl	c 205	47.4	3.1	887	9	US-10-479-081-15	Sequence 15, Appl
c 133	49.4	3.2	7657	3	US-09-070-327A-33	Sequence 33, Appl	c 206	47.4	3.1	6025	5	US-10-239-676-44	Sequence 44, Appl
c 134	49.2	3.2	419	3	US-09-960-352-11234	Sequence 11234, A	c 207	47.4	3.1	6767	7	US-10-221-714A-330	Sequence 330, App
c 135	49.2	3.2	526	8	US-10-363-345A-25807	Sequence 25807, A	c 208	47.4	3.1	7659	6	US-10-311-455-161	Sequence 161, App
c 136	49.2	3.2	526	8	US-10-363-345A-25808	Sequence 25808, A	c 209	47.4	3.1	510510	8	US-10-741-600-17606	Sequence 17606, A
c 137	49.2	3.2	526	9	US-10-363-483A-25807	Sequence 25807, A	c 210	47.4	3.1	3673778	6	US-10-312-841-1	Sequence 1, Appl
c 138	49.2	3.2	526	9	US-10-363-483A-25808	Sequence 25808, A	c 211	47.2	3.1	581	7	US-10-425-114-4514	Sequence 4514, App
c 139	49.2	3.2	6816	8	US-10-723-860-7676	Sequence 7676, App	c 212	47.2	3.1	5433	7	US-10-221-613-350	Sequence 350, App
c 140	49.2	3.2	8056	8	US-10-473-126-240	Sequence 240, App	c 213	47.2	3.1	6831	6	US-10-311-455-1460	Sequence 1460, App
c 141	49.2	3.2	13449	6	US-10-311-455-1358	Sequence 1358, App	c 214	47.2	3.1	8420	7	US-10-221-714A-379	Sequence 379, App
c 142	49.2	3.2	15387	6	US-10-311-455-157	Sequence 157, App	c 215	47.2	3.1	11745	6	US-10-240-453-206	Sequence 206, App
c 143	49.2	3.2	3673778	6	US-10-312-841-2	Sequence 2, Appl	c 216	47.2	3.1	17934	6	US-10-311-455-1692	Sequence 1692, App
c 144	49	3.2	484	8	US-10-425-115-172345	Sequence 172345,	c 217	47	3.1	739	8	US-10-425-115-55020	Sequence 55020, A
c 145	49	3.2	8943	7	US-10-257-166-48	Sequence 48, Appl	c 218	47	3.1	6464	6	US-10-311-455-487	Sequence 487, App
c 146	48.8	3.2	337	3	US-09-960-352-6976	Sequence 6976, App	c 219	47	3.1	7823	5	US-10-239-676-198	Sequence 198, App
c 147	48.8	3.2	516	3	US-09-960-352-5785	Sequence 5785, App	c 220	47	3.1	7823	6	US-10-311-455-2034	Sequence 2034, App
c 148	48.8	3.2	3089	9	US-10-954-778-160	Sequence 160, App	c 221	47	3.1	7823	6	US-10-240-453-292	Sequence 292, App
c 149	48.8	3.2	3931	5	US-10-006-780-1	Sequence 1, Appl	c 222	47	3.1	13627	7	US-10-433-793-5	Sequence 5, Appl
c 150	48.8	3.2	4985	6	US-10-094-240-10	Sequence 10, Appl	c 223	47	3.1	14919	7	US-10-221-714A-227	Sequence 227, App
c 151	48.8	3.2	4985	6	US-10-056-405-10	Sequence 10, Appl	c 224	46.8	3.0	416	8	US-10-425-115-174155	Sequence 174155,
c 152	48.8	3.2	9510	6	US-10-240-485-115	Sequence 115, App	c 225	46.8	3.0	509	8	US-10-363-345A-3319	Sequence 3319, App
c 153	48.8	3.2	9510	6	US-10-221-714A-159	Sequence 159, App	c 226	46.8	3.0	509	8	US-10-363-345A-3320	Sequence 3320, App
c 154	48.8	3.2	32392	8	US-10-706-635-27	Sequence 27, Appl	c 227	46.8	3.0	509	9	US-10-363-483A-3319	Sequence 3319, App
c 155	48.6	3.2	441	7	US-10-437-963-98795	Sequence 98795, A	c 228	46.8	3.0	509	9	US-10-363-483A-3320	Sequence 3320, App
c 156	48.6	3.2	868	7	US-10-437-963-42302	Sequence 42302, A	c 229	46.8	3.0	577	8	US-10-437-963-34329	Sequence 34329, A
c 157	48.6	3.2	6107	7	US-10-221-613-304	Sequence 304, App	c 230	46.8	3.0	647	7	US-10-425-115-40312	Sequence 40312, A
c 158	48.6	3.2	6115	6	US-10-311-455-1774	Sequence 1774, App	c 231	46.8	3.0	2187	7	US-10-724-972A-617	Sequence 617, App
c 159	48.6	3.2	7544	5	US-10-239-676-5	Sequence 5, Appl	c 232	46.8	3.0	6095	6	US-10-311-455-334	Sequence 334, App
c 160	48.6	3.2	7544	6	US-10-240-453-13	Sequence 13, Appl	c 233	46.8	3.0	6095	6	US-10-240-485-28	Sequence 28, Appl
c 161	48.6	3.2	188971	7	US-10-235-192A-27	Sequence 27, Appl	c 234	46.8	3.0	6095	7	US-10-221-714A-32	Sequence 32, Appl
c 162	48.4	3.2	423	8	US-10-425-115-113227	Sequence 113227, A	c 235	46.8	3.0	6486	7	US-10-433-793-80	Sequence 80, Appl
c 163	48.4	3.2	553	8	US-10-363-345A-22741	Sequence 22741, A	c 236	46.8	3.0	7057	6	US-10-311-455-1821	Sequence 1821, App
c 164	48.4	3.2	553	8	US-10-363-345A-22742	Sequence 22742, A	c 237	46.8	3.0	7057	6	US-10-240-485-147	Sequence 147, App
c 165	48.4	3.2	553	8	US-10-363-483A-22741	Sequence 22741, A	c 238	46.8	3.0	7057	6	US-10-221-613-317	Sequence 317, App
c 166	48.4	3.2	553	9	US-10-363-483A-22742	Sequence 22742, A	c 239	46.8	3.0	7057	7	US-10-221-714A-323	Sequence 323, App
c 167	48.4	3.2	2184	7	US-10-282-122A-34760	Sequence 34760, A	c 240	46.8	3.0	8254	6	US-10-311-455-837	Sequence 837, App
c 168	48.4	3.2	5886	6	US-10-311-455-2185	Sequence 2185, App	c 241	46.8	3.0	9145	6	US-10-311-455-861	Sequence 861, App
c 169	48.4	3.2	16750	6	US-10-311-455-493	Sequence 493, App	c 242	46.8	3.0	5000	8	US-10-706-635-23	Sequence 23, Appl

243	46.6	3.0	1316	8	US-10-425-115-109626	Sequence 109626,	C 316	45.4	3.0	547	4	US-09-925-065A-354362	Sequence 354362,
C 244	45.6	3.0	6036	6	US-10-311-455-1081	Sequence 1081, Ap	C 317	45.4	3.0	8201	6	US-10-311-455-279	Sequence 279, App
C 245	46.6	3.0	6036	7	US-10-221-613-151	Sequence 151, App	C 318	45.4	3.0	8201	6	US-10-240-452-27	Sequence 27, Appl
C 246	46.4	3.0	341	7	US-10-021-323-451	Sequence 451, App	C 319	45.4	3.0	12007	6	US-10-311-455-689	Sequence 689, App
C 247	46.4	3.0	488	8	US-10-425-115-70463	Sequence 70463, A	C 320	45.4	3.0	12592	6	US-10-221-613-58	Sequence 58, Appl
C 248	46.4	3.0	629	6	US-10-125-968-78	Sequence 78, Appl	C 321	45.4	3.0	13038	6	US-10-311-455-1247	Sequence 1247, Ap
C 249	46.4	3.0	802	8	US-10-425-115-647	Sequence 647, App	C 322	45.4	3.0	15161	7	US-10-221-613-385	Sequence 385, App
C 250	46.4	3.0	807	8	US-10-425-115-126857	Sequence 126857,	C 323	45.2	2.9	396	7	US-10-021-323-17801	Sequence 17801, A
C 251	46.4	3.0	1524	9	US-10-712-533A-9	Sequence 9, Appl	C 324	45.2	2.9	478	8	US-10-357-930-8272	Sequence 8272, Ap
C 252	46.4	3.0	6160	6	US-10-311-455-1506	Sequence 1506, Ap	C 325	45.2	2.9	541	4	US-09-925-065A-518241	Sequence 518241,
C 253	46.4	3.0	6247	7	US-10-257-166-4	Sequence 4, Appl	C 326	45.2	2.9	606	4	US-09-925-065A-407077	Sequence 407077,
C 254	46.4	3.0	7522	6	US-10-311-455-888	Sequence 888, App	C 327	45.2	2.9	606	4	US-09-925-065A-407077	Sequence 407078,
C 255	46.4	3.0	15743	6	US-10-240-453-269	Sequence 269, App	C 328	45.2	2.9	1030	7	US-10-282-122A-35330	Sequence 35330, A
C 256	46.4	3.0	17594	6	US-10-311-455-1999	Sequence 1999, App	C 329	45.2	2.9	1496	3	US-09-764-891-9190	Sequence 9190, Ap
C 257	46.4	3.0	37515	7	US-10-433-733-28	Sequence 28, Appl	C 330	45.2	2.9	1496	5	US-10-091-572-766	Sequence 766, App
C 258	46.4	3.0	115515	6	US-10-311-455-2147	Sequence 2147, Ap	C 331	45.2	2.9	2665	4	US-09-925-065A-712735	Sequence 712735,
C 259	46.2	3.0	385	3	US-09-960-352-1739	Sequence 1739, Ap	C 332	45.2	2.9	2665	4	US-09-925-065A-712736	Sequence 712736,
C 260	46.2	3.0	424	5	US-10-198-846-2929	Sequence 2929, Ap	C 333	45.2	2.9	5834	3	US-09-764-860-976	Sequence 976, App
C 261	46.2	3.0	479	3	US-09-960-352-12872	Sequence 12872, A	C 334	45.2	2.9	5834	3	US-09-764-860-976	Sequence 976, App
C 262	46.2	3.0	641	3	US-09-969-034-389	Sequence 389, App	C 335	45.2	2.9	5834	5	US-10-091-572-769	Sequence 769, App
C 263	46.2	3.0	5487	6	US-10-311-455-1571	Sequence 1571, Ap	C 336	45.2	2.9	5834	5	US-10-074-095-976	Sequence 976, App
C 264	46.2	3.0	7057	6	US-10-311-455-1822	Sequence 1822, Ap	C 337	45.2	2.9	5834	6	US-10-212-872-976	Sequence 976, App
C 265	46.2	3.0	7057	6	US-10-240-485-148	Sequence 148, App	C 338	45.2	2.9	5834	6	US-10-212-872-976	Sequence 1170, Ap
C 266	46.2	3.0	7057	7	US-10-221-613-318	Sequence 318, App	C 339	45.2	2.9	6183	6	US-10-311-455-1170	Sequence 1170, Ap
C 267	46.2	3.0	7057	7	US-10-221-714A-324	Sequence 324, App	C 340	45.2	2.9	6775	7	US-10-433-793-190	Sequence 190, App
C 268	46.2	3.0	8079	7	US-10-240-589C-122	Sequence 122, App	C 341	45.2	2.9	8781	6	US-10-311-455-1660	Sequence 1660, Ap
C 269	46.2	3.0	18154	6	US-10-311-455-228	Sequence 228, App	C 342	45	2.9	537	7	US-10-021-323-8120	Sequence 8120, Ap
C 270	46.2	3.0	50000	8	US-10-706-635-26	Sequence 26, Appl	C 343	45	2.9	564	7	US-10-437-963-7175	Sequence 7175, Ap
C 271	46	3.0	494	8	US-10-357-930-10012	Sequence 10012, A	C 344	45	2.9	677	7	US-10-437-963-72100	Sequence 72100, A
C 272	46	3.0	3970	8	US-10-723-860-6160	Sequence 6160, A	C 345	45	2.9	1305	7	US-10-369-339-73	Sequence 73, Appl
C 273	46	3.0	5647	6	US-10-311-455-1539	Sequence 1539, Ap	C 346	45	2.9	1305	7	US-10-956-157-281	Sequence 281, App
C 274	46	3.0	5647	7	US-10-221-613-281	Sequence 281, App	C 347	45	2.9	1330	9	US-10-956-157-281	Sequence 5516, Ap
C 275	46	3.0	5768	7	US-10-221-613-61	Sequence 61, Appl	C 348	45	2.9	1330	9	US-09-925-065A-679743	Sequence 679743,
C 276	46	3.0	7498	6	US-10-311-455-230	Sequence 230, App	C 349	45	2.9	1740	4	US-09-925-065A-679744	Sequence 679744,
C 277	46	3.0	7657	5	US-10-239-676-185	Sequence 185, App	C 350	45	2.9	1830	8	US-10-706-635-67	Sequence 67, Appl
C 278	46	3.0	7657	7	US-10-311-455-1995	Sequence 1995, Ap	C 351	45	2.9	5527	6	US-10-311-455-290	Sequence 290, App
C 279	46	3.0	11787	7	US-10-240-589C-52	Sequence 52, Appl	C 352	45	2.9	5527	6	US-10-240-452-38	Sequence 38, Appl
C 280	46	3.0	17738	6	US-10-311-455-1511	Sequence 1511, Ap	C 353	45	2.9	5542	6	US-10-311-455-1994	Sequence 1994, Ap
C 281	46	3.0	49379	7	US-10-741-601-5746	Sequence 5746, Ap	C 354	45	2.9	6876	6	US-10-311-455-954	Sequence 954, App
C 282	46	3.0	49379	8	US-10-741-601-17905	Sequence 17905, A	C 355	45	2.9	6944	5	US-10-172-086-112	Sequence 112, App
C 283	46	3.0	337344	8	US-10-388-838-58	Sequence 28737, A	C 356	45	2.9	6944	7	US-10-311-507-114	Sequence 114, App
C 284	45.8	3.0	321	7	US-10-424-599-23196	Sequence 23196, A	C 357	45	2.9	6944	8	US-10-480-846-112	Sequence 112, App
C 285	45.8	3.0	627	7	US-10-021-323-13664	Sequence 13664, A	C 358	45	2.9	12592	7	US-10-221-613-58	Sequence 58, Appl
C 286	45.8	3.0	1039	8	US-10-425-115-58802	Sequence 58802, A	C 359	45	2.9	15872	7	US-10-221-714A-242	Sequence 242, App
C 287	45.8	3.0	648	3	US-09-969-034-4434	Sequence 4434, Ap	C 360	45	2.9	18683	6	US-10-311-455-286	Sequence 286, App
C 288	45.8	3.0	706	8	US-10-363-345A-28737	Sequence 28737, A	C 361	45	2.9	32392	8	US-10-706-635-24	Sequence 24, Appl
C 289	45.8	3.0	706	9	US-10-363-483A-28737	Sequence 28737, A	C 362	45	2.9	50000	8	US-10-706-635-24	Sequence 124, App
C 290	45.8	3.0	706	9	US-10-363-483A-28737	Sequence 28737, A	C 363	45	2.9	83391	7	US-10-433-793-124	Sequence 6528, Ap
C 291	45.8	3.0	1039	8	US-10-425-115-58802	Sequence 58802, A	C 364	45	2.9	83391	7	US-09-960-352-6528	Sequence 29301, A
C 292	45.8	3.0	1060	7	US-10-424-599-29814	Sequence 29814, A	C 365	45	2.9	451	3	US-09-918-985-23301	Sequence 47977, A
C 293	45.8	3.0	5107	6	US-10-311-455-1039	Sequence 1039, Ap	C 366	44.8	2.9	451	3	US-10-424-599-47977	Sequence 106527,
C 294	45.8	3.0	5364	7	US-10-257-166-87	Sequence 87, Appl	C 367	44.8	2.9	592	7	US-09-925-065A-106527	Sequence 57885, A
C 295	45.8	3.0	6754	7	US-10-221-613-266	Sequence 266, App	C 368	44.8	2.9	592	7	US-10-424-599-57885	Sequence 126557,
C 296	45.8	3.0	8759	8	US-10-473-126-250	Sequence 250, App	C 369	44.8	2.9	673	8	US-10-425-115-126557	Sequence 58, Appl
C 297	45.8	3.0	8759	8	US-10-473-126-250	Sequence 250, App	C 370	44.8	2.9	927	8	US-10-706-635-58	Sequence 12233, A
C 298	45.8	3.0	8759	8	US-10-473-126-378	Sequence 378, App	C 371	44.8	2.9	1599	8	US-10-198-846-12223	Sequence 45, Appl
C 299	45.8	3.0	12405	5	US-10-239-676-35	Sequence 35, Appl	C 372	44.8	2.9	1656	5	US-10-486-319A-45	Sequence 67, Appl
C 300	45.8	3.0	12405	6	US-10-240-453-43	Sequence 43, Appl	C 373	44.8	2.9	3051	9	US-10-486-319A-67	Sequence 1, Appl
C 301	45.8	3.0	12405	7	US-10-221-613-101	Sequence 101, App	C 374	44.8	2.9	3051	9	US-10-250-987-1	Sequence 691, App
C 302	45.8	3.0	17534	7	US-10-257-166-108	Sequence 108, App	C 375	44.8	2.9	3422	7	US-10-311-455-691	Sequence 351, App
C 303	45.8	3.0	17848	5	US-10-239-676-28	Sequence 28, Appl	C 376	44.8	2.9	5739	6	US-10-221-613-353	Sequence 1199, Ap
C 304	45.8	3.0	17848	6	US-10-240-453-38	Sequence 38, Appl	C 377	44.8	2.9	9233	6	US-10-311-455-1199	Sequence 109, App
C 305	45.8	3.0	17848	6	US-10-257-166-58	Sequence 58, Appl	C 378	44.8	2.9	13125	6	US-10-240-485-109	Sequence 430, App
C 306	45.8	3.0	513509	3	US-09-754-853A-4	Sequence 4, Appl	C 379	44.8	2.9	13125	6	US-10-221-714A-430	Sequence 5719, Ap
C 307	45.6	3.0	375	8	US-10-357-930-44930	Sequence 44930, A	C 380	44.8	2.9	14615	7	US-10-741-601-5719	Sequence 17839, A
C 308	45.6	3.0	603	7	US-10-282-122A-27293	Sequence 27293, A	C 381	44.8	2.9	398287	8	US-10-741-600-17839	Sequence 1, Appl
C 309	45.6	3.0	765	8	US-10-425-115-85265	Sequence 85265, A	C 382	44.8	2.9	398287	8	US-09-790-988-1	Sequence 3931, Ap
C 310	45.6	3.0	6794	7	US-10-221-613-133	Sequence 133, App	C 383	44.8	2.9	640681	3	US-09-733-627A-2931	Sequence 22930, A
C 311	45.6	3.0	23272	3	US-09-960-870-6	Sequence 6, Appl	C 384	44.6	2.9	351	3	US-10-674-124A-430	Sequence 41993, A
C 312	45.6	3.0	23272	3	US-09-960-858-6	Sequence 6, Appl	C 385	44.6	2.9	428	8	US-10-437-963-41993	Sequence 40082, A
C 313	45.6	3.0	23272	3	US-10-251-668-6	Sequence 6, Appl	C 386	44.6	2.9	521	7	US-10-357-930-40082	
C 314	45.6	3.0	580073	6	US-10-205-220-1	Sequence 1, Appl	C 387	44.6	2.9	556	8		
C 315	45.4	3.0	411	3	US-09-960-352-14521	Sequence 14521, A	C 388	44.6	2.9				

389	44.6	2.9	556	8	US-10-357-930-40182	Sequence 40182, A	c 462	44.2	2.9	15674	6	US-10-311-455-335	Sequence 335, App
390	44.6	2.9	556	8	US-10-357-930-42124	Sequence 42124, A	c 463	44.2	2.9	15674	6	US-10-240-485-29	Sequence 29, Appl
391	44.6	2.9	556	8	US-10-357-930-43620	Sequence 43620, A	c 464	44.2	2.9	15782	6	US-10-240-453-10	Sequence 10, Appl
392	44.6	2.9	638	4	US-09-925-065A-74515	Sequence 74515, A	c 465	44.2	2.9	17280	7	US-10-221-714A-497	Sequence 497, App
393	44.6	2.9	1319	7	US-10-424-599-142270	Sequence 142270, A	c 466	44.2	2.9	61020	7	US-10-221-714A-514	Sequence 514, App
394	44.6	2.9	3990	8	US-10-425-115-129439	Sequence 129439, A	c 467	44.2	2.9	83391	7	US-10-433-793-123	Sequence 123, App
395	44.6	2.9	4152	8	US-10-706-635-9	Sequence 9, Appl	c 468	44.2	2.9	83391	7	US-10-433-793-124	Sequence 124, App
396	44.6	2.9	4947	8	US-10-425-115-31146	Sequence 31146, A	c 469	44.2	2.9	442	3	US-09-960-352-12911	Sequence 12911, A
397	44.6	2.9	5820	6	US-10-311-455-512	Sequence 512, App	c 470	44.2	2.9	452	3	US-09-987-899-125	Sequence 125, App
398	44.6	2.9	6503	6	US-10-311-455-744	Sequence 744, App	c 471	44.2	2.9	452	3	US-10-425-115-64074	Sequence 64074, A
399	44.6	2.9	6621	5	US-10-172-086-9	Sequence 9, Appl	c 472	44.2	2.9	539	3	US-09-983-965-2109	Sequence 2109, App
400	44.6	2.9	6621	7	US-10-221-613-53	Sequence 53, Appl	c 473	44.2	2.9	606	4	US-09-925-065A-407076	Sequence 407076, A
401	44.6	2.9	6621	7	US-10-311-507-15	Sequence 15, Appl	c 474	44.2	2.9	606	4	US-09-925-065A-407079	Sequence 407079, A
402	44.6	2.9	6621	8	US-10-480-846-9	Sequence 9, Appl	c 475	44.2	2.9	787	7	US-10-424-599-70401	Sequence 70401, A
403	44.6	2.9	6621	8	US-10-473-126-123	Sequence 123, App	c 476	44.2	2.9	885	7	US-10-767-701-20477	Sequence 20477, A
404	44.6	2.9	6621	8	US-10-473-126-237	Sequence 237, App	c 477	44.2	2.9	963	8	US-10-425-115-176206	Sequence 176206, A
405	44.6	2.9	8961	6	US-10-240-453-302	Sequence 302, App	c 478	44.2	2.9	1656	6	US-10-253-904-1	Sequence 1, Appl
406	44.6	2.9	14551	6	US-10-240-485-138	Sequence 138, App	c 479	44.2	2.9	1656	6	US-10-392-970-1	Sequence 1, Appl
407	44.6	2.9	14568	6	US-10-311-455-203	Sequence 203, App	c 480	44.2	2.9	1656	10	US-11-109-793-1	Sequence 1, Appl
408	44.6	2.9	19787	6	US-10-311-455-1423	Sequence 1423, App	c 481	44.2	2.9	2342	4	US-09-925-065A-695871	Sequence 695871, A
409	44.6	2.9	50000	8	US-10-706-635-25	Sequence 25, Appl	c 482	44.2	2.9	2342	4	US-09-925-065A-695872	Sequence 695872, A
410	44.4	2.9	456	8	US-10-767-795-527	Sequence 527, App	c 483	44.2	2.9	2411	6	US-10-253-904-15	Sequence 15, Appl
411	44.4	2.9	489	3	US-09-918-995-15384	Sequence 15384, A	c 484	44.2	2.9	2411	6	US-10-392-970-47	Sequence 47, Appl
412	44.4	2.9	507	7	US-10-437-963-69134	Sequence 69134, A	c 485	44.2	2.9	2411	10	US-11-109-793-47	Sequence 47, Appl
413	44.4	2.9	535	8	US-10-363-345A-28883	Sequence 28883, A	c 486	44.2	2.9	5276	6	US-10-311-455-124	Sequence 124, App
414	44.4	2.9	535	8	US-10-363-345A-28884	Sequence 28884, A	c 487	44.2	2.9	5361	3	US-09-742-096-2	Sequence 2, Appl
415	44.4	2.9	535	9	US-10-363-483A-28883	Sequence 28883, A	c 488	44.2	2.9	5464	7	US-10-240-454-37	Sequence 37, Appl
416	44.4	2.9	535	9	US-10-363-483A-28884	Sequence 28884, A	c 489	44.2	2.9	5467	6	US-10-311-455-2082	Sequence 2082, App
417	44.4	2.9	588	7	US-10-021-323-6082	Sequence 6082, App	c 490	44.2	2.9	5528	7	US-10-415-253-1	Sequence 1, Appl
418	44.4	2.9	611	4	US-09-925-065A-638356	Sequence 638356, A	c 491	44.2	2.9	6152	3	US-09-742-096-1	Sequence 1, Appl
419	44.4	2.9	693	8	US-10-363-345A-18695	Sequence 18695, A	c 492	44.2	2.9	6306	5	US-10-239-676-224	Sequence 224, App
420	44.4	2.9	693	8	US-10-363-345A-18696	Sequence 18696, A	c 493	44.2	2.9	6306	6	US-10-240-453-332	Sequence 332, App
421	44.4	2.9	693	9	US-10-363-483A-18695	Sequence 18695, A	c 494	44.2	2.9	6361	6	US-10-311-455-1114	Sequence 1114, App
422	44.4	2.9	693	9	US-10-363-483A-18696	Sequence 18696, A	c 495	44.2	2.9	12507	6	US-10-311-455-271	Sequence 271, App
423	44.4	2.9	729	6	US-10-349-680-112	Sequence 112, App	c 496	44.2	2.9	12705	6	US-10-311-455-122	Sequence 122, App
424	44.4	2.9	841	8	US-10-425-115-42884	Sequence 42884, A	c 497	44.2	2.9	13249	6	US-10-311-455-89	Sequence 89, Appl
425	44.4	2.9	3441	7	US-10-424-599-55147	Sequence 55147, A	c 498	44.2	2.9	13503	6	US-10-311-455-2043	Sequence 2043, App
426	44.4	2.9	6631	6	US-10-240-453-214	Sequence 214, App	c 499	44.2	2.9	34769	7	US-10-221-714A-501	Sequence 501, App
427	44.4	2.9	7369	8	US-10-473-126-131	Sequence 131, App	500	44.2	2.9	513509	3	US-09-754-853A-4	Sequence 4, Appl
428	44.4	2.9	7369	8	US-10-486-319A-34	Sequence 34, Appl							
429	44.4	2.9	9110	7	US-10-221-714A-115	Sequence 115, App							
430	44.4	2.9	9219	7	US-10-311-455-2400	Sequence 2400, App							
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432	44.4	2.9	10369	6	US-10-311-455-365	Sequence 365, App							
433	44.4	2.9	10369	6	US-10-221-714A-25	Sequence 25, Appl							
434	44.4	2.9	12025	6	US-10-311-455-1271	Sequence 1271, App							
435	44.4	2.9	15548	6	US-10-311-455-2127	Sequence 2127, App							
436	44.4	2.9	19659	6	US-10-311-455-739	Sequence 739, App							
437	44.4	2.9	24259	7	US-10-221-714A-415	Sequence 415, App							
438	44.4	2.9	177556	3	US-09-952-213D-6	Sequence 6, Appl							
439	44.4	2.9	177556	10	US-11-033-666-6	Sequence 6, Appl							
440	44.2	2.9	432	8	US-10-425-115-138737	Sequence 138737, A							
441	44.2	2.9	452	4	US-09-925-065A-272979	Sequence 272979, A							
442	44.2	2.9	480	3	US-09-960-352-5301	Sequence 5301, App							
443	44.2	2.9	599	9	US-10-972-079-15484	Sequence 15484, A							
444	44.2	2.9	622	7	US-10-424-599-3380	Sequence 3380, App							
445	44.2	2.9	2431	6	US-10-311-455-2241	Sequence 2241, App							
446	44.2	2.9	5185	6	US-10-311-455-1007	Sequence 1007, App							
447	44.2	2.9	5452	6	US-10-311-455-1122	Sequence 1122, App							
448	44.2	2.9	5477	5	US-10-172-086-109	Sequence 109, App							
449	44.2	2.9	5477	7	US-10-311-507-107	Sequence 107, App							
450	44.2	2.9	5477	8	US-10-480-846-109	Sequence 109, App							
451	44.2	2.9	6221	7	US-10-221-714A-226	Sequence 226, App							
452	44.2	2.9	6641	6	US-10-311-455-288	Sequence 288, App							
453	44.2	2.9	6641	6	US-10-240-452-36	Sequence 36, Appl							
454	44.2	2.9	7143	7	US-10-311-455-956	Sequence 956, App							
455	44.2	2.9	8076	7	US-10-257-166-36	Sequence 36, Appl							
456	44.2	2.9	8759	8	US-10-473-126-104	Sequence 104, App							
457	44.2	2.9	8759	8	US-10-473-126-232	Sequence 232, App							
458	44.2	2.9	11047	5	US-10-239-676-188	Sequence 188, App							
459	44.2	2.9	11047	5	US-10-311-455-1958	Sequence 1958, App							
460	44.2	2.9	11047	6	US-10-240-453-276	Sequence 276, App							
461	44.2	2.9	13326	6	US-10-311-455-1685	Sequence 1685, App							

ALIGNMENTS

RESULT 1

US-10-757-745-5
; Sequence 5, Application US/10757745
; Publication No. US20050101769A1
; GENERAL INFORMATION:
; APPLICANT: Vlaams Internuiversitair Instituut Voor Biotechnologie VZW
; TITLE OF INVENTION: CD-40 INTERACTING AND TRAF-INTERACTING PROTEINS
; FILE REFERENCE: 2676-4555US
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: US/09/697,863A
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: PCT/EP99/03025
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: BPO 98201392.2
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1530)..(1531)
; OTHER INFORMATION: N stands for any nucleotide.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (209)..(1534)

Qy	391	TGATATCTCTGTTTCCTAAAATGCCAAAACGACAGGGTGATTTTTTGCATTTTTTAAATAT	450
Db	1519	TCGATTTCTGTTTCCTAAAATGCCAAAACGACAGGGTGATTTTTTGCATTTTTTAAATGT	1578
Qy	451	GAAGAAGGTGAAACACACACACAGAAAATATGAAGTGAGCAAAAATCCTGCAGATTGTC	510
Db	1579	GAAGAAGGTGAAACACACACAGAAAATATGAAGTGAGCAAAAATCCTGCAGATTGTC	1638
Qy	511	TAAGGCAAAAGGAACCAATTTTCAGTATATAGAACCAACCAATCATTTGAAGAAAAGCCATC	570
Db	1639	TAAGGCAAAAGGAACCAATTTTCGNGTATATTGAACAACCAATCATTTGAAGAAAAGCCATC	1698
Qy	571	ACTTTCATCAAAAGAAAGAAATAGATAAATCTTGTCCTTCAGATGTTGGAAATGAAAACA	630
Db	1699	ACTTTCATCAAAAGAAAGAAATAGATAATCTTGTCCTTCAGATGTTGGAAATGAAAACA	1758
Qy	631	AGCATTTATGTTTACAGAACAATACAAATGGCTTGAATATAAAGMAGGTAAATTTAGATG	690
Db	1759	AGCATTTATGTTTACAGAACAATACAAATGGCTTGAATATAAAGMAGGTAAATTTAGGATG	1818
Qy	691	TAAGGATTTGTTACAGAGTTCCGCCATTTGGGATCGAAAAGCAGAAAAGCATGTCCTATGTC	750
Db	1819	TAAGGATTTGTTACAGAGTTCCGCCATTTGGGATCGAAAAGCAGAAAAGCATGTCCTATGTC	1878
Qy	751	CAAGGAATTGAATTCGATATTTAGTAAACCCCTAATAGGCAAGTAAATAAACTACTAGGCAAGC	810
Db	1879	CAAGGAATTGAATTCGATATTTAGTAAACCCCTAATAGGCAAGTAAATAAACTACTAGGCAAGC	1938
Qy	811	TTCTCTACGAAAAAAAATTAGGGAACATGATGTTTCTAAAGCCCATCGTAAATTCAGGA	870
Db	1939	TTCTCTACGAAAAAAAATTAGGGAACATGATGTTTCTAAAGCCCATCGTAAATTCAGGA	1998
Qy	871	TTTGTGTAAGGAATCAACTAATGATCCAAATTTGTAAATTTAGTGATATAACCAAAATAATAA	930
Db	1999	TTTGTGTAAGGAATCAACTAATGATCCAAATTTGTAAATTTAGTGATATAACCAAAATAATAA	2058
Qy	931	AAATATTGATCTACTGCTAAAGTTTTTCAATPACTGTTTACAGTTTAGTAAAAACATAACAG	990
Db	2059	AAATATTGATCTACTGCTAAAGTTTTTCAATPACTGTTTACAGTTTAGTAAAAACATAACAG	2118
Qy	991	ACCTTTATCTGATATTGAGGGGGCAAGAAATACAGAAAAAAATGGAGAGGTAAATTG	1050
Db	2119	ACCTTTATCTGATATTGAGGGGGCAAGAAATACAGAAAAAAATGGAGAGGTAAATTG	2178
Qy	1051	TTTAAATAACGTTTACAGTGCACAAAGAAATAGCAGAACATATTCGAAAAAGAAATGAAGAT	1110
Db	2179	TTTAAATAACGTTTACAGTGCACAAAGAAATAGCAGAACATATTCGAAAAAGAAATGAAGAT	2238
Qy	1111	GAAGATATTTAAGAAATATTATAGAAGAGAAATGCCAAAATCTGTATCATAAATTTGATGAGGC	1170
Db	2239	GAAGATATTTAAGAAATATTATAGAAGAGAAATGCCAAAATCTGTATCATAAATTTGATGAGGC	2298
Qy	1171	ATCTACAGTTTCAAAGAAAAACACCTAGTGAATTTATCTCCAGTGCACAAATTCAGTCAGC	1230
Db	2299	ATCTACAGTTTCAAAGAAAAACACCTAGTGAATTTATCTCCAGTGCACAAATTCAGTCAGC	2358
Qy	1231	TCCTGCACCTGTATGTTATTTGTGGCTTTTAAAGAAATGGTGTCACATATAGCAGAGTG	1290
Db	2359	TCCTGCACCTGTATGTTATTTGTGGCTTTTAAAGAAATGGTGTCACATATAGCAGAGTG	2418
Qy	1291	TATTTGTCAAATCATTTATGACTACTTTAAATGATTTGTGGTTTTTACAAATGAATATTTGAA	1350
Db	2419	TATTTGTCAAATCATTTATGACTACTTTAAATGATTTGTGGTTTTTACAAATGAATATTTGAA	2478
Qy	1351	AGCAAAATTAATGCAATTTTGTTCFGATGGTGCTTAATACAANCCTGGGAAGAAAGTCTGG	1410
Db	2479	AGCAAAATTAATGCAATTTTGTTCFGATGGTGCTTAATACAANCCTGGGAAGAAAGTCTGG	2538
Qy	1411	AGTAGCTACAAATTTGTAGAAAAATTTTTCCTGGAATCATCATTTTGGAACTGTTTAAATCA	1470
Db	2539	AGTAGCTACAAATTTGTAGAAAAATTTTTCCTGGAATCATCATTTTGGAACTGTTTAAATCA	2598
Qy	1471	TCGATTACAAATTTGTCATTTGATGTTCTATATCCGAAAAATAAAACAAATTAATCATTTTAA	1529

Db 2599 TCGATTACAATTGTCCTTGATGTTCTATATCCGAATATAACCAAAATTAAATCATTTAA 2657

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RESULT 3

US-10-242-535A-52672

; Sequence 52672, Application US/10242535A

; Publication No. US20040013663A1

; GENERAL INFORMATION:

; APPLICANT: ChondroGene Inc.

; APPLICANT: Liew, C.C.

; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

; FILE REFERENCE: 4231/2005

; CURRENT APPLICATION NUMBER: US/10/242,595A

; CURRENT FILING DATE: 2002-09-12

; PRIOR APPLICATION NUMBER: US 10/085,783

; PRIOR FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: US 60/305,340

; PRIOR FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 60/275,017

; PRIOR FILING DATE: 2001-03-12

; PRIOR APPLICATION NUMBER: US 60/271,955

; PRIOR FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 58994

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 52672

; LENGTH: 352

; TYPE: DNA

; ORGANISM: Human

US-10-242-535A-52672

RESULT 4
US-10-085-783A-52672
; Sequence 52672, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13

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; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52672
; LENGTH: 352
; TYPE: DNA
; ORGANISM: Human
; US-10-085-783A-52672

Query Match      21.4%; Score 329; DB 7; Length 352;
Best Local Similarity 99.2%; Pred. No. 5.1e-61;
Matches 351; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1175 ACAGTTTCAAGAAACCAACCTAGTGATTTATCTCCAGTGCACAAATTCAGTCAGCTCCT 1234
DB 1 ACAGTTTCAAGAAACCAACCTAGTGATTTATCTCCAGTGCACAAATTCAGTCAGCTCCT 60
QY 1235 GCACCTGTTATGTTATTTTGGCTTTAAAGAAATTTGGTGTCAACTATAGCAGAGTGATT 1294
DB 61 GCACCTGTTATGTTATTTTGGCTTTAAAGAAATTTGGTG-CAACTATAGCAGAGTGATT 119
QY 1295 GTCAATACATTAATGACTACTTTAAATGATTTGTTTACAAATGAATATTTGAAAGCA 1354
DB 120 GTCAATACATTAATGACTACTTTAAATGATTTGTTTACAAATGAATATTTGAAAGCA 179
QY 1355 AATTTAATTCATTTTGTCTGATGGTGCTAATACAAACCTGGGAAGAAAGTCTGGAGTA 1414
DB 180 AATTTAATTCATTTTGTCTGATGGTGCTAATACAACTCTGGGAAGAAAGTCTGGAGTA 239
QY 1415 GCTCAAAATTTGTAGAAATTTCTCTGAAATCATCATTTGGAACCTGTTTAAATCATCGA 1474
DB 240 GCTCAAAATTTGTAGAAATTTCTCTGAAATCATCATTTGGAACCTGTTTAAATCATCGA 299
QY 1475 TTCAATTCCTCACTTGATGATTTCTATATCCGAAATTAACAAATTAATCATTTA 1528
DB 300 TTCAATTCCTCACTTGATGATTTCTATATCCGAAATTAACAAATTAATCATTTA 352

RESULT 5
US-10-362-463-1
; Sequence 1, Application US/10362463
; Publication No. US20040059089A1
; GENERAL INFORMATION:
; APPLICANT: Akzo No. US20040059089A1el N.V.
; TITLE OF INVENTION: COACTIVATION OF NUCLEAR RECEPTORS
; FILE REFERENCE: 2000.569WO
; CURRENT APPLICATION NUMBER: US/10/362,463
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: EP202905.6
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: EPI201771.1
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4999
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-362-463-2

Query Match      20.7%; Score 317.6; DB 7; Length 4999;
Best Local Similarity 90.9%; Pred. No. 5.8e-58;
Matches 360; Conservative 0; Mismatches 34; Indels 2; Gaps 2;

QY 1 AGAGAAAGAGGCTCCGGGAGATAGCGGACCAAGTGGGGCTGCCCTCTCTTTTGAAGCGGT 60
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QY 61 TTT-CGTCTCTTTCCGCCAGTGGCTCCAGCTCACGAGGGGGGGTCCCGGTAGCGG 119
DB 76 TTTGGTCTCTTTCCGCCGCTGGCGTCCGCTCACGAGGGGGGGTCCCGGTAGCGG 135
QY 120 AGGCGGTGCAGGGGGGAAAGGGGAGTGTGTGGCGGTGCGGAG-TAGGGAAGAGGAGG 178
DB 136 AGGCGGTGCAGGGGGGAAAGGGGATTCGTGGCGACGCGGGGGGCAAGGAGCAGAGGAGC 195
QY 179 AGTGGTGTGTTCGCGCGGCTCGGAGACATGGAGACCCGGGGTCCGAATATAGAA 238
DB 196 AGTGGTGTGTTCGCGCGGCTCGGAGACATGGAGACCCGGGGTCCGAGATATAGAA 255
QY 239 TCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAAAGGATGAAAAATGAAGACGAC 298
DB 256 TCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAAAGGATGAAAAATGAAGACGAC 315
QY 299 ATTCAAGTTTGTCAAGTGAAGGACCAATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGT 358
DB 316 ATTCAAGTTTGTCAAGTGAAGGACCAATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGT 375

RESULT 6
US-10-362-463-2
; Sequence 2, Application US/10362463
; Publication No. US20040059089A1
; GENERAL INFORMATION:
; APPLICANT: Akzo No. US20040059089A1el N.V.
; TITLE OF INVENTION: COACTIVATION OF NUCLEAR RECEPTORS
; FILE REFERENCE: 2000.569WO
; CURRENT APPLICATION NUMBER: US/10/362,463
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: EP202905.6
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: EPI201771.1
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4999
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-362-463-2

Query Match      20.7%; Score 317.6; DB 7; Length 4999;
Best Local Similarity 90.9%; Pred. No. 5.8e-58;
Matches 360; Conservative 0; Mismatches 34; Indels 2; Gaps 2;

QY 1 AGAGAAAGAGGCTCCGGGAGATAGCGGACCAAGTGGGGCTGCCCTCTCTTTTGAAGCGGT 60
DB 16 AGAGAAAGCGGCTCCGGGGGCATAGCGGGGCAGTAAGGGCCGCTCTCTCTTTGAAGAGT 75
QY 61 TTT-CGTCTCTTTCCGCCAGTGGCTCCAGCTCACGAGGGGGGGTCCCGGTAGCGG 119
DB 76 TTTGGTCTCTTTCCGCCGCTGGCGTCCGCTCACGAGGGGGGGTCCCGGTAGCGG 135
QY 120 AGGCGGTGCAGGGGGGAAAGGGGAGTGTGTGGCGGTGCGGAG-TAGGGAAGAGGAGG 178
DB 136 AGGCGGTGCAGGGGGGAAAGGGGATTCGTGGCGACGCGGGGGGCAAGGAGCAGAGGAGC 195
QY 179 AGTGGTGTGTTCGCGCGGCTCGGAGACATGGAGACCCGGGGTCCGAATATAGAA 238
DB 196 AGTGGTGTGTTCGCGCGGCTCGGAGACATGGAGACCCGGGGTCCGAGATATAGAA 255
QY 239 TCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAAAGGATGAAAAATGAAGACGAC 298
DB 256 TCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAAAGGATGAAAAATGAAGACGAC 315
QY 299 ATTCAAGTTTGTCAAGTGAAGGACCAATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGT 358
DB 316 ATTCAAGTTTGTCAAGTGAAGGACCAATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGT 375
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Qy 359 GGTGATGATGAACACCTTAGCGCTATTATAGTGAT 394
Db 376 AGTGATGATGAAGACGCTAGCACCTCTATAGTGAT 411

RESULT 7
US-10-362-463-3
; Sequence 3, Application US/10362463
; Publication No. US20040059089A1
; GENERAL INFORMATION:
; APPLICANT: Akzo No. US20040059089A1el N.V.
; TITLE OF INVENTION: COACTIVATION OF NUCLEAR RECEPTORS
; FILE REFERENCE: 2000,569WO
; CURRENT APPLICATION NUMBER: US/10/362,463
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: EP202905.6
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: EP1201771.1
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 5144
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-362-463-3

Query Match 20.7%; Score 317.6; DB 7; Length 5144;
Best Local Similarity 90.9%; Pred. No. 5.9e-58;
Matches 360; Conservative 0; Mismatches 34; Indels 2; Gaps 2;

Qy 1 AGAGAAAGAGGCTCCGGGGAGATAGCGGACAGTGAGGGTGCCTCTTTTGAAGCGGT 60
Db 16 AGAGAAAGCGCTCCGGGGGCATAGCGGGCCAGTAAGGGCGCTCTCTTTGAAGAGGT 75
Qy 61 TTT-CGTCTCTTTCCGCCAGTGGCTCCAGCTCAGCGAGGCGGGTCCCGGTAGCGG 119
Db 76 TTTCGCTCTCTTTCCGCCAGTGGCTCAGCGAGGCGGGTCCCGGTAGCGG 135
Qy 120 AGGCGGTGCAGGCGGGGAGGAGTGTGGCGGCTGCGGAG-TAGGGACAGCAGGAC 178
Db 136 AGGCGGTGCAGGCGGGGAGGAGTGTGGCGGATTCGTGGCGACGCGCGCAAGGACAGCAGGAGC 195
Qy 179 AGTGGTGTCTGTCAGCGCGGCGCTCGGAGACATGGGAGACCCGGGTGCGGAAATAGAA 238
Db 196 AGTGGTGTCTGTCAGCGCGGCGCTCGGAGACATGGGAGACCCGGGTGCGGAGATAGAA 255
Qy 239 TCTGTCCCTCCAGCTCGGCTGAGGATCTGAGTCAACACGATGAAATGAAGACGAC 298
Db 256 TCTGTCCCTCCAGCTCGGCTGAGGATCTGAGTCAACACGATGAAATGAAGACGAC 315
Qy 299 ATTCAAGTTTGTCAAGTGAAGACCATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGT 358
Db 316 ATTCAAGTTTGTCAAGTGAAGACCATTAGCACCTGTTCTTGAATACATCGATCTGGTCTGT 375
Qy 359 GGTGATGATGAACACCTTAGCGCTATTATAGTGAT 394
Db 376 AGTGATGATGAAGACGCTTAGCACCTCTTATAGTGAT 411

RESULT 9
US-09-918-995-28032
; Sequence 28032, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28032
; LENGTH: 448
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(448)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-28032

Query Match 20.1%; Score 308; DB 3; Length 448;
Best Local Similarity 81.4%; Pred. No. 2.1e-56;
Matches 402; Conservative 0; Mismatches 11; Indels 81; Gaps 1;

Qy 128 CAGGGCGGAAGGAGTGTGGCGGCTGCGGAGTAGGAGACAGCAGGAGCAGTGGTCT 187
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Db 35 CGGGGCAANNNGGNGGNGCGGCTCGCGAGTAGGGACAGCAGCAGCAGTGCTGCT 94
QY 188 GTACGCGCGCGCTCGGAGACATGGAGACCCGGGGTCGGAATAATAGAAATCTGTCCCT 247
Db 95 GTACGCGCGCGCTCGGAGACATGGAGACCCGGGGTCGGAATAATAGAAATCTGTCCCT 154
QY 248 CCAGCTGGCCCTGAGGCATCTGAGTCAACAAACGGAATGAAGACGACATTCAGTTT 307
Db 155 CCAGCTGGCCCTGAGGCATCTGAGTCAACAAACGGAATGAAGACGACATTCAGTTT 214
QY 308 GTACGTGAAGGACCAATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGGTGATGAT 367
Db 215 GTACG----- 219
QY 368 GAAACCCCTAGCGCTATTATAGTAGTATCTGTCTTAAATGCCAAACGACAGGCT 427
Db 220 -----TATTCGTCTTAAATGCCAAACGACAGGCT 253
QY 428 GATTTTTTGCATTTTTTAAATATGAAGAGGTGAAACACAGACAGAAATAATGAAGTG 487
Db 254 GATTTTTTGCATTTTTTAAATGTGAAGAGGTGAAACACAGACAGAAATAATGAAGTG 313
QY 488 AGCAAAATCTACTGCAGATTGTCTAAGCAAAAGAACCAATTCGAGTATATAGAACAA 547
Db 314 AGCAAAATCTACTGCAGATTGTCTAAGCAAAAGAACCAATTCGAGTATATAGAACAA 373
QY 548 CCAATCATTGAAGAAAGCCATCTTTCATCAAGAAAGAAATAGATAATCTGTGCTT 607
Db 374 CCAATCATTGAAGAAAGCCATCTTTCATCAAGAAAGAAATAGATAATCTGTGCTT 433
QY 608 CCAGATTGTTGAA 621
Db 434 CCAGATTGTTGAA 447

RESULT 10
US-10-450-763-17121
; Sequence 17121, Application US/10450763
; Publication No. US200501967541
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 17121
; LENGTH: 3363
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (771)...(211)
; OTHER INFORMATION: 98% homologous to Escherichia coli seryl-tRNA
; OTHER INFORMATION: synthetase, accession number X05017, Smith-Waterman Score=934.
US-10-450-763-17121

Query Match 19.6%; Score 301.4; DB 9; Length 3363;
Best Local Similarity 91.2%; Pred. No. 1.5e-54;
Matches 331; Conservative 0; Mismatches 31; Indels 1; Gaps 1;

QY 33 GTGAGGGCTGCCCTCTTTTGAAGCGGTTTT-CGTCTCTTCGCGCAGTGGCTCCAGC 91
Db 1 GTAAGGGCGGCTCTCTCTTTGAAGAGTTTTTGCGTCTCTTCGCGGTTGGGCGC 60
QY 92 TCACGAGGGCGGCTCCCGGTAGCGGAGGGGTGCGAGGGCGGAGGTGCTGTC 151

Db 61 TCACGAGGGCGGCTCCCGGTAGCGCAGCGGTGCGAGGAGGGGATTCGTGGC 120
QY 152 GGCTGCGGCGAGTGGGACAGCAGGACAGTGGTCTGTACGCGCGGCGTGGAGACATG 211
Db 121 GACGCGGCGGACAGGACAGCAGGACAGTGGTCTGTACGCGCGGCGTGGAGACATG 180
QY 212 GGAGACCGGGGTGCGGAATAATAAGAAATCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAG 271
Db 181 GGAGACCGGGGTGCGGAGATAATAAGAAATCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAG 240
QY 272 TCAACAACCGGATGAAATGAAGACGACATTCAGTTTGTCACTGAAGGCCATCGAGACCT 331
Db 241 TCAACAACCGGATGAAATGAAGACGACATTCAGTTTGTCACTGAAGGCCATTCAGACCT 300
QY 332 GTTCTTGAATACATCGATCTGGTCTGTGGTATGATGAACCCCTAGCGCCTATTATAGT 391
Db 301 GTTCTTGAATACATTCGATCTGGTCAGCAGTGTATGAAGACCTTAGCACCTCTTATACT 360
QY 392 GAT 394
Db 361 GAT 363

RESULT 11
US-10-775-169-139
; Sequence 139, Application US/10775169
; Publication No. US20040175743A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dörner, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 139
; LENGTH: 4961
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-139

Query Match 13.6%; Score 208.2; DB 8; Length 4961;
Best Local Similarity 94.3%; Pred. No. 2.9e-34;
Matches 216; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 166 GGACAGCAGGAGCAGTGGTGTCTGTCAGCGCGGCGTGGAGACATGGGAGACCCGGGTC 225
Db 1 GGACAGCAGGAGCAGTGGTGTCTGTCAGCGCGGCGTGGAGACATGGGAGACCCGGGTC 60
QY 226 GGAATAATAGAAATCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAAACGATGA 285
Db 61 GGAGATAATAGAAATCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAAACGATGA 120
QY 286 AAATGAAGACGACATTCAGTTTGTCACTGAAGGCCATCGAGACCTGTCTTGAATACAT 345
Db 121 AAATGAAGACGACATTCAGTTTGTCACTGAAGGCCATTCAGACCTGTCTTGAATACAT 180
QY 346 CGATCTGCTGTGTGTATGATGAACCCCTAGCGCCTATTATAGTGTAT 394
Db 181 TGATCTGTGTGAGTGTATGAGACCTTAGCACCTCTTATAGTGTAT 229

RESULT 12
US-10-450-763-17122
; Sequence 17122, Application US/10450763
; Publication No. US200501967541
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc


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; SEQ ID NO 9
; LENGTH: 3183
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-362-463-9

Query Match
Best Local Similarity 10.8%; Score 165.2; DB 7; Length 3183;
Matches 173; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 209 ATGGGAGACCGGGTCGGAATAATAGAAATCTGCTCCAGCTGGCCCTGAGGCATCT 268
Db 1 ATGGGAGACCGGGTCGGAATAATAGAAATCTGCTCCAGCTGGCCCTGAGGCATCT 60

QY 269 GAGTCAACACGGATGAATAAGACGACATTCAGTTTGTTCAGTGAAGGACCATCGAGA 328
Db 61 GAGTCAACACGGATGAATAAGACGACATTCAGTTTGTTCAGTGAAGGACCATTCAGA 120

QY 329 CCTGTTCTTGAATACATCATCTGCTGTGTGTGATGATGAAACCCCTAGGCCCTATTAT 388
Db 121 CCTGTTCTTGAATACATTCATTCAGTCTGTCAGCAGTGAATGAAGCCTTAGCACCTTTAT 180

QY 389 AGTGAT 394
Db 181 ACTGAT 186

RESULT 16
US-10-362-463-10
; Sequence 10, Application US/10362463
; Publication No. US20040059089A1
; GENERAL INFORMATION:
; APPLICANT: Akzo No. US20040059089A1el N.V.
; TITLE OF INVENTION: COACTIVATION OF NUCLEAR RECEPTORS
; FILE REFERENCE: 2000,569WO
; CURRENT APPLICATION NUMBER: US/10/362,463
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: EP202905.6
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: EP1201771.1
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 3183
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-362-463-10

Query Match
Best Local Similarity 10.8%; Score 165.2; DB 7; Length 3183;
Matches 173; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 209 ATGGGAGACCGGGTCGGAATAATAGAAATCTGCTCCAGCTGGCCCTGAGGCATCT 268
Db 1 ATGGGAGACCGGGTCGGAATAATAGAAATCTGCTCCAGCTGGCCCTGAGGCATCT 60

QY 269 GAGTCAACACGGATGAATAAGACGACATTCAGTTTGTTCAGTGAAGGACCATCGAGA 328
Db 61 GAGTCAACACGGATGAATAAGACGACATTCAGTTTGTTCAGTGAAGGACCATTCAGA 120

QY 329 CCTGTTCTTGAATACATCATCTGCTGTGTGTGATGATGAAACCCCTAGGCCCTATTAT 388
Db 121 CCTGTTCTTGAATACATTCATTCAGTCTGTCAGCAGTGAATGAAGCCTTAGCACCTTTAT 180

QY 389 AGTGAT 394
Db 181 ACTGAT 186

RESULT 17
US-10-450-763-15209
; Sequence 15209, Application US/10450763
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; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 15209
; LENGTH: 394
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: SIMILAR
; LOCATION: (79) ..(183)
; OTHER INFORMATION: 100% homologous to Homo sapiens Human secreted protein, SEQ
; OTHER INFORMATION: ID NO: 5728, accession number G01647, Smith-Waterman Score=180.
US-10-450-763-15209

Query Match
Best Local Similarity 10.7%; Score 164.8; DB 9; Length 394;
Matches 166; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 147 GTGGCGGCTGCGGAGTAGGACAGCAGGAGCAGTGTGTCTCAGCCGCGCGTCCGAG 206
Db 17 GTGGCGGCTGCGGAGTAGGACAGCAGTGTGTCTCAGCCGCGCGTCCGAG 76

QY 207 ACATGGGAGACCGGGGTCCGAAATAATAGAAATCTGTCCCTCCAGCTGGCCCTGAGGCAT 266
Db 77 ACATGGGAGACCGGGGTCCGAGATAATAGAAATCTGTCCCTCCAGCTGGCCCTGAGGCAT 136

QY 267 CTGAGTCAACACGGATGAAATGAAGACGACATTCAGTTTGTTCAGTG 314
Db 137 CTGAGTCAACACGGATGAAATGAAGACGACATTCAGTTTGTTCAGTG 184

RESULT 18
US-10-450-763-17120
; Sequence 17120, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 17120
; LENGTH: 394
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: SIMILAR
; LOCATION: (79) ..(183)
; OTHER INFORMATION: 100% homologous to Homo sapiens Human secreted protein, SEQ
; OTHER INFORMATION: ID NO: 5728, accession number G01647, Smith-Waterman Score=180.
US-10-450-763-17120

Query Match
Best Local Similarity 10.7%; Score 164.8; DB 9; Length 394;
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Db 707 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 648
Qy 685 AGGATGTAAGGATTGTTTCAGCAGTTCGGCATTCGGGATCGAAGCAGAAAAGCAGTGTCCA 744
Db 647 AAACCTAATAAACAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 588
Qy 745 TGTGTCAGGAATGGATGTCATATTTAGTAACCCCTAAATGGCGAGTAAATAAACTACTAG 804
Db 587 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 528
Qy 805 GCAAGCTTCTCTACGAAAAAAAAAATAGGGACATGATGTTTCTAAAGCCCATGTTAAAT 864
Db 527 AAAATAATGAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 468
Qy 865 TCAGGATTTGTTAAAGGATCACTAATGATTCATTTGTAATTTAGTGCATAAACAAA 924
Db 467 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 408
Qy 925 TAATAAAAAATATTGATGCTACTGTAAAAAGTTTTCATACTCTTTTACAGTTTAGTAAACA 984
Db 407 AAAATAAATAAATAAAAAAAAAAAGAAACATATAAATAAATAACAA--TAAAAA 350
Qy 985 TAAACAGACCTTTATCTCATATTTAGGGGGCGAAGAGAAATACAGGAAAAAATGAGAGGT 1044
Db 349 AAAAAAAAAAATAAAAAAAAAATTGACAAACAAAAAAAAAAAAAAAAAATAAATAA 290
Qy 1045 AAATGTTTAAATACACGTTACAGTGCACAAAGAAATAGCAGAACATATTCGAAAGAAAT 1104
Db 289 AAATTTATACGTAATAAAAAAAAAAAGATTTAAAAATAAAAAAAAAAAAAAAAAA 230
Qy 1105 GAAGATGAAGATATTTAAGATATTTATAGAGAGAAATGCCAAAA 1148
Db 229 AAAAAAAAAAAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 186
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RESULT 21

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US-10-085-117-286
; Sequence 286, Application US/10085117
; Publication No. US2003023334A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 286
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-117-286
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Query Match 4.2%; Score 65; DB 6; Length 202802;
Best Local Similarity 54.6%; Pred. No. 0.02;
Matches 214; Conservative 0; Mismatches 171; Indels 7; Gaps 4;

Qy 1080 TAGCAGACATATTGCAAAAGAAATGAAGATCAAGATATTTAAGAAATATTATAGAGAGA 1139
Db 75092 TTGCAAAACATATATCTACTAGATGCAAAATATGCAITTTGGAGAA--CTTATAATCAGG 75150
Qy 1140 ATGCCAAAATCTGTATCATTAATTGTAGGCGATCTACAGTTTCAAGAGAAACCACCCCTAG 1199
Db 75151 AAGGTAAATTTCACTGATATTATGATGCTGCTCAACATTTTCATAGAAATGTTTAA 75210
Qy 1200 TGATTTATCTCAGTGCAAAATTCAGTCAGCTCCGCACTGCTGATTTATTTGCGCTT 1259
Db 75211 TAAATTTACTTAAATGCAATATTTCAAGACTTCAAGACAGTGTGATGGTTTTATTGATT 75270
Qy 1260 TAAAGAATTTGGTGTCAACTATATAGAGAGTGTATTGTCAATACATATTAGTACTTTAA 1319
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Db 75271 TCATGAAGCTGGAAGGAACAACATCTGA---AATATATTAAACTTTATTAGTCATACTCA 75327
Qy 1320 ATGATTTGTGTTTTTACAAATGAATATTGAAAGCAATTTAAATGCAATTTTGTCTCATG 1379
Db 75328 AGAAAAATGGTTTTCAATAGAAATACTTACATGAAAACCT--TGTGAATGTTTTCACATG 75386
Qy 1380 GTGCTAATAAANCCCTGGGAAGAAAGTCTGGAGTAGCTACAAAAATTTGTTAGAAAAATTTTC 1439
Db 75387 GTGCAAGTATAGTGTAGGAGAAA--AAGTTGCTTAGCTGAAATTTCTAGAAAAACTTTC 75444
Qy 1440 CTGAAATCATCTTTGGAACACTGTTTAAATCAT 1471
Db 75445 TAGTGTTTTCAITTTGATGCTGCTCACTTAT 75476

RESULT 22
US-10-425-115-16756/c
; Sequence 16756, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 16756
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1081)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_115279C.1
US-10-425-115-16756
```

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Query Match 4.1%; Score 63.6; DB 8; Length 1081;
Best Local Similarity 42.9%; Pred. No. 0.0028;
Matches 291; Conservative 0; Mismatches 388; Indels 0; Gaps 0;

Qy 444 TAAATATGAAGAAGGTGAAACACAGACACAGAAAAATAATGAAGTCAGCAAAATCAGTCA 503
Db 907 TAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 848
Qy 504 GATTGCTTAAGGCAAGAACCAACATTTTCGAGTATATAGAACCAACCATCATTTGNAGAAA 563
Db 847 GAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 788
Qy 564 AGCCATCACTTTTCATCAAGAAAGAAATAGATAATCTTGTCTTCCAGATTTGTGGAATG 623
Db 787 AAAAAAGCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 728
Qy 624 AAAAAACAGCAATTTATGTTTACAGAACAAATCAAAATGGCTTTGAAATAAAGAAAGTAAAT 683
Db 727 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 668
Qy 684 TAGGATGTAAGGATTTGTCAGCAGTTCGGCATTTGGGTTCGAAAGCAGAAAGCATGTCC 743
Db 667 AACAAAAAATAAAGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 608
Qy 744 ATGTGTCGAAGGATGATTCATATTTAGTAACCCCTTAATGGCAGTAAATAAACTACTTA 803
Db 607 ACAAACAAAAATAAAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 548
Qy 804 GGCAAGCTTCTCTACGAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 863
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1792, 4861..4862
; OTHER INFORMATION: n is a or g or c or t
US-10-221-714A-409

Query Match      4.1%; Score 62.8; DB 7; Length 7442;
Best Local Similarity 44.9%; Pred. No. 0.011;
Matches 323; Conservative 0; Mismatches 392; Indels 5; Gaps 2;

Qy 444 TAAATATGAGAGGTGAAAACAGACACAGAAAATATGAAGTGAAGCAAAATCACTGCA 503
Db 2812 TAATTTCTCTAAATTTAAATAAAAAAATAAAAAATCAAAAAAATAAAAAATCTTAAAAA 2753

Qy 504 GATTGCTTAAGCGCAAGCAACACATTTTCGAGTATATAGAACCAACCAATCATTCGAGAAA 563
Db 2752 AAATAAATCTTAAAAAATAAATAAATTTTAAATAAAAAAATAAAAAATCTTAAAAA 2693

Qy 564 AGCCATCACTTTTCATCAAGAAAGAAATAGATAATCTTTGCTTCCAGATTGTTGGAATG 623
Db 2692 AAAAAACAATCTATTAAAAAATAAATAAATCTAATAAAAAAATAAAAAATCTAAAAAT 2633

Qy 624 AAAAAACAGCAATTTATGTTTACAGAACAAATCAAAATGCGCTTGAAATAAAGAGGTAAAT 683
Db 2632 AAAAAAC--GAAATTTAAAAAATAAAAAATAAAAAATCTAAAAAATAAAAAATCTAAAA 2575

Qy 684 TAGGATGTAAGGATTTGTTGACGAGTTTCGGCATTTGGGATCGAAAGCAGAAAGCATGTCC 743
Db 2574 AAAAAAATAAATAATCTAAAAAATAAAAAAATAAAGCAAAATTTAAAAAATAAATAATCTAAAA 2515

Qy 744 ATGTGTCACAGGAATGGATTCGATATTTAGTAACCCCTTAATGGCGAGTAAATAAACTACTA 803
Db 2514 AAAAAAATAAATAATCTAAAAAATAAATAAATAAATTTGAAATAAAAAAATAAATAAATAA 2455

Qy 804 GCGAGCTTCTCTACGAAAAAATAATAGGGAACATGATGTTTCTTAAAGCCCATGTTAAAA 863
Db 2454 AAAAAAATAAATAATCTAAAAAATAAAAAAATAAAGCAAAATCTAAAAAATAAATAAATAA 2395

Qy 864 TTCAGATTGTTTAAAGCAATCACTAATGATTCATTTGTAATTTAGTGCATTAACAAA 923
Db 2394 AAAAAAATAAATAATCTAAAAAATAAAAAAATAAACAATATAAAAAAATAAATAATTTAAAA 2335

Qy 924 ATAATAAAAAATTTGATGCTACTGTGTAAGGTTTTCATATCTGTTTACAGTTTGTAGTAAAC 983
Db 2334 AAAAAAATAAATAATCTAAAAAATAAAAAAATAAATAATCTAAAAAATAAATAATTTAAAA 2275

Qy 984 ATAACAGACCTTTATCTGATATTGAGGGGCGAAGAGATTACAGGAAA---AAATGGAG 1040
Db 2274 AAAAAAATAAATAATCTAAAAAATAAAAAAATAAATAAATAAATAAATAAATAAATAAATA 2215

Qy 1041 AGGTAATTTGTTTAAATACAGTTTACAGTGCACAGAAATAGCAGACATATTGCAAAAG 1100
Db 2214 AATAAATAATCTAAAAAATAAAAAAATAAACAATCTAAAAAATAAAAAAATAAATAAATA 2155

Qy 1101 AAATCAAGTGAAGATTTTAAAGATATTATAGAGAGAAATGCCAAATCTGTATCATAA 1160
Db 2154 AATAAATAATTTAAAAAATAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATA 2095

RESULT 25
US-10-473-126-339/c
; Sequence 339, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 339
; LENGTH: 3683
```

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-339

Query Match      4.1%; Score 62.6; DB 8; Length 3683;
Best Local Similarity 43.8%; Pred. No. 0.0085;
Matches 320; Conservative 0; Mismatches 409; Indels 2; Gaps 1;

Qy 462 AARACAGACACAGAAAATTAATGAGTGAAGCAAAATCACTGCAGATTGCTGAAGCAAGG 521
Db 3487 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3428

Qy 522 AACACACATTTTCGAGTATATAGAACCAACCAATCATTTGAAGAAAGCCATCACTTTCATCAA 581
Db 3427 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3368

Qy 582 AGAAAGAAATAGATAATCTTTGCTTCCAGATTGCTGGAATGAAATGAAACCAAGCATTTATGT 641
Db 3367 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3308

Qy 642 TTACAGAACCAATCAAAATGCTTGAATTAAGAGGCTTAATTTAGGATGTAAGGATTGTT 701
Db 3307 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3248

Qy 702 CAGCAGTTTCGGCATTTTCGGGATCGAAAGCAGAAAGCATGTCATGTGTCGAAGGAATGGA 761
Db 3247 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3188

Qy 762 TTGCATATTTAGTAACCCCTTAATGGCAGTAAATAAACTACTAGGCAAGCTTCTCTACGAA 821
Db 3187 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3128

Qy 822 AAAAAATTTAGGGAACATGATGTTTCTTAAGCCCATGGTAA--AATTCAGGATTGTTTAAA 879
Db 3127 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3068

Qy 880 GGAATCAACTAATCATTTCAATTTGTAATTTAGTGCATAAACAAAAATAAATAAATAATTTGA 939
Db 3067 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3008

Qy 940 TGCTACTGTAAAAGTTTTTCAATCTGTTTACAGTTTGTAGTAAACATACACACCTTTATC 999
Db 3007 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2948

Qy 1000 TGATATTGAGGGGCGAAGAGATTTACAGGAAAAAATAATGGAGAGGTAAATTTGTTTAAATAC 1059
Db 2947 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2888

Qy 1060 ACGTTACAGTGCACACAGAAATAGCAGACATATTGCAAAAGAAATGAAGATGAAGATATT 1119
Db 2887 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2828

Qy 1120 TAAGAATATTATAGAGAGAAATGCAAAATCTGTATCATTAATTTGATGAGGCATCTACAGT 1179
Db 2827 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2768

Qy 1180 TTCAAGAGAAA 1190
Db 2767 TAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2757

RESULT 26
US-10-311-455-1670/c
; Sequence 1670, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detecti
; TITLE OF INVENTION: cytosine methylation
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; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 386
; LENGTH: 8056
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-386

Query Match          3.9%; Score 59.2; DB 8; Length 8056;
Best Local Similarity 44.6%; Pred. No. 0.069;
Matches 309; Conservative 0; Mismatches 381; Indels 3; Gaps 2;

QY 843 TTTCTAAGCCCATGTAATAATTCAGGATTTCTTAAAGGAATCAACTAATGATCAATTT 902
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3378 TTTTAAATCATCATTTTCAAAATTTTATTCATTTTTTTTACATTAACAATATATTTTTTTT 3319
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 903 GTAATTTAGTGCATAAACAATAATAAATAATATTGATGCTACTGTAAAGTTTTCAATA 962
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3318 TTCAAAAATAATACACAACATACAAAATTTTTTTTACATCAATTAATTAATAATAA 3259
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 963 CTGTTTACAGTTTAGTAAACAATAACAGACCTTTATCTGATATCGAGGGGCAAGAGAT 1022
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3258 TAATCAAAATTTAAAAAAATAATAATAATTTAAATTTTATTTACAAATTCAAACAACA 3199
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1023 TACAGGAAAAATGAGAGGTAAATTTGTTAAATACAGCTTACAGTGCACAAGNATAG 1082
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3198 AAATTTTATTAATAATAATTTATTTTAAATTTATATATAAACAATTTTCAATCATCA 3139
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1083 CAGACATATTCGAAAGAAATGAAGATCAAGATATTTAAGAAATATTATAGAAGAGATG 1142
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3138 TTAATTTCAATTTAAAAAAATTAATTTTTTATTAATTAACATTAATAATAATAATTA 3079
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1143 CCAAAATCTGATCAATAATGATAGGCACTACAGTTTCAAGAAAAACCCCTAGTGA 1202
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3078 CAAATTTTCATCACA-ATTATAACATTTATTTTATTTTAAATTTATATTTATAAAAAATTTA 3020
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1203 TTTATCTCAGTGCACAATTCAGTCAGCTCCTGCACCTGTTATGTTATTTGGCTTAA 1262
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3019 AACATCATCATTTTAAATATATATCAATTTTCAATAAATTTTTTTTTTTTAAACAAT 2960
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1263 AAGAATTTGTGTCACCTATAGCAGAGTGATTTGTCAATACATTTATGACTACTTTAAAG 1322
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2959 AATAATTCATTTAAATTTTACATTTCAAAAATTTTAAATTTTCAATTTTCAATTTTCAAT 2900
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1323 ATTGTGTTTTCAAATGAATATTTGAAAGCAAAATTTAATGCAATTTTCTGATGGTG 1382
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2899 TTTTATTTTTCACAAAAATTTTTTTCATAAAATAATTCAAATTTTAAATATTTTAT 2840
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1383 CTAATACAANC--CTGGGAAGAAGTCTGGAGTAGCTACAAAATGTTAGAAAATTTTCC 1440
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2839 AAAAAAATATCATTTTATTTATTAATAACAATTTTAAATAACAATAATTCATTTAAATTTAT 2780
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1441 TGAATTCATCATTTGCAACTGTTTAAATCATGATTACAAATTTGTCATTTGATGATCTAT 1500
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2779 AAAAAATAACAATTAATAATTTTTTTTATTTTATTAATAATTTTATTAACAATTTAT 2720
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1501 ATCCGAAATAAACAAATTAATCAATTTAAANNTA 1533
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2719 TTATTAAAAAATAAATAATTAATTTTAAAAA 2687
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 29
US-09-925-065A-316174/c
; Sequence 316174, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
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; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 316174
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-316174

Query Match          3.8%; Score 59; DB 4; Length 577;
Best Local Similarity 52.6%; Pred. No. 0.02;
Matches 122; Conservative 1; Mismatches 109; Indels 0; Gaps 0;

QY 1301 ACATTATTGACTACTTTTAAATGATTGCTTTTACAAATGAATATTTGAAAGCAAAATTTA 1360
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 429 AAATTTATATATCTTTTTCATTTTGGAAAGTTTTCTTCAAGACRTATTTATATGAAAACTTT 370
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1361 ATTGCATTTTCTGATGCTTAATACAACTGGAAGAACTCTGGAGTAGCTACA 1420
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 369 ATTGAACCTGTACATATGTCGCCAGTCATTTGCTGGGAAAATGCTGGAAGTATCAGGA 310
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1421 AAATTTGTAGAAAAATTTTCTGAAATCATCATTTTGGAACTGTTTAAATCATCGATTACAA 1480
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 309 AAAATAAACACAAATTTCTAGTAAATTTCTCTTATCTATCTATGCAAGAAATCCAA 250
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1481 TTGTCATTTGATGATCTTATATCCGAAATAAAACAAATTAATCATTTAAANT 1532
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 249 TTATTTCTGAATAACATAATCAATTAATTAATCAATTAATAATAATAGATTTAAAT 198
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 30
US-10-311-455-240/c
; Sequence 240, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detecting
; Cytosine Methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 240
; LENGTH: 6419
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-240

Query Match          3.8%; Score 59; DB 6; Length 6419;
Best Local Similarity 42.6%; Pred. No. 0.066;
Matches 308; Conservative 0; Mismatches 415; Indels 0; Gaps 0;

QY 445 AAATATGAAGAAGGTGMAAACACACAGACAGAAAAATAATGAAGTGAGCAAAAAATCATCTGCAG 504
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 09:59:45 ; Search time 277.691 Seconds
(without alignments)
9832.267 Million cell updates/sec

Title: US-10-757-745-5
Perfect score: 1536
Sequence: 1 agagaaagagctcgaggga.....attaatcatttaantataa 1536

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/prodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/prodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/prodata/1/ina/PCrus COMB.seq.*
- 7: /cgn2_6/prodata/1/ina/pp COMB.seq.*
- 8: /cgn2_6/prodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1533	99.8	1336	3	US-09-697-863A-5
2	270.8	17.6	274	3	US-09-513-999C-1651
3	62.4	4.1	1141	3	US-09-806-708B-22
4	59.8	3.9	1141	3	US-09-806-708B-22
5	59.2	3.9	7218	2	US-08-232-463-14
6	57.8	3.8	3057	3	US-09-601-198-55
7	56.6	3.7	50000	3	US-09-662-254B-25
8	56.2	3.7	396	3	US-09-640-173-53
9	56.2	3.7	396	3	US-09-713-550-53
10	56.2	3.7	396	3	US-09-825-294-53
11	56.2	3.7	396	3	US-09-970-966-53
12	54.2	3.5	14066	3	US-09-601-198-56
13	53.4	3.5	612	3	US-09-902-540-1357
14	53.2	3.5	19124	2	US-08-487-826B-13
15	51.6	3.4	1039	3	US-09-902-540-1280
16	51.2	3.3	731	2	US-08-451-405A-2
17	51.2	3.3	832	3	US-09-621-976-2813
18	51	3.3	1413	3	US-09-601-198-116
19	50	3.2	11091	3	US-09-134-001C-2243
20	49.4	3.2	1560	3	US-09-134-000C-1158
21	48.8	3.2	32392	3	US-09-662-254B-27
22	48.4	3.2	1055	3	US-09-806-708B-23
23	48.4	3.2	4673	2	US-07-638-431-1
24	48.4	3.2	4673	6	PCT-US92-00018-1
					Sequence 5, Appli
					Sequence 1651, Ap
					Sequence 22, Appl
					Sequence 14, Appl
					Sequence 55, Appl
					Sequence 25, Appl
					Sequence 53, Appl
					Sequence 53, Appl
					Sequence 53, Appl
					Sequence 56, Appl
					Sequence 1357, Ap
					Sequence 13, Appl
					Sequence 1280, Ap
					Sequence 2, Appli
					Sequence 2813, Ap
					Sequence 1163, Ap
					Sequence 2243, Ap
					Sequence 1158, Ap
					Sequence 27, Appl
					Sequence 23, Appl
					Sequence 1, Appli
					Sequence 1, Appli

Sequence 288, App
Sequence 2057, Ap
Sequence 2131, Ap
Sequence 362, Ap
Sequence 23, Appl
Sequence 186, Appl
Sequence 25, Appl
Sequence 15, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1543, A
Sequence 15349, A
Sequence 15350, A
Sequence 15350, A
Sequence 15507, A
Sequence 15508, A
Sequence 15509, A
Sequence 548, App
Sequence 547, App
Sequence 23, Appl
Sequence 9489, Ap
Sequence 33, Appl
Sequence 33, Appl
Sequence 23, Appl
Sequence 79, Appl
Sequence 79, Appl
Sequence 3, Appli
Sequence 16536, A
Sequence 29, Appl
Sequence 35, Appl
Sequence 12776, A
Sequence 15940, A
Sequence 9722, Ap
Sequence 1669, Ap
Sequence 5, Appli
Sequence 26, Appl
Sequence 1933, Ap
Sequence 165, App
Sequence 15845, A
Sequence 6, Appli
Sequence 15, Appl
Sequence 12901, A
Sequence 7789, Ap

98	42	2.7	601	3	US-09-949-016-145318	Sequence 145318,	171	41.2	2.7	2038	2	US-08-181-271A-1	Sequence 1, Appli
99	42	2.7	601	3	US-09-949-016-145319	Sequence 145319,	172	41.2	2.7	2038	2	US-08-449-315-1	Sequence 1, Appli
100	42	2.7	601	3	US-09-949-016-145320	Sequence 145320,	173	41.2	2.7	2038	2	US-08-444-803-1	Sequence 1, Appli
101	42	2.7	601	3	US-09-949-016-196337	Sequence 196337,	174	41.2	2.7	2038	2	US-08-449-043-1	Sequence 1, Appli
102	42	2.7	601	3	US-09-949-016-196338	Sequence 196338,	175	41.2	2.7	2038	2	US-08-456-265A-1	Sequence 1, Appli
103	42	2.7	601	3	US-09-949-016-196339	Sequence 196339,	176	41.2	2.7	2038	2	US-08-455-416-1	Sequence 1, Appli
104	42	2.7	601	3	US-09-949-016-196340	Sequence 196340,	177	41.2	2.7	2038	2	US-08-455-244-1	Sequence 1, Appli
105	42	2.7	601	3	US-09-949-016-196365	Sequence 196365,	178	41.2	2.7	2038	2	US-08-454-876-1	Sequence 1, Appli
106	42	2.7	601	3	US-09-949-016-196366	Sequence 196366,	179	41.2	2.7	2038	2	US-08-457-364-1	Sequence 1, Appli
107	42	2.7	1485	3	US-09-543-681A-601	Sequence 601, App	180	41.2	2.7	2038	2	US-08-456-262-1	Sequence 1, Appli
108	42	2.7	451924	3	US-09-949-016-12896	Sequence 12896, A	181	41.2	2.7	2038	2	US-08-456-240-1	Sequence 1, Appli
109	42	2.7	451925	3	US-09-949-016-17305	Sequence 17305, A	182	41.2	2.7	2038	2	US-08-455-736-1	Sequence 1, Appli
110	41.8	2.7	660	2	US-07-991-867B-32	Sequence 32, Appl	183	41.2	2.7	2038	2	US-08-971-217-1	Sequence 1, Appli
111	41.8	2.7	660	2	US-08-107-755A-32	Sequence 32, Appl	184	41.2	2.7	2038	3	US-09-350-600-1	Sequence 1, Appli
112	41.8	2.7	660	2	US-08-544-332-32	Sequence 32, Appl	185	41.2	2.7	2038	3	US-09-906-234-1	Sequence 1, Appli
113	41.8	2.7	660	3	US-09-370-861A-32	Sequence 32, Appl	186	41.2	2.7	2100	3	US-09-134-001C-1217	Sequence 1217, Ap
114	41.8	2.7	1511	2	US-07-991-867B-8	Sequence 8, Appli	187	41.2	2.7	2163	3	US-09-662-254B-38	Sequence 38, Appl
115	41.8	2.7	1511	2	US-08-107-755A-8	Sequence 8, Appli	188	41.2	2.7	2358	3	US-09-248-796A-6328	Sequence 6328, Ap
116	41.8	2.7	1511	2	US-08-544-332-8	Sequence 8, Appli	189	41.2	2.7	50000	3	US-09-662-254B-24	Sequence 24, Appl
117	41.8	2.7	1511	3	US-09-370-861A-8	Sequence 8, Appli	190	41	2.7	700	3	US-09-735-271-1038	Sequence 1038, Ap
118	41.8	2.7	1511	3	US-09-248-796A-8910	Sequence 8910, Ap	191	41	2.7	1194	3	US-09-601-198-77	Sequence 77, Appl
119	41.8	2.7	4810	3	US-08-852-629-11	Sequence 11, Appl	192	41	2.7	1916	3	US-09-508-824-16	Sequence 16, Appl
120	41.8	2.7	4838	3	US-08-852-629-15	Sequence 15, Appl	193	41	2.7	1916	3	US-09-508-824-22	Sequence 22, Appl
121	41.8	2.7	8920	2	US-08-446-855A-1	Sequence 1, Appli	194	41	2.7	2332	3	US-09-508-824-2	Sequence 2, Appli
122	41.8	2.7	8920	3	US-09-150-741-1	Sequence 1, Appli	195	41	2.7	147382	3	US-09-949-016-14624	Sequence 14624, A
123	41.8	2.7	15346	3	US-09-949-016-15309	Sequence 15309, A	196	40.8	2.7	1074	3	US-09-861-451A-49	Sequence 49, Appl
124	41.8	2.7	1664976	3	US-08-916-421B-1	Sequence 1, Appli	197	40.8	2.7	3561	3	US-09-248-796A-2080	Sequence 2080, Ap
125	41.8	2.7	1664976	3	US-09-692-570-1	Sequence 1, Appli	198	40.8	2.7	18492	3	US-09-949-016-17450	Sequence 17450, A
126	41.6	2.7	601	3	US-09-949-016-30532	Sequence 30532, A	199	40.8	2.7	18494	3	US-09-949-016-12863	Sequence 12863, A
127	41.6	2.7	601	3	US-09-949-016-37151	Sequence 37151, A	200	40.8	2.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
128	41.6	2.7	601	3	US-09-949-016-37165	Sequence 37165, A	201	40.8	2.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
129	41.6	2.7	601	3	US-09-949-016-145869	Sequence 145869,	202	40.6	2.6	2826	3	US-09-390-134B-30	Sequence 30, Appl
130	41.6	2.7	601	3	US-09-949-016-146137	Sequence 146137,	203	40.6	2.6	3256	3	US-09-719-085A-3	Sequence 3, Appli
131	41.6	2.7	601	3	US-09-949-016-146405	Sequence 146405,	204	40.6	2.6	62908	3	US-09-949-016-17554	Sequence 17554, A
132	41.6	2.7	601	3	US-09-949-016-196367	Sequence 196367,	205	40.6	2.6	136254	3	US-09-949-016-15341	Sequence 15341, A
133	41.6	2.7	1605	3	US-03-248-796A-4757	Sequence 4757, Ap	206	40.6	2.6	153866	3	US-09-949-016-16919	Sequence 16919, A
134	41.6	2.7	1648	3	US-08-799-451-667	Sequence 667, App	207	40.6	2.6	212139	3	US-09-949-016-16065	Sequence 16065, A
135	41.6	2.7	2132	3	US-08-844-188-39	Sequence 39, Appl	208	40.6	2.6	451924	3	US-09-949-016-12896	Sequence 12896, A
136	41.6	2.7	2132	3	US-09-378-088A-39	Sequence 39, Appl	209	40.6	2.6	451925	3	US-09-949-016-17305	Sequence 17305, A
137	41.6	2.7	2132	3	US-09-548-334A-39	Sequence 39, Appl	210	40.4	2.6	2142	3	US-09-107-532A-905	Sequence 905, App
138	41.6	2.7	2132	3	US-09-547-621-39	Sequence 39, Appl	211	40.2	2.6	339	3	US-09-543-681A-655	Sequence 655, App
139	41.6	2.7	2132	3	US-09-643-596B-39	Sequence 39, Appl	212	40.2	2.6	601	3	US-09-949-016-196418	Sequence 196418,
140	41.6	2.7	2132	3	US-10-412-200B-39	Sequence 39, Appl	213	40.2	2.6	658	3	US-08-998-416-595	Sequence 595, App
141	41.6	2.7	2132	3	US-10-099-278-39	Sequence 39, Appl	214	40.2	2.6	1296	3	US-09-107-532A-3402	Sequence 3402, Ap
142	41.6	2.7	107085	3	US-09-949-016-13157	Sequence 13157, A	215	40.2	2.6	1296	3	US-09-134-000C-3111	Sequence 3111, Ap
143	41.6	2.7	152393	3	US-09-949-016-14514	Sequence 14514, A	216	40.2	2.6	1956	3	US-08-559-896B-1	Sequence 1, Appli
144	41.6	2.7	152393	3	US-09-949-016-14515	Sequence 14515, A	217	40.2	2.6	1956	3	US-09-351-794A-1	Sequence 1, Appli
145	41.6	2.7	156894	3	US-09-949-016-12765	Sequence 12765, A	218	40.2	2.6	4285	3	US-09-410-464-1	Sequence 1, Appli
146	41.6	2.7	156894	3	US-09-949-016-12766	Sequence 12766, A	219	40.2	2.6	9369	3	US-10-237-551-190	Sequence 190, App
147	41.6	2.7	156895	3	US-09-949-016-16957	Sequence 16957, A	220	40.2	2.6	9369	3	US-10-237-551-247	Sequence 247, App
148	41.6	2.7	156895	3	US-09-949-016-16958	Sequence 16958, A	221	40.2	2.6	88245	3	US-09-949-016-13835	Sequence 13835, A
149	41.6	2.7	156895	3	US-09-949-016-16959	Sequence 16959, A	222	40.2	2.6	89892	3	US-09-949-016-13667	Sequence 13667, A
150	41.6	2.7	205044	3	US-09-949-016-15851	Sequence 15851, A	223	40.2	2.6	154746	3	US-09-827-688-8	Sequence 8, Appli
151	41.6	2.7	205044	3	US-09-949-016-15852	Sequence 15852, A	224	40.2	2.6	236341	3	US-09-949-016-13978	Sequence 13978, A
152	41.6	2.7	205044	3	US-09-949-016-15853	Sequence 15853, A	225	40.2	2.6	246230	3	US-09-949-016-17019	Sequence 17019, A
153	41.6	2.7	223471	3	US-09-949-016-12387	Sequence 12387, A	226	40.2	2.6	246230	3	US-09-949-016-17020	Sequence 17020, A
154	41.6	2.7	223471	3	US-09-949-016-12724	Sequence 12724, A	227	40.2	2.6	246230	3	US-09-949-016-17021	Sequence 17021, A
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156	41.4	2.7	27752	3	US-09-949-016-16444	Sequence 16444, A	229	40.2	2.6	278866	3	US-09-949-016-13923	Sequence 13923, A
157	41.2	2.7	519	3	US-09-248-796A-7830	Sequence 7830, Ap	230	40.2	2.6	278866	3	US-09-949-016-13924	Sequence 13924, A
158	41.2	2.7	601	3	US-09-949-016-30533	Sequence 30533, A	231	40.2	2.6	278866	3	US-09-949-016-13925	Sequence 13925, A
159	41.2	2.7	601	3	US-09-949-016-30534	Sequence 30534, A	232	40.2	2.6	278866	3	US-09-949-016-13926	Sequence 13926, A
160	41.2	2.7	601	3	US-09-949-016-37152	Sequence 37152, A	233	40.2	2.6	278866	3	US-09-949-016-14699	Sequence 14699, A
161	41.2	2.7	601	3	US-09-949-016-37153	Sequence 37153, A	234	40.2	2.6	278866	3	US-09-949-016-14700	Sequence 14700, A
162	41.2	2.7	601	3	US-09-949-016-37166	Sequence 37166, A	235	40.2	2.6	278866	3	US-09-949-016-14701	Sequence 14701, A
163	41.2	2.7	601	3	US-09-949-016-37167	Sequence 37167, A	236	40.2	2.6	278866	3	US-09-949-016-14702	Sequence 14702, A
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166	41.2	2.7	601	3	US-09-949-016-146138	Sequence 146138,	239	40	2.6	614	3	US-09-902-540-1318	Sequence 1318, Ap
167	41.2	2.7	601	3	US-09-949-016-146139	Sequence 146139,	240	40	2.6	672	3	US-09-830-230A-276	Sequence 276, App
168	41.2	2.7	601	3	US-09-949-016-146406	Sequence 146406,	241	40	2.6	724	3	US-08-998-416-683	Sequence 683, App
169	41.2	2.7	601	3	US-09-949-016-146407	Sequence 146407,	242	40	2.6	726	3	US-09-830-230A-275	Sequence 275, App
170	41.2	2.7	1498	3	US-03-807-258-17	Sequence 17, Appl	243	40	2.6				

c 244	40	2.6	732	3	US-08-998-416-1036	Sequence 1036, Ap	317	39	2.5	171700	3	US-09-949-016-12276	Sequence 12276, A
245	40	2.6	854	3	US-08-998-416-534	Sequence 534, App	318	39	2.5	171701	3	US-09-949-016-15835	Sequence 15835, A
246	40	2.6	860	3	US-08-998-416-287	Sequence 287, App	c 319	39	2.5	340380	3	US-09-949-016-14179	Sequence 14179, A
c 247	40	2.6	53332	3	US-08-801-861-3	Sequence 3, Appl	320	38.8	2.5	453	3	US-09-134-001C-2262	Sequence 2262, Ap
c 248	40	2.6	53332	3	US-10-786-065-3	Sequence 3, Appl	c 321	38.8	2.5	486	3	US-09-248-796A-13914	Sequence 13914, A
c 249	40	2.6	53332	3	US-10-786-065-3	Sequence 3, Appl	c 322	38.8	2.5	601	3	US-09-949-016-156603	Sequence 156603, A
250	40	2.6	126176	3	US-09-949-016-16137	Sequence 16137, A	323	38.8	2.5	906	3	US-09-495-406-14	Sequence 14, Appl
251	40	2.6	126176	3	US-09-949-016-16138	Sequence 16138, A	324	38.8	2.5	906	3	US-09-816-028A-26	Sequence 26, Appl
c 252	40	2.6	162841	3	US-09-949-016-13733	Sequence 13733, A	325	38.8	2.5	906	3	US-10-303-132-26	Sequence 26, Appl
c 253	39.8	2.6	601	3	US-09-949-016-93802	Sequence 93802, A	326	38.8	2.5	906	3	US-10-303-134-26	Sequence 26, Appl
c 254	39.8	2.6	601	3	US-09-949-016-93803	Sequence 93803, A	327	38.8	2.5	906	3	US-10-303-118-26	Sequence 26, Appl
c 255	39.8	2.6	1707	3	US-09-543-681A-2794	Sequence 2794, Ap	328	38.8	2.5	906	3	US-10-303-128-26	Sequence 26, Appl
c 256	39.8	2.6	1785	3	US-09-601-198-156	Sequence 156, App	329	38.8	2.5	1270	3	US-09-270-767-2929	Sequence 2929, Ap
c 257	39.8	2.6	1850	3	US-08-617-860B-32	Sequence 32, Appl	330	38.8	2.5	1270	3	US-09-270-767-18211	Sequence 18211, A
c 258	39.8	2.6	3357	3	US-09-976-594-1005	Sequence 1005, Ap	331	38.8	2.5	2264	3	US-08-262-220-5	Sequence 5, Appl
c 259	39.8	2.6	4098	2	US-08-605-106-4	Sequence 4, Appl	332	38.8	2.5	2264	3	US-08-471-733-5	Sequence 5, Appl
c 260	39.8	2.6	137394	3	US-09-949-016-13872	Sequence 13872, A	333	38.8	2.5	2264	3	US-08-468-878-5	Sequence 5, Appl
c 261	39.8	2.6	137743	3	US-09-949-016-12178	Sequence 12178, A	334	38.8	2.5	2264	3	US-08-750-494-5	Sequence 5, Appl
c 262	39.8	2.6	203093	3	US-09-949-016-14445	Sequence 14445, A	335	38.8	2.5	2264	3	US-08-470-638-5	Sequence 5, Appl
c 263	39.6	2.6	289	3	US-09-007-005-17	Sequence 17, Appl	336	38.8	2.5	5852	2	US-07-867-103-2	Sequence 2, Appl
c 264	39.6	2.6	289	3	US-09-244-796-17	Sequence 17, Appl	c 337	38.8	2.5	6243	2	US-09-056-075-1	Sequence 1, Appl
c 265	39.6	2.6	378	3	US-09-248-796A-11672	Sequence 11672, A	c 338	38.8	2.5	11474	3	US-09-495-406-1	Sequence 1, Appl
c 266	39.6	2.6	705	3	US-09-248-796A-9940	Sequence 9940, Ap	c 339	38.8	2.5	11474	3	US-09-816-028A-1	Sequence 1, Appl
c 267	39.6	2.6	1107	3	US-09-248-796A-11324	Sequence 11324, A	c 340	38.8	2.5	11474	3	US-10-303-162-1	Sequence 1, Appl
c 268	39.6	2.6	2118	3	US-09-601-198-59	Sequence 59, Appl	c 341	38.8	2.5	11474	3	US-10-303-134-1	Sequence 1, Appl
c 269	39.6	2.6	6152	3	US-08-973-462-1	Sequence 1, Appl	c 342	38.8	2.5	11474	3	US-10-303-118-1	Sequence 1, Appl
c 270	39.6	2.6	8868	3	US-08-815-803-7	Sequence 7, Appl	c 343	38.8	2.5	11474	3	US-10-303-128-1	Sequence 1, Appl
c 271	39.6	2.6	18651	3	US-09-949-002-592	Sequence 592, App	c 344	38.8	2.5	113382	3	US-09-949-016-15996	Sequence 15996, A
c 272	39.6	2.6	18682	3	US-09-949-002-786	Sequence 786, App	c 345	38.8	2.5	113382	3	US-09-949-016-15997	Sequence 15997, A
c 273	39.6	2.6	19877	2	US-08-816-155B-8	Sequence 8, Appl	c 346	38.8	2.5	231129	3	US-09-949-016-16110	Sequence 16110, A
c 274	39.6	2.6	19877	2	US-09-079-587-8	Sequence 8, Appl	c 347	38.8	2.5	266293	3	US-09-949-016-11934	Sequence 11934, A
c 275	39.6	2.6	343552	3	US-09-949-016-13498	Sequence 13498, A	c 348	38.6	2.5	564	3	US-09-248-796A-2884	Sequence 2884, Ap
c 276	39.4	2.6	601	3	US-09-949-016-93804	Sequence 93804, A	c 349	38.6	2.5	601	3	US-09-949-016-28913	Sequence 28913, A
c 277	39.4	2.6	601	3	US-09-949-016-176727	Sequence 176727, A	c 350	38.6	2.5	601	3	US-09-949-016-14624	Sequence 14624, A
c 278	39.4	2.6	765	3	US-09-134-000C-3120	Sequence 3120, Ap	c 351	38.6	2.5	601	3	US-09-949-016-125860	Sequence 125860, A
c 279	39.4	2.6	777	3	US-09-107-532A-835	Sequence 835, App	c 352	38.6	2.5	601	3	US-09-949-016-174936	Sequence 174936, A
c 280	39.4	2.6	1028	3	US-08-118-200-1	Sequence 1, Appl	c 353	38.6	2.5	601	3	US-09-949-016-174937	Sequence 174937, A
c 281	39.4	2.6	1028	3	US-08-458-745-1	Sequence 1, Appl	c 354	38.6	2.5	1059	3	US-09-543-681A-2446	Sequence 2446, Ap
c 282	39.4	2.6	3817	3	US-09-270-767-14234	Sequence 14234, A	c 355	38.6	2.5	1536	3	US-09-248-796A-4586	Sequence 4586, Ap
c 283	39.4	2.6	148609	3	US-09-949-016-12860	Sequence 12860, A	c 356	38.6	2.5	1774	3	US-09-149-476-94	Sequence 94, Appl
c 284	39.4	2.6	148609	3	US-09-949-016-16787	Sequence 16787, A	c 357	38.6	2.5	1866	3	US-09-673-395A-24	Sequence 24, Appl
c 285	39.4	2.6	193169	3	US-09-949-016-15091	Sequence 15091, A	c 358	38.6	2.5	6609	3	US-10-172-502-1	Sequence 1, Appl
c 286	39.4	2.6	317366	3	US-09-949-016-16001	Sequence 16001, A	c 359	38.6	2.5	15037	3	US-09-949-016-16692	Sequence 16692, A
c 287	39.4	2.6	390920	3	US-09-949-016-14720	Sequence 14720, A	c 360	38.6	2.5	18773	3	US-09-949-016-14164	Sequence 14164, A
c 288	39.2	2.6	663	3	US-08-998-416-191	Sequence 191, App	c 361	38.6	2.5	36643	3	US-09-949-016-11860	Sequence 11860, A
c 289	39.2	2.6	1230	4	US-09-747-385-5	Sequence 5, Appl	c 362	38.6	2.5	36821	3	US-09-949-016-16403	Sequence 16403, A
c 290	39.2	2.6	3450	3	US-09-662-254B-47	Sequence 47, Appl	c 363	38.6	2.5	45197	3	US-09-949-016-16404	Sequence 16404, A
c 291	39.2	2.6	92681	3	US-09-949-016-14772	Sequence 14772, A	c 364	38.6	2.5	113379	3	US-09-949-016-17561	Sequence 17561, A
c 292	39.2	2.6	94142	3	US-09-949-016-16553	Sequence 16553, A	c 365	38.6	2.5	113379	3	US-09-949-016-17562	Sequence 17562, A
c 293	39.2	2.6	134987	3	US-09-949-016-15348	Sequence 15348, A	c 366	38.6	2.5	113153	3	US-09-949-016-12378	Sequence 12378, A
c 294	39.2	2.6	134987	3	US-09-949-016-15349	Sequence 15349, A	c 367	38.6	2.5	133719	3	US-09-949-016-15092	Sequence 15092, A
c 295	39.2	2.6	134987	3	US-09-949-016-15350	Sequence 15350, A	c 368	38.6	2.5	580073	3	US-08-545-528D-1	Sequence 1, Appl
c 296	39.2	2.6	134987	3	US-09-949-016-15507	Sequence 15507, A	c 369	38.6	2.5	640681	3	US-09-790-988-1	Sequence 1, Appl
c 297	39.2	2.6	134987	3	US-09-949-016-15508	Sequence 15508, A	c 370	38.6	2.5	601	3	US-09-949-016-141806	Sequence 141806, A
c 298	39.2	2.6	134987	3	US-09-949-016-15509	Sequence 15509, A	c 371	38.4	2.5	723	3	US-09-248-796A-6004	Sequence 6004, Ap
c 299	39.2	2.6	141248	3	US-09-949-016-12241	Sequence 12241, A	c 372	38.4	2.5	825	3	US-09-252-931A-11824	Sequence 11824, A
c 300	39	2.5	504	3	US-09-248-796A-1506	Sequence 1506, Ap	c 373	38.4	2.5	1557	3	US-09-830-230A-108	Sequence 108, App
c 301	39	2.5	601	3	US-09-949-016-28914	Sequence 28914, A	c 374	38.4	2.5	1617	3	US-09-830-230A-107	Sequence 107, App
c 302	39	2.5	601	3	US-09-949-016-107700	Sequence 107700, A	c 375	38.4	2.5	1692	3	US-09-134-001C-79	Sequence 79, Appl
c 303	39	2.5	601	3	US-09-949-016-125861	Sequence 125861, A	c 376	38.4	2.5	1842	3	US-09-328-352-3065	Sequence 3065, Ap
c 304	39	2.5	773	3	US-08-998-416-385	Sequence 385, App	c 377	38.4	2.5	2187	3	US-09-252-931A-11888	Sequence 11888, A
c 305	39	2.5	831	3	US-09-662-254B-69	Sequence 69, Appl	c 378	38.4	2.5	2796	3	US-09-710-279-4335	Sequence 4335, Ap
c 306	39	2.5	1050	3	US-09-662-254B-31	Sequence 31, Appl	c 379	38.4	2.5	2906	3	US-09-662-254B-60	Sequence 60, Appl
c 307	39	2.5	1262	3	US-09-949-016-3641	Sequence 3641, Ap	c 380	38.4	2.5	29717	3	US-09-949-016-16284	Sequence 16284, A
c 308	39	2.5	4114	3	US-09-710-279-3572	Sequence 3572, Ap	c 381	38.4	2.5	45249	3	US-09-949-016-16288	Sequence 16288, A
c 309	39	2.5	6243	2	US-09-056-075-1	Sequence 1, Appl	c 382	38.4	2.5	58407	3	US-08-916-431B-2	Sequence 2, Appl
c 310	39	2.5	15019	3	US-09-949-016-13571	Sequence 13571, A	c 383	38.4	2.5	58407	3	US-09-692-570-2	Sequence 2, Appl
c 311	39	2.5	20935	3	US-09-949-016-13583	Sequence 13583, A	c 384	38.4	2.5	60376	3	US-09-949-016-12423	Sequence 12423, A
c 312	39	2.5	77388	3	US-09-949-016-13496	Sequence 13496, A	c 385	38.4	2.5	363032	3	US-09-949-016-12415	Sequence 12415, A
c 313	39	2.5	115388	3	US-09-949-016-14981	Sequence 14981, A	c 386	38.4	2.5	363032	3	US-09-949-016-15754	Sequence 15754, A
c 314	39	2.5	127771	3	US-09-949-016-14982	Sequence 14982, A	c 387	38.4	2.5	444	3	US-09-601-198-141	Sequence 141, App
c 315	39	2.5	144322	3	US-09-949-016-15316	Sequence 15316, A	c 388	38.2	2.5	601	3	US-09-949-016-69236	Sequence 69236, A
c 316	39	2.5	168575	3	US-09-426-290-1	Sequence 1, Appl	c 389	38.2	2.5	601	3		

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c 432 37.8 2.5 2166 3 US-09-601-198-95
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c 434 37.8 2.5 2994 2 US-08-548-159-4
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c 462 37.6 2.4 601 3 US-09-949-016-144644

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Sequence 12838, A Sequence 12838, A Sequence 12838, A
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Sequence 84623, A Sequence 84623, A Sequence 84623, A
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Sequence 9100, App Sequence 9100, App Sequence 9100, App
Sequence 126, App Sequence 126, App Sequence 126, App
Sequence 1688, App Sequence 1688, App Sequence 1688, App
Sequence 153, App Sequence 153, App Sequence 153, App
Sequence 598, App Sequence 598, App Sequence 598, App
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ALIGNMENTS

RESULT 1
US-09-697-863A-5
; Sequence 5, Application US/09697863A
; Patent No. 6812203
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut Voor Biotechnologie VZW
; TITLE OF INVENTION: CD-40 INTERACTING AND TRAF-INTERACTING PROTEINS
; FILE REFERENCE: 2676-4555US
; CURRENT APPLICATION NUMBER: US/09/697,863A
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: PCT/EP99/03025
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EPO 98201392.2
; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1530)..(1531)
; OTHER INFORMATION: N stands for any nucleotide.
; NAME/KEY: CDS
; LOCATION: (209)..(1534)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc_feature

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; LOCATION: (1392)..(1392)
; OTHER INFORMATION: N stands for any nucleotide.
US-09-697-863A-5

Query Match      99.8%; Score 1533; DB 3; Length 1536;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGAAAGGCTCCGGGAGATAGCGACAGTCAGGCGTCCCTCTTTTGAAGCGGT 60
DB 1 AGAGAAAGGCTCCGGGAGATAGCGACAGTCAGGCGTCCCTCTTTTGAAGCGGT 60

QY 61 TTTTCGTCTCTTTCCGCGAGTGGCTCCAGCTCAGCGAGGGGCGGTCCTCGGTAGCGGA 120
DB 61 TTTTCGTCTCTTTCCGCGAGTGGCTCCAGCTCAGCGAGGGGCGGTCCTCGGTAGCGGA 120

QY 121 GCGGTGTCAGGCGGGAAGGAGTGGTGGCGGTCGCGGATGAGGACAGCAGGAGCAG 180
DB 121 GCGGTGTCAGGCGGGAAGGAGTGGTGGCGGTCGCGGATGAGGACAGCAGGAGCAG 180

QY 181 TGGTGTCTGTCAGGCGGCGCTCGGAGACATGGGAGACCGGGGTCGGAATAATAGATC 240
DB 181 TGGTGTCTGTCAGGCGGCGCTCGGAGACATGGGAGACCGGGGTCGGAATAATAGATC 240

QY 241 TGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACACGATGAAATGAAGACGACAT 300
DB 241 TGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACACGATGAAATGAAGACGACAT 300

QY 301 TCAGTTTGTTCAGTGAAGGACCATCGAGACCTGTTCTTGAATACATCGATCTGGTGTGG 360
DB 301 TCAGTTTGTTCAGTGAAGGACCATCGAGACCTGTTCTTGAATACATCGATCTGGTGTGG 360

QY 361 TGATGATGAAAACCTTAGCGGCTATATAGTATATCTGTTTCTTAAATCCGAAACG 420
DB 361 TGATGATGAAAACCTTAGCGGCTATATAGTATATCTGTTTCTTAAATCCGAAACG 420

QY 421 ACAGGCTGATTTTTCATTTTAAATATGAAGAGGTGAAAACAGACACAGAAAATAA 480
DB 421 ACAGGCTGATTTTTCATTTTAAATATGAAGAGGTGAAAACAGACACAGAAAATAA 480

QY 481 TGAAGTGAGCAAAAATCACTCGAGATTGTCTAAGGCAAAAGAACCAATTCAGTATAT 540
DB 481 TGAAGTGAGCAAAAATCACTCGAGATTGTCTAAGGCAAAAGAACCAATTCAGTATAT 540

QY 541 AGAACCAACCAATCAITGAAGAAAAGCCATCTTTTCATCAAAAGAAATAGATAATCT 600
DB 541 AGAACCAACCAATCAITGAAGAAAAGCCATCTTTTCATCAAAAGAAATAGATAATCT 600

QY 601 TGTGCTTCAGATTGTTGGAATGAAAACAGCAATTTATGTTTACAGAACCAATACAAATG 660
DB 601 TGTGCTTCAGATTGTTGGAATGAAAACAGCAATTTATGTTTACAGAACCAATACAAATG 660

QY 661 GCTTGAATAAAGAAAGGTAAATTAGGATGTAAGGATTTGTTTCAGCAGTTTCGGCATTTGG 720
DB 661 GCTTGAATAAAGAAAGGTAAATTAGGATGTAAGGATTTGTTTCAGCAGTTTCGGCATTTGG 720

QY 721 ATCGAAAGCAGAAAAGCATGTCCATGTGTCAGGAATGGAATGCAATTTAGTACCC 780
DB 721 ATCGAAAGCAGAAAAGCATGTCCATGTGTCAGGAATGGAATGCAATTTAGTACCC 780

QY 781 TAAATGCGAGTAAATAAATCTAGGCAAGCTTCTACGAAAATAAATTAGGAAACATGA 840
DB 781 TAAATGCGAGTAAATAAATCTAGGCAAGCTTCTACGAAAATAAATTAGGAAACATGA 840

QY 841 TGTTCCTAAAGCCCATGTTAAATTCAGGATTTGTTTAAAGGAATCAACTAATGATTCAT 900
DB 841 TGTTCCTAAAGCCCATGTTAAATTCAGGATTTGTTTAAAGGAATCAACTAATGATTCAT 900

QY 901 TTGTAATTTAGTCATAAACAATAATTAATAATTTGATGCTACTGTAAGAGTTTCAA 960
DB 901 TTGTAATTTAGTCATAAACAATAATTAATAATTTGATGCTACTGTAAGAGTTTCAA 960

QY 961 TACTGTTTACAGTTTAAACATACAGACCTTTATCTGATATTTGAGGGGCGCAAGAGA 1020
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DB 961 TACTGTTTACAGTTTAAACATACAGACCTTTATCTGATATTTGAGGGGCGCAAGAGA 1020
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DB 1021 ATTACAGGAAAAAATGGAGAGGTAAATTTGTTTAAATACAGTTTACAGTGCACCAAGAAAT 1080
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QY 1141 TGCCAAATCTGTATCATATAATGATGAGGCACTCTACAGTTTCAAGAAAAACCAACCTTAGT 1200
DB 1141 TGCCAAATCTGTATCATATAATGATGAGGCACTCTACAGTTTCAAGAAAAACCAACCTTAGT 1200
QY 1201 GATTATCTCCAGTGCACAAATTCAGTCAGCTCCGACCTGTCATGTTATTTGTCGCTTT 1260
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QY 1381 TGCTAATAACANCCCTGGGAAGAAAGTCTGGAGTAGCTACAAATTTGTAGAAAATTTTCC 1440
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QY 1441 TGAATCATCATTTTGGAACTGTTTAAATCATCGATTACAAATTTGTCACCTTGATGATCTAT 1500
DB 1441 TGAATCATCATTTTGGAACTGTTTAAATCATCGATTACAAATTTGTCACCTTGATGATCTAT 1500
QY 1501 ATCCGAAATAAACAATAATTAATCATTTTAANNATATA 1536
DB 1501 ATCCGAAATAAACAATAATTAATCATTTTAANNATATA 1536

RESULT 2
US-09-513-999C-1651
; Sequence 1651, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 1651
; LENGTH: 274
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 108..272
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 43
; OTHER INFORMATION: k=g or t
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: 45
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 52
; OTHER INFORMATION: r=a or g
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: x=a or g
US-09-513-999C-1651

Query Match 17.6%; Score 270.8; DB 3; Length 274;
Best Local Similarity 97.1%; Pred. No. 2.6e-55;
Matches 266; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 102 GCGGTCCTCCGTACGCGAGCGGTGCGAGCGGGAAGGAGGTGGTGGCGGTGCGGCA 161
Db 1 GCGGTCCTCCGTACGCGAGCGGTGCGAGCGGGAAGGAGGTGGTGGCGGTGCGGCR 60

Qy 162 GTAGGACAGCAGGAGCAGTGTCTGTCTGTCAGCGCGCGCGTGGGAGACATCGGACCCGG 221
Db 61 GYAGGACAGCAGGAGCAGTGTCTGTCTGTCAGCGCGCGCGTGGGAGACATCGGACCCGG 120

Qy 222 GGTGCGAAATTAATAGATCTGCTCCCTCCAGCTGCGCCCTGAGGCATCTGAGTCAACACGG 281
Db 121 GGTGCGARATTAATAGATCTGCTCCCTCCAGCTGCGCCCTGAGGCATCTGAGTCAACACGG 180

Qy 282 ATGAATATGAAGACACATTCAGTTGTCAGTGAAGACCATCGAGACCTGTTCTTGAAT 341
Db 181 ATGAATATGAAGACACATTCAGTTGTCAGTGAAGACCATCGAGACCTGTTCTTGAAT 240

Qy 342 ACATCGATCTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 375
Db 241 ACATCGATCTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 274

RESULT 3
US-09-806-708B-22
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
US-09-806-708B-22
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Query Match 4.1%; Score 62.4; DB 3; Length 1141;
Best Local Similarity 12.1%; Pred. No. 4.7e-05;
Matches 124; Conservative 357; Mismatches 538; Indels 2; Gaps 2;

Qy 408 AAATGCAAAACGACAGGGTGATTTTTTGCATTTTTTAAATATGAAGAAGGTGAAACAG 467
Db 61 WARMYKYRRWYNNKSRWKGWYKKBBCANNYSBRYHARRWKDKMTAYBMTMTNKWGK 120

Qy 468 ACACAGAAATAATGAAGTGAGCAAAATACATGCGAGTTGTCTAAGGCAAGAACCCAC 527
Db 121 TGRHRYWRWMBDVTVDHVVYVAMNNAWTTMCMDKDDKRTWVKKNNAATGWDGDDTK 180

Qy 528 ATTTGAGATATAGAACAACCAATCATTTGAAGAAAAGCCATCATTTCATCAAGAAAG 587
Db 181 YHMNNNGCBVTVMVRYKTRDRWSBKRMNYGMBWKNWSYDVYTVVWDDCKRKVR 240

Qy 588 AAATAGATAATC-TTGTGCTTCCAGATTGTTGGAATGAAACAAAGCATTTATGTTTACA 646
Db 241 WVRTRGRMYVWABTAHRRYNNNGWTBAMAYRRWTMNNNNNNNAKAMCKEAKYWGWNRA 300

Qy 647 GAAACAATACAAATGGCTTGAATTAAGAGGTAAATTAGAGTGTAGGATTTGTTACGA 706
Db 301 BVNSTCTTWKSKTTKVRTSCWANNCRAGDANKDKWKSAAAGVYVNNNNNNNNWYTKA 360

Qy 707 GTTCGGCATTTGGGATCGAAGCAGAAAAGCATGTCCATGTGTCGAAGGATGGATTGCA 766
Db 361 RHBARDWVWHSAAWKHANAHAHYSRKKWTBYRKTVMVNNNNNGTWMKRWAWYWKMDMD 420

Qy 767 TATTAGTAACCCCTAATGGCAGTAATAAACTACTAGGCAAGCTTCTCTACGAAAAAAA 826
Db 421 WBGTYNNNNGRTYTGWTKKWYKWKANNCKWRADWHTCTHNNNTTWKMTYWN 480

Qy 827 ATTAGGAAACATGATTTTCTAAAGCCCATGGTAAATTCAGGATTTGTTAAAGGAATCA 886
Db 481 NCYKSMKNGKSHRBAAAVYTWVWRRYAHANNNNNDYWKACTWYKYBVCSKWNNTY 540

Qy 887 ACTAATGATTCATTTGTAATTTAGTCATAAACAATAATAAATAATATATGATGCTACT 946
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Qy 947 GTAAAAGTTTTCAATCTGTTTACAGTTTGTAGTAAACATACACAGACCTTTTATCGAT 1006
Db 500 WBHRAGAAYWMBMYBAKCHCKWYKAKKYAGAGSNNNNNNNNNNNNNNNNNNATCAR 659

Qy 1007 GAGGGGCAAGAGAAATTACAGGAAAAAATGAGAGAGTAAATTTGTTTAAATACACGTTAC 1066
Db 660 DDYAAASRWYAMANAkWYKYKBAANNAYYTHANNWGWGNNNAIDTRRTWKNNNNNNAGT 719

Qy 1067 AGTCAACAAGAAATAGCAGACATATTGCAAAAGAAATGAAGATGAAGATATTAAAGA 1126
Db 720 WKNNNNNNNAKNSAAKYYAAAANKHWRWANKWMRGWHADAAALBTDDKRNNGAYTK 779

Qy 1127 ATTATAGAAGAGATGCAAAATCTGTATCATATAATTGATGAGGCATCTACAGTTTCAA 1186
Db 780 YTTNNNTYRGVVTNTAARDGWANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 839

Qy 1187 AAAACACCTAGTGTATTATCTCCAGTGCAATTCAGTCAGCTCTCTGACCTGTTATG 1246
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Qy 1247 TTATTGTGCTTTTAAAGAAATTTGTCGTCACACTATAGCAGAGTGTATTGTTCAATTA 1306
Db 900 ATKNNNATYNRGTAWRTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 959

Qy 1307 TTGACTACTTTAAATGATGTTGTTTAAACAATGAATATTGAAAGCAAAATTTAAATGCA 1366
Db 960 TKGCMWNTTTCRKYKNCCTWYTWMTTTRITWYAAATWKTNNATGSTRCNATGKNNNY 1019

Qy 1367 TTTTGTCTGATGGTGCTAATACAANCCTGGGAAAGAAAGTCTGGAGTAGCTACAAAATTG 1426
Db 1020 WTGKTRWTAYRMATRWKAWKVMATGWSNTNSYARWAYKTRAYKGYWYNACAWRWRG 1079
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QY 1427 T 1427
Db 1080 K 1080

RESULT 4
US-09-806-708B-22/c
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)-(1141)
; OTHER INFORMATION: Consensus sequence of A.t., L.a., and B.n. FAE1 promoters
US-09-806-708B-22

Query Match 3.9%; Score 59.8; DB 3; Length 1141;
Best Local Similarity 12.5%; Pred. No. 0.0002;
Matches 127; Conservative 355; Mismatches 527; Indels 7; Gaps 3;

QY 506 TTGCTAAGCAAGAACACATTCGAGTATATAGAACACCAATCATTTGAGAAAG 565
Db 1123 YKCANNNNNNGMGKMDNRMDATKWSATGTAWTTHAKRGATMCWYWTGTGTRRWCNR 1064

QY 566 CATCATCTTCATCAAGAAAGAAATAGATAATCTTGTCTCCAGATTGTTGGATGAA 625
Db 1063 TYA--MRTYTRSNANWSKATBMMWTKMYATKYRTAYAMWCANNNNNMCAATNGYAK 1006

QY 626 AAACAGCATTTATGTTTACAGAACCAATCAATGCTTGAATAAAGAAAGTAAATTA 685
Db 1005 SCATNNAMYATRWAAAYAAKWARWAGNNMYGAAAGNKGWCMALMATGCBWADTAG 946

QY 686 GGATGTAAGGATTTGTCAGAGTTCGGCATTTGGGATCGAAAGCAGAAAGCATGTCAT 745
Db 945 KMCNNNNNNWTTDVRMMAMKAKNNNNNNAYWTACYNRAATNNKMAATHMMKWTGHAHSKER 886

QY 746 GTGTCCAAGGATGGATTGCATATTTAGTAAACCCCTAATGCGCAGTAATAAACTACTAGG 805
Db 885 TRHHTTCRRTKYNNNNNNNARTVYVYHHAARRMMNAWTRTNNNNNNNNNACRTRTW 826

QY 806 CAACTCTCTACGAAAAAAATTAGGAAACATGATGTTCTTAAAGCCCATGTGTAATAAT 865
Db 825 ABKHSKCNNNNNNNNNNNNTWCHYTTANABBCYRANNNDAAAPMARTCNMYHAATV 766

QY 866 CAGGATTTGTTAAGGAATCAATATGATTCATTTGTTGATTTAGTGCATATAACAAAT 925
Db 765 TTHDWCYKTMNTWYMDMTTMBTTTTRNTTSTNNNNNNNNNNNNNNNNNNNNNNNNW 706

QY 926 AATAAAAAATTCATCTACTGTAAGATTTTCAATCTGTTTACATGTTTAGTAAACAT 985
Db 705 YAHATNNWGCWNNTDARETNTTVMRRMMNTKTRWYSTTTRRHRYTGATNNNNNNNN 646

QY 986 AACAGACCTTTATCTCATATTGAGGGGCAAGAGAATTACAGAAAAAAATGAGAGGTA 1045
Db 645 NNNNNNSCCTCTRMNTMRTWTKGDGNTVKVKYKRDCTTCTYVDVWADSW--VWYANWM 588

QY 1046 AATTTGTTTAAATACGTTTACAGTGCACAGAAATAGCAGAAATATTCGAAAGAAATG 1105
Db 587 RCRDVTYTRNTYCKSYAHSYMYWNSNNAMWYRRYSARNWSSMARMTTRNNNNWMSGBVRM 528

RESULT 5
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single


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; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
; US-08-232-463-14

Query Match          3.9%; Score 59.2; DB 2; Length 7218;
Best Local Similarity 12.9%; Pred. No. 0.00062;
Matches 63; Conservative 219; Mismatches 202; Indels 4; Gaps 1;

Qy 357 GTGTGATGATGAAACCCCTAGCCCTATTATAG- ---TGATAFTCTGTTTCCTAAATG 412
Db 1559 GTGTGATGTGACTAGCTAGCATCGCTCTAGACGCACTATTTCAGTTTCAAATAACG 1500
Qy 413 CCAAAACGACGGGTGATTTTTCATTTTAAATATGAAGAAGGTGAAACAGACACA 472
Db 1499 GCATGTAGGCATCACTGTAATTACCTATCTATGCAAGTAGTTAAAGAGATAGAAGATTT 1440
Qy 473 GAAATAATGAAGTGAGCAAAATCACTGCAGATTGCTAAGGCAAAAGGAACACATTC 532
Db 1439 GGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1380
Qy 533 GAGTATATAGAACCAACCAATCATTTGAAAGAAAGCCATCACTTTCATCAAGAAAGAAATA 592
Db 1379 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1320
Qy 593 GATAATCTTGCTTCAGATGTTGGAATGAAACCAAGCAATTTATGTTTACAGAACAA 652
Db 1319 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1260
Qy 653 TACAAATGGCTTGAAATAAAGAGGTAAATAGAGTGAAGGATGTCAGCAGTTCGG 712
Db 1259 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1200
Qy 713 CATTTGGATGCAAGCAGCAAGCATGCTCATGTGTCCAAGGAATGCAATTTA 772
Db 1199 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1140
Qy 773 GTAACCCCTAATGGCAGTAATAAACTACTAGGCAAGCTTCTCAGCAAAATAATAGG 832
Db 1139 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1080
Qy 833 GAACATGA 840
Db 1079 RRRRRRR 1072

RESULT 6
US-09-601-198-55/c
; Sequence 55, Application US/09601198
; Patent No. 6531583
; GENERAL INFORMATION:
; APPLICANT: Cassell, Gail H.
; APPLICANT: Chen, Eliseon Y.
; APPLICANT: Glass, Jennifer S.
; APPLICANT: Glass, John I.
; APPLICANT: Heiner, Cheryl R.
; APPLICANT: Lefkowitz, Elliot
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
; FILE REFERENCE: UAB-13452/22
; CURRENT APPLICATION NUMBER: US/09/601,198
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/073,189
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 3057
; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
US-09-601-198-55

Query Match          3.8%; Score 57.8; DB 3; Length 3057;
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Best Local Similarity 43.9%; Pred. No. 0.00092;
Matches 294; Conservative 0; Mismatches 372; Indels 3; Gaps 1;

Qy 668 ATAAAGAGAGGTAAATATTAGATGTAAGGATTTGTTACGAGTTCGGCATTTGGGATCGAAA 727
Db 1317 ATACAAACAATTAATTTAGTAAGAAAGATAATAAATGGATTCTTGAAGGAGAAATATCT 1258
Qy 728 GCAGAAAGCATGTCCATGTGTCCAAGGAATGGATTGCATATTTAGTAACCCCTAATGGC 787
Db 1257 AATTTAGAGCCAAATACAGAATACATTTTATCTCAATAAAATATTCAGACCACACAGGC 1198
Qy 788 AGTAATAAAACTACTAGGCAAGCTTCTCTACGAAAAAAATTTAGGGAACATGATGTTCT 847
Db 1197 AATGATCTATTTCATACAGAAATTAACACACAAACATTAACATTATTGAACAAAAATCAAAT 1138
Qy 848 AAGCCCATGGTAAAAATTCAGGATTTGTTTAAAGGAATCACTAATGATCAATTTGTAAT 907
Db 1137 AAAATTTTAAAGTATTGATCCATATATCGAATCAATTTACTTTATGAAAAAATCAAT 1078
Qy 908 TTAGTGCATAAACCAAAATATAAAATNTTGATGCTACTGTAAAAAGTTTTCAATCTACTGTT 967
Db 1077 GATTTAAGAGAAGAATTATTAAATTAAGGATATAAAGATTAACAATGATGGT 1018
Qy 968 TACAGTTTGTAAAAACATAACAGA- --CCTTTATCTGATATTGAGGGGGCAAGAGAATTA 1024
Db 1017 GATAGATTAGTATTAGGTATAGATACAATAATCAACTTCTAAAAAAGAAAGTAAAGCTTA 958
Qy 1025 CAGGAAAAAATGGAGAGGTAATTTGTTTAAATACACGTTACAGTTCGCAACAGAAATAGCA 1084
Db 957 ACTTTAAATAAAAAATCAAGAAGATTATAGCGTTTAATATTGAAAAATTTAACTTAATCGT 898
Qy 1085 GAACATATTCCAAGAAAGATCAAGATATTTAAGAAATATTATAGAAGAGAATGCC 1144
Db 897 GAATATATCTTTAAAAAATAATTATTAATAAATCAATACTAATAATAATATTACTTCAATA 838
Qy 1145 AAAATCTGTATCATTAATTGATGAGGCATCTACAGTTTTCAAAGAAAAACCCCTAGTGATT 1204
Db 837 GATATTAGTAATAATTAATGATATAACATTTGTTGTTGAACCAAGTGTGACAAAAATTAAT 778
Qy 1205 TATCTCAGTGCAAAATTCAGTCAGCTCCTGACCTGTTATGTTATTTTGGCTTTAAAA 1264
Db 777 AAATTTAAAAAATATTAACAAATTTTGTATGAAAAAACAATTTGATCAAGAATAATGGAA 718
Qy 1265 GAATTTGGTGTCAACTATAGCAGAGTGATGTGCAATACATTTTACTACTTTTAAATGAT 1324
Db 717 TTTAATAATTACTAATGATGATGATGATTTTCTCAATCATTAATTAAATTCATATAAAAT 658
Qy 1325 TGTGGTTTTT 1333
Db 657 CGTGTATT 649

RESULT 7
US-09-662-254B-25/c
; Sequence 25, Application US/09662254B
; Patent No. 6933145
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Li, Yi
; APPLICANT: Bawden, Alison Louise
; TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous
; TITLE OF INVENTION: Vertebrate Cells
; FILE REFERENCE: UF-221C1XCI
; CURRENT APPLICATION NUMBER: US/09/662,254B
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 09/086,651
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/224,479
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 50000
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; TYPE: DNA
; ORGANISM: Ambacta moorei entomopoxvirus
US-09-662-254B-25

Query Match      3.7%; Score 56.6; DB 3; Length 5000;
Best Local Similarity 42.6%; Pred. No. 0.0061;
Matches 293; Conservative 0; Mismatches 394; Indels 0; Gaps 0;

QY 455 AAGTGAAGAAACAGACACAGAAATAATGAAGTGGAGCAAAATCACTGAGATTGCTTAAG 514
DB 38911 AATGATATAATGGATTGTTAGTTAATAATTTTAAATGATTATAACAATAATAAAAAATCTATT 38952

QY 515 GCAAAGGAACACACATTTCCAGGTATATAGAACAAACCAATCATTTGAAGAAAAGCCATCACTT 574
DB 38851 GATGAAAATAATAGATGATATAATAATATAACAGATGAATTAATACACATCTATCATCT 38792

QY 575 TCATCAAGAAGAATAAGATAATCTTGCTTCAGATTGTTGGAATGAAACAAAACAGCA 634
DB 38791 TTAGATGTTTAAATATCTCCATATCAAAATCTTAGAACTTATATGAATGATATAGATACT 38732

QY 635 TTTATGTTTACAGACAATACAAATGGCTTGAAATAAAGAGGTAAATTAGGATGAAG 694
DB 38731 ATGATTGAATCTATATATGATAAATATGATAAACAATAATTAATAATCTATATCAGGAAACT 38672

QY 695 GATTGTTACAGCAGTTTCGGCATTTGGGATCGAAAGCAGAAAGCATGTCCATGTGTCCAAAG 754
DB 38671 GAAAACTACAGCATCATTTAAACAAATGTAAATCTAGATTTTCGACAAATTATCTGAT 38612

QY 755 GAATGGATTGCAATTTAGTACCCTTAATGGCAGTAATAAATCTAGGCAAGCTTCT 814
DB 38611 GTTAGTAATTCGATTGATGAAATAATATGATAATTTTATAAATAATCAGAGTCTATTATA 38552

QY 815 CTACGAAAAAAATTAGGGAACATGATGTTCTTAAAGCCATGGTAAATTCAGGATTG 874
DB 38551 AATAAATAAAGCATAAAGAAAGTTATTTTATATACTAGTCGAAAGATATATCTAAAAAT 38492

QY 875 TTAAGAGGAATCAACTAATGATTCAATTTGTAATTTAGTCATAAACAATAATAAATAAT 934
DB 38491 ATAAATTAACATAATGATGATTCTAATTAATTAATTAACATATATAGAAAAATTAAT 38432

QY 935 ATTGATGCTACTGTAAAAAGTTTTTACATCTGTTTACAGTTTATAGTAAAAACATAACAGCCT 994
DB 38431 AGTGGTGATGAACAAATTTGATAGATATAAAAAATATTTGATTTATCAGACATATTAAA 38372

QY 995 TTATCTGATATTGAGGGGCAAGAGAAATACAGGAAAAAAATGGAGAGGTAATTTGTTTA 1054
DB 38371 ATTTTATAAATAAATAATATTACCAGAAATTAATAAAAAATTTTTTAAACGGAGAAATATGTA 38312

QY 1055 AATACACGTTACAGTGCAACAGAAATAGCAGACATATTGCAAAAGAAATGAAGATGAAG 1114
DB 38311 AACTCTGATAAATTTAAAAAATATTATTAATGAAGTGTATTAAATAATAATAATACAGAT 38252

QY 1115 ATATTTAAGAATATTATAAGAGAGAAAT 1141
DB 38251 TATATATTAAATATTATAAAATCTAAT 38225

RESULT 8
US-09-640-173-53/c
; Sequence 53, Application US/09640173
; Patent No. 6613515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 21021.484C2
; CURRENT APPLICATION NUMBER: US/09/640,173
; CURRENT FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 396

; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-713-550-53

Query Match      3.7%; Score 56.2; DB 3; Length 396;
Best Local Similarity 39.0%; Pred. No. 0.0091;
Matches 154; Conservative 0; Mismatches 241; Indels 0; Gaps 0;

QY 741 TCCATGTGTCGAAGGAATGGATTCATATTTAGTAACCCCTAATGGCAGTAAATAAACTA 800
DB 395 TGCNTNNNNCNAAANNNAAGGGGCGCAAGNNNNNNAANNNAAGNNNNNNNNNNNNNNNN 336

QY 801 CTAGCGAAGCTTCTCTAGCAAAAAAATTTAGGGAACATGATGTTTCTAAAGCCCATGTA 860
DB 335 CTCGNNNNCCNNNNNNNAANNANTATNAAGNANNATNNNNNNNNNNNNNNNNNNNTTTA 276

QY 861 AAATTCAGGATTTGTTAAAGGAATCAACTAATGATTTCAATTTGTAATTTAGTGCATAAAC 920
DB 275 TNNTTCTTNTCTTTTNTGAAATTAANAAGNAAANAANAANAANNNTAAARAAA 216

QY 921 AAAATAATAAAAAATTTGATGCTACTGTGAAAAAGTTTTTCAATCTGTTTACAGTTTAGTAA 980
DB 215 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 156

QY 981 AACATAACAGACCTTTTATCTGATTTAGGGGGGCAAGAGAAATTCAGGAAAAAATGGAG 1040
DB 155 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 96

QY 1041 AGGTAATTTGTTAAATACACGTTTACAGTCGCAACAAGAAATAGCAACAATTTGCAAAAG 1100
DB 95 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 36

QY 1101 AAATGAAGATGAAGATATTTAAGAAATATTATAGAA 1135
DB 35 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 1

RESULT 9
US-09-713-550-53/c
; Sequence 53, Application US/09713550
; Patent No. 6617109
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 21021.484C4
; CURRENT APPLICATION NUMBER: US/09/713,550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 396

; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-713-550-53

Query Match      3.7%; Score 56.2; DB 3; Length 396;
Best Local Similarity 39.0%; Pred. No. 0.0091;
Matches 154; Conservative 0; Mismatches 241; Indels 0; Gaps 0;

QY 741 TCCATGTGTCGAAGGAATGGATTCATATTTAGTAACCCCTAATGGCAGTAAATAAACTA 800
DB 395 TGCNTNNNNCNAAANNNAAGGGGCGCAAGNNNNNNAANNNAAGNNNNNNNNNNNNNNNN 336
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Qy	801	CTAGGCAAGCTTCTCTACGAAAAAAATTAGGGACATGATGTTCTTAAAGCCCATGGTA	860
Db	335	CTCGNNCCNNNTNNNNAANNANTATNAGNANNTNNNNNTNNNGTNNNTNTTA	276
Qy	861	AAATTCAAGGATTTGTTTAAAGGAATCAACTAATGATTCAAATTGTGTAATTTAGTGCATAAAC	920
Db	275	TNTTTTCTTNTCTTTTTTNTGAAATTAATAAANAAGGNAAAAAAANAANNTAAAAAAA	216
Qy	921	AAAATAATAAAAAATATTGATGCTACTGTAAAAAGTTTTCAATCTGTTTTACAGTTTACTAA	980
Db	215	AAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	156
Qy	981	AACATAACAGACCTTTTACTGTATTTGAGGGGCAAGAGAATTACAGAAAAAAATCGAG	1040
Db	155	AAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	96
Qy	1041	AGGTAAATTGTTTAAATACAGTTTACAGTGCACAGAATAGCAGAAACATATTGCAAAAG	1100
Db	95	AAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	36
Qy	1101	AAATGAAGATGAAGATATTTTAAGAAATATTATAGAA	1135
Db	35	AAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	1

```

RESULT 10
US-09-825-294-53/c
Sequence 53, Application US/09825294
Patent No. 6710170
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF OVARIAN CANCER
FILE REFERENCE: 210121.484CS
CURRENT APPLICATION NUMBER: US/09/825,294
CURRENT FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 53
LENGTH: 396
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(396)
OTHER INFORMATION: n = A,T,C or G
US-09-825-294-53

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Db      155 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 96
Qy      1041 AGGTAAATGTTTAAATACACGTTACAGTGCAACAAGATAGCAGAACATATTGCAAAAG 1100
Db      95 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 36
Qy      1101 AAATGAGAGTGAAGATATTTTAAAGAAATATTATAGAA 1135
Db      35 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 11
US-09-970-966-53/c
; Sequence 53, Application US/09970966
; Patent No. 6720146
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Molesh, David Alan
; APPLICANT: Fling, Steven P.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C6
; CURRENT APPLICATION NUMBER: US/09/970,965
; CURRENT FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 224, 225, 228, 235, 240, 246, 257, 266, 274, 279, 281, 282,
; LOCATION: 283, 285, 287, 288, 290, 291, 292, 293, 294, 295, 296, 297,
; LOCATION: 300, 301, 303, 307, 311, 313, 314, 317, 318, 319, 320, 321,
; LOCATION: 323, 324, 328, 329, 330, 336, 337, 338, 339, 340, 341
; OTHER INFORMATION: n = A, T, C or G
; NAME/KEY: misc_feature
; LOCATION: 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 356,
; LOCATION: 357, 358, 359, 362, 363, 364, 365, 366, 367, 373, 380, 381,
; LOCATION: 382, 385, 387, 388, 389, 390, 392
; OTHER INFORMATION: n = A, T, C or G
; US-09-970-966-53

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	Query Match	3.7%;	Score 56.2;	DB 3;	Length 396;
	Best Local Similarity	39.0%;	Pred. No. 0.00091;		
	Matches 154;	Conservative 0;	Mismatches 241;	Indels 0;	Gaps 0;
Qy	741	TCCATGTGTC	CAGGAA	TGCA	TATTTAGTAA
Db	395	TGCNTNNNN	CNAANN	AAAGGG	GCAGNNNNN
Qy	801	CTAGGCAAG	CTTCTCTACG	AAAAA	ATTAGGGA
Db	335	CTCGNNN	CCNNTNNNN	NAANN	TATNAGNANN
Qy	861	AAATTCAGG	ATTTGTTTAA	AGGA	TCAACTAAT
Db	275	TNTTTTCT	TNTTCTTTTNTG	ATTA	AAAAA
Qy	921	AAATATAA	AAATATTTGAT	CGCTACTG	TAAAGTTT
Db	215	AAAAA	AAAAA	AAAAA	AAAAA
Qy	981	AACATAA	CAGACCTTTATCTG	ATTTCTGAGG	GGCAAGAA
Db	155	AAAAA	AAAAA	AAAAA	AAAAA
Qy	1041	AGGTA	AAATGTTTAAATAC	AGTTTACAGT	GCACAGAA
Db	95	AAAAA	AAAAA	AAAAA	AAAAA

RESULT 14
US-08-487-826B-13
; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Welliams, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-487-826B-13

Query Match 3.5%; Score 53.2; DB 2; Length 19124;
Best Local Similarity 49.4%; Pred. No. 0.026;
Matches 167; Conservative 0; Mismatches 168; Indels 3; Gaps 1;
Qy 861 AAATTCAGGATTTCTTAAAGAACTCACTAATGATTCAAATTTGTAATTTAGTCGATAAAC 920
Db 15432 AAAAACAAATTTATTAATAAGTAAAGAAAGAAATGAAATATAAATAAATAATTTATTAAA 15491
Qy 921 AAAATAATAAATAATTTGATGCTACTGTAAAGTTTTCATACCTGTTTACAGTTTAGTAA 980
Db 15492 ATAAAAAATAAATAAATAAAGGAAATAATTTTAAAAATAATAAATAATTAAT 15551
Qy 981 AACATAACAGACCTTTATCTGATATTGAGGGGCAAGAGAAATTCAGGAAAAAATGGAG 1040
Db 15552 AAAATATAAA--TTTGTAGATAAATAAATAAGAAAGATTATCAAAAAAATAATTAATA 15608
Qy 1041 AGGTAAATGTTTAAATACAGTTACAGTGAACAAGNATAGCAGACATATTCGCAAAAG 1100
Db 15609 AAAAATTTTATATAAATAAATAAATGATTATATAAATAAATAAATAAAGAAAGAAAAA 15668
Qy 1101 AAATCAAGATGAAGATATTTAAGAAATATTATAGAGAGAAATGCCAAATACTCTGTATCA 1160
Db 15669 AAAACATTAATAAATAAATAAATAATATATATATATAAATAAATAAATAAATAAATAAT 15728

Qy 1161 TTGATGAGGCATCTACAGTTTCAAGAAACACCCCTA 1198
Db 15729 TAAATAAATAATATATATATATCAATAAATAAATAAATAATTA 15766
RESULT 15
US-09-902-540-1280
; Sequence 1280, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1280
; LENGTH: 1039
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1039)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1280

Query Match 3.4%; Score 51.6; DB 3; Length 1039;
Best Local Similarity 42.6%; Pred. No. 0.018;
Matches 318; Conservative 0; Mismatches 426; Indels 2; Gaps 1;
Qy 445 AAATATGAAGAGTGAAGAAACAGACAGACAGAAATAATGAAGTGAGCAAAATCACTGCAG 504
Db 249 AAAACAATATCATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 308
Qy 505 ATTGTCTTAAGGCAAGGAACCAATTTTCGAGTATATAGAACCAACCAATCATTTGAAGAAA 564
Db 309 ATAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 368
Qy 565 GCCATCATCTTCATCAAGAAAGAAATAGATAATCTTGTCTTCCAGATTTTGGATGA 624
Db 369 AAAACAAAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 428
Qy 625 AAAACAAGCATTTTATGTTTACAGAACAAATCAAAATGCTTTGAAATAAAGAAGTAAATT 684
Db 429 AAAAAAATAATATGTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 488
Qy 685 AGGATGTAAAGATTTGTTTCAGCAGTTTCGGCATTTTGGGATCGAAAGCAGAAAGCATGTCCA 744
Db 489 AAAAAAATAAATGAAACAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 548
Qy 745 TGTGTCCAAGAAATGGATTCGATATTTAGTAACCCCTTAATGGCAGTAAATAAACTACTAG 804
Db 549 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 608
Qy 805 GCAGCTTCTACGAAAAAATAATAGGGAACATGATGTTTCTAAAGCCCATGTTAAAT 864
Db 609 AAAAAAACNC--CGCATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 666
Qy 865 TCAGGATTTGTTAAAGGAATCAACTATATGATTCAAATTTGTAATTTAGTGCATAAACAATA 924
Db 667 TGTITTTTCTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 726
Qy 925 TAATAAATAATTCATCTACTGTAAAGTTTTCATATCTGTTTACAGTTTAGTTAGTAAACA 984
Db 727 TAACAAAGGCTCTAATCAACACCCCAATATAACAAAAAATCCTAAAAACAAAAAATAAATA 786
Qy 985 TAACAGACCTTTTCTGATATTGAGGGGCAAGAGAAATTACAGGAAAAAATAATGGAGGTT 1044

Db 787 ATAAAAATATAAACCTTCTTAAAAAATAAAAAATTAACAACTAAAAAATGAGGAAA 846
Qy 1045 AAATTGTTTAAATACAGCTTACAGTGCACACAGATACAGACATATTCAGAAAGAAAT 1104
Db 847 ATAAAAAACAATAAATCTTAAAAAATAAAAAAACCATAAATAAAAAAATAAAAA 906
Qy 1105 GAAGATGAAGATATTTAAGATATTTATAGAGAGATGCAAAATCTGTATCATATTTGA 1164
Db 907 GAAAAAATAAATTAACAATAATCCAAAAAATAAAAAAATAAACCAATAAAAAAATA 966
Qy 1165 TGAGCATCTACAGTTTCAAGAAA 1190
Db 967 AAAAAACATAAACTAATAAAAAA 992

RESULT 16

US-08-451-405A-2
; Sequence 2, Application US/08451405A
; Patent No. 5736358

GENERAL INFORMATION:

; APPLICANT: FASEL, NICOLAS JOSEPH
; APPLICANT: REYMOND, CHRISTOPHE DOMINIQUE
; TITLE OF INVENTION: DICTYOSTELID EXPRESSION VECTOR AND
; TITLE OF INVENTION: METHOD FOR EXPRESSING A DESIRED PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE WEBB LAW FIRM
; STREET: 700 KOPPERS BUILDING, 436 SEVENTH AVENUE
; CITY: PITTSBURGH
; STATE: PENNSYLVANIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 15219-1818

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISK
; COMPUTER: Midwest Micro 486-50
; OPERATING SYSTEM: DOS
; SOFTWARE: WORDPERFECT 6.1

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/451,405A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,273
; FILING DATE: 15-JAN-1993
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 731
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: UNKNOWN

US-08-451-405A-2

Query Match 3.3%; Score 51.2; DB 2; Length 731;
Best Local Similarity 50.7%; Pred. No. 0.019;
Matches 154; Conservative 0; Mismatches 143; Indels 7; Gaps 1;

Qy 895 TTCATTTGTAATTTAGTCATTAACAAATAATAAATAATTTGCTACTGTAAGCT 954
Db 87 TTTTATTTTATTTTAAAAAATAAATAATTAAGATTAATAATTTCTATTTGAAGGAGT 146
Qy 955 TTTCAATCTGTTTACAGTTTATAGTAAACATACACACCTTTATCTGATATTGAGGGGC 1014
Db 147 TTTTATTTGTAATTTAAAAATATATTAACATAGTGAACCTAAAAATAGATTTGTGACGT 206
Qy 1015 -----AAGAGAAATACAGGAAAAAATGGAGGTAATTTGTTTAAATACACGTTACA 1067
Db 207 ATATGATAGAAAAATCTTAAAAAATAAATTTTGAATTTGGAATGGAACAACCAACC 266
Qy 1068 GTCCACACAGATAGCAGAACATATTTGCCAAAAGAAATGAAGATGAAGATATTAAAGATA 1127
Db 267 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 326
Qy 1128 TTATAGAGAGATGCCAAATCTGTATCATATTTGATGAGGATCTACAGTTTCAAGA 1187

Db 327 AAAAAAAGGTATTTTAAAGAAATTTTAAAAATATTTATATATATCTTTAAATGTGCAA 386
Qy 1188 AAC 1191
Db 387 ACAC 390

RESULT 17

US-09-621-976-2813
; Sequence 2813, Application US/09621976
; Patent No. 6639063

GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399

US-09-621-976-2813

Query Match 3.3%; Score 51.2; DB 3; Length 832;
Best Local Similarity 20.6%; Pred. No. 0.02;
Matches 107; Conservative 169; Mismatches 238; Indels 5; Gaps 1;

Qy 946 TGTAAGTGTTCATATCTGTTTACAGTTTAGTAAACATAACACACCTTTATCTGATAT 1005
Db 1 YRWYWKYTTWYAKCWTWKWSWSYMYMKTYWRWRKWKKKAMWKYKWTWTWY 60
Qy 1006 TGAGGGGCAAGAGATTAACAGAAAAATGAGAGGTAAATTTGTTTAAATACACGTTA 1065
Db 61 RYAMMGTYKKKAMCRKTKKKKKKYMMWYWGWSRSYAMWTRTWTGYYRSMYWR 120
Qy 1066 CAGTCAACAAGATAGCAGAACATATTCGAAAAAGAAATGAAGATGAAGATATTAAGAA 1125
Db 121 YRCWKKAYYRKTTCYSSKGWTKWKKAWTTWKKTYWATRYMMWCMWTKWRAS 180
Qy 1126 TATTATAGAAGAGATGCAAAATCTGTATCATATTTGATGAGGATCTACAGTTTCAA 1185
Db 181 WWCWGWKARKWSTWRSRSYASARSACRCCYSCSWGMSWKYMWWRWGWATGAGM 240
Qy 1186 GAAACACCCCTAGTGATTTATCTCCAGTGACAAATTCAGTCAGCTCCTGACCTGTTAT 1245
Db 241 KAWRASCMMRRYAGSKTSYSKMMWCWTRSWKYCYTKARWTGYCYRKG-----GWWGK 295
Qy 1246 GTTATTTTGGCTTTTAAAGAAATTTGTTCAACTATAGCAGAGTGTATTTGTAACAT 1305
Db 296 RGRWYASKYMMWKRMMWCMWARMYRSTGTFRASMMWRWYTTMMWKMWYAWARAAWRA 355
Qy 1306 ATTGACTACTTTAAATGATTTGGTTTACAAATGAATTTTGAAGAGCAATTTAATTCG 1365
Db 356 MMWAWRACAAATATAATTTATTTATGGTACAAATTTCTGTACTTTAGCAAACTGGAGT 415
Qy 1366 ATTTGTTCTGTGCTGTAAATACAACTCGGAAGAAAGTCTGGAGTAGTAGTACAAAAAT 1425
Db 416 AGTTCATAGTCAAGAGTCAGTTAATTTCTTAGAGAAAGTTTGTGTTTGTGGCAACA 475
Qy 1426 GTTAGAAAAATTTCTCGAAATCATCATTTTGAACCTGTTT 1464
Db 476 TTTTATAGCTTGTGTGAGTTCTTTTATTTAATGATT 514

RESULT 18

```
US-09-601-198-116/c
; Sequence 116, Application US/09601198
; Patent No. 6531583
; GENERAL INFORMATION:
; APPLICANT: Caselli, Gail H.
; APPLICANT: Chen, Elieon Y.
; APPLICANT: Glass, Jennifer S.
; APPLICANT: Glass, John I.
; APPLICANT: Heiner, Cheryl R.
; APPLICANT: Lefkowitz, Elliot
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
; TITLE OF INVENTION: UREALYTICUM
; FILE REFERENCE: URB-13452/22
; CURRENT APPLICATION NUMBER: US/09/601,198
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/073,189
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 116
; LENGTH: 1413
; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
US-09-601-198-116

Query Match      3.3%; Score 51; DB 3; Length 1413;
Best Local Similarity 45.3%; Pred. No. 0.028;
Matches 186; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

Qy 629 CAAGCAATTTGTTTACAGACACATACAAATGGCTTGAAATAAAGAGGCTAAATTAGGA 688
Dy 564 CAATCAGTAATTTAAGAGAAATTAATAAAATTTTCACAAATAAAAAACAATAAAAAA 505
Qy 689 TGTAAAGGATGTTTCCAGCAGTTTGGGCATTTGGGATCGAAAGCAGAAAGCATGTCCATGTG 748
Dy 504 CAATGAAGTTATCTCCCATTTAATAAGAGAAATTAATAATTTATTTGATCACAACCA 445
Qy 749 TCCAAGGAATGGATGTCATATTTAGTAACCCCTTAATGGCAGTATATAAACTACTAGGCAA 808
Dy 444 ACTATTAAAGAGCGTAATTTAAATAATTTAAACCTCATTTATATATAATAAAAAATTTTAA 385
Qy 809 GCTTCTCTACGAAAAAATTTAGGAACATGATGTTTCTAAAGCCCATGCTAAATTCAG 868
Dy 384 ACTATGGTTATAAAATTTGTTGGACATGATGATGATGATGATGATGATGATGATGATGAT 325
Qy 869 GATTGTTTAAAGGAATCAATGATTCATATTTGTAATTTAGTGCAATAAACCAAAATAAT 928
Dy 324 GGTTTAAACCTGATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 265
Qy 929 AAAAATATGATGCTACTGTAAAGTTTTCATCTGTTTCAATCTGTTTACAGTTTGTAGTAA 988
Dy 264 CAAGGTGTGTTGTAATTTTAAAGAGTTGATTAATATGATTAATTTAGAAAAAATTAAT 205
Qy 989 AGACCTTTAATCTGATTTAGGGGGCAGAGAAATTCAGGAAAAAATGGA 1039
Dy 204 AAGCTCTCTAATGATGATGAAAAAGCGGAATTTGTTGATAAAAAATTTTGCA 154

RESULT 19
US-09-134-001C-2243
; Sequence 2243, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
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; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2243
; LENGTH: 11091
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2243

Query Match      3.3%; Score 50; DB 3; Length 11091;
Best Local Similarity 45.3%; Pred. No. 0.12;
Matches 182; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

Qy 807 AAGCTTCTCTACGAAAAAATTTAGGGAACATCATGTTTCTAAAGCCCATGGTAAATTC 866
Dy 3848 ATGCATACAGCAAAATGTAATTTAGTAAGTGTGTAATGCTACACGAATAATCAATTTG 3907
Qy 867 AGGATTTGTTTAAAGGAATCAATTAATGATTTCAATTTTGAATTTAGTGCATAAACAAATA 926
Dy 3908 ATGGTATTTGAGTGATGGTAGACAAAGCATAAATCAATTCACCTGATACATCAATTA 3967
Qy 927 ATAAAAATATTTGATGCTACTGTAAAAAGTTTTCATTAATCTGTTTACAGTTTGTAGTAA 986
Dy 3968 AAAGAAATGCTAAAAATGATATTGATATTAAAGCAGCTGATAAGAAAAATAAAAAATTC 4027
Qy 987 ACAGACCTTTATCTGATATTGAGGGGCAAGAGAAATTTACAGGAAAAAATTTGGAGAGTAA 1046
Dy 4028 GAATAAATGATGCTACAGATGAAGAAATTTCAAGAGCGGAATCGTAAATTTGAAGAAGCTA 4087
Qy 1047 ATTGTTTAAATACACGTTTACAGTGCACCAAGAAATAGCAGAACATATTTGCAAAAAGAA 1106
Dy 4088 AGATTGAAGCAAAAGATAATATTTCACGCAATAGTAGATCAAGTAAATGAAGCGGA 4147
Qy 1107 AGATGAAGATATTTAAGATATTTATAGAGAGAAATGCCAAAAATCTGTATCATTAATTG 1166
Dy 4148 AAACATAATGGAATAAAAAATAAGAAATATATAACACGCAACTACTGTGAAATCTGAAG 4207
Qy 1167 AGCATCTACAGTTTCAAGAAAAACCCACCTAGTGTGATTTATC 1208
Dy 4208 CTAGACAGCAGTACAGATTAAGCAATTAAGCAATTAATC 4249

RESULT 20
US-09-134-000C-1158
; Sequence 1158, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1158
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1158

Query Match      3.2%; Score 49.4; DB 3; Length 1560;
Best Local Similarity 51.6%; Pred. No. 0.071;
Matches 113; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

Qy 459 TGAAGCAAGACAGCAAGAAATAATGAAGTAGAGCAAAAAATCACTGCAGATTTGCTAAGGCAA 518
Dy 914 TGAAGCAAGACAGCAAGAAATTAATCAGCAGCAACAAATTTTAAACAGGTCGTTATGCAA 973
Qy 519 AGGAACCAATTTTCGAGTATATAGAACAAACCAATTCATTTGAAGAAAAAGCCATCATCTTCAT 578
Dy 974 CGGATACATATTACGATATAAAAAATTTAAACCGGTGTTGTTGAACCTCAATTAATCAATGAAT 1033
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Qy	579	CAAGAAGAAATAGATAATCTTGCTCCAGATGCTTGAATGAAACAAGCATTTA	638
Db	1034	ACGATCAAGAAAGAAAGAAACCAAGTAGTACTAATTTGGCAGAGAAAGAAACCTTCGT	1093
Qy	639	TGTTTACAGAACCAATACAAATGGCTTGAAATAAAAAGAG	677
Db	1094	TTGNTAGGAAGCAGTCAAGAACAGCTAANAAGAGAG	1132

RESULT 21
 US-09-662-254B-27
 ; Sequence 27, Application US/09662254B
 ; Patent No. 693145
 ; GENERAL INFORMATION:
 ; APPLICANT: Moyer, Richard W.
 ; APPLICANT: Li, Yi
 ; APPLICANT: Bowden, Alison Louise
 ; TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous
 ; TITLE OF INVENTION: Vertebrate Cells
 ; FILE REFERENCE: UP-221C1XC1
 ; CURRENT APPLICATION NUMBER: US/09/662.254B
 ; CURRENT FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: 09/086,651
 ; PRIOR FILING DATE: 1998-05-29
 ; PRIOR APPLICATION NUMBER: 60/224,479
 ; PRIOR FILING DATE: 2000-08-10
 ; NUMBER OF SEQ ID NOS: 80
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 27
 ; LENGTH: 32392
 ; TYPE: DNA
 ; ORGANISM: Amsacta moorei entomopoxvirus
 US-09-662-254B-27

Query Match	3.2%	Score 48.8;	DB 3;	Length 32392;
Best Local Similarity	44.2%	Pred. No. 0.38;	307;	Indels 1;
Matches	244;	Conservative	0;	Mismatches

Qy	625	AAAAACAAGCATTTATGTTTACAGAACCAATACAAATGGCTTGAAATAAAAAGAGTAAATT	684
Db	7618	ACATATAAATTAAGTAGTATATGATATTAATTTAAATTCATCGAATTTACAAATATTAATA	7677
Qy	685	AGGATGTAAAGGATTTGTCAGCAGTTCCGCAATTCGGGATCGAAAGCAGCATGTCCA	744
Db	7678	TTTGCTACTATAATATATATATTGATTTTAAATTTATTTAAACCTTGTTAAATATAAAATATA	7737
Qy	745	TGTGTCAGAGGAATGGATTCGATATTTAGTAAACCCCTAAATGCGCAGTAAATAAACTACTAG	804
Db	7738	TGAAATTTAATAAATATAAATAAAAAAATAAATAACGTTTTGATGTAAATATATATATTA	7797
Qy	805	GCAAGCTTCTCTACGAAAAAAAATTTAGGGAACATGATGTTTTCTAAAGCCCATGTTAAAT	864
Db	7798	AGTTTAAAGTTTATATATCATTTAAAAATTTGAAATATGCAATATAGATAATTTGAAAAA	7857
Qy	865	TCAGGATTTGTTAAAGGAATCAACTAAT - GATTCAAATTTGTAATTTAGTGCATAAACAAA	923
Db	7858	TCAGTAAATTTTAACTATTGGAAGTATTACACTTAAATAATATTGATATAGTAAATATA	7917
Qy	924	ATAATAAAATATTGATGCTACTGTAAAAGTTTTCAATACATGTTTTACAGTTTAGTAAAC	983
Db	7918	ATTTTATAGAAAAATTAATTTAAATTTAAATCGAATTTAAATTTAGATAAATATATATAATA	7977
Qy	984	ATAACAGACCTTTATCTGATATTGAGGGGCGAAGAGAAATTCACGGAAAAAATCGAGAGG	1043
Db	7978	ATAAATAATCTTTTAAATTTGTTTTAAAAAATTAATAAATTTATCATTTAAAAACAACATA	8037
Qy	1044	TAAATTTGTTTAAATACACGTTTACAGTGCACAAGAAATAGCAGAACATATTCGCAAAAGAA	1103
Db	8038	TTATTGATATAAACCACTTATTATATCTTAAATAATTTAAATTTATTAATAATAAATAATA	8097
Qy	1104	TGAAGATGAAGATATTTAAGAAATATATATAGAGAGAAATGCCAAATCTGTATCATATTTG	1163
Db	8098	ATAATATAAAGATATTAATATTTTAAAGATATTTTAAAAAATAAATATTCGATTTATATATAG	8157

	Query Match	3.2%	Score 48.4;	DB 2;	Length 4673;
	Best Local Similarity	48.2%;	Pred. No. 0.2;		
	Matches 136;	Conservative 0;	Mismatches 146;	Indels 0;	Gaps 0;
Qy	878	AAGGAATCACTAATGATTGCAATTTGCTAAATTTAGTCGATACACAAAATAATAAAAAATATT	937		
Db	4286	AAAAATGGACATGCACTACAAATATGAGAAAATGAAATAAATTTGGAAAAATGAT	4227		
Qy	938	GATGCTACTCTAAAAAGTTTTCAATFACTGTTTTACAGTTTTAGTTAAACACATAACAGACCTTTA	997		
Db	4226	ATTGCTTCTCTTAAAAATAAAATTAATTTTAAATGATTTAAAAAAAATAATCGATTCCTTA	4167		
Qy	998	TCTGATATTGAGGGGCGACAGAAATTCAGAAAAAAATCGAGAGGTAAATTTGTTTAAAT	1057		
Db	4166	TTTTTTTTGTAAAAATGAAAGAGATAATTAATATTTAAAAAAAATGCTCATATTTTTTTCAAAA	4107		

Query Match 3.2%; Score 48.4; DB 6; Length 4673;
Best Local Similarity 48.2%; Pred. No. 0.2;
Matches 136; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

Qy 878 AAGGAATCAACTAATGATTCATTTGGTAATTTTGTGTCATAACAAAAATAATAAAATATT 937

Db 4286 AAAAAATGGACACATCACTACAAAATTAATGAAGAAAATGAAAATTAATTTGGAAAATGAT 4227
Qy 938 GATGCTACTGTAAGTTTTCATCTACTGTTTACAGCTTTTAGTAAACATAACAGACCTTTA 997
Db 4226 ATTGCTCTCTTTAAAAATAAAATTAATTTTAATGATTTTAAAAAATAAAATCGATCTTA 4167
Qy 998 TCTGATATTGAGGGGCGCAAGAGATTACAGGAAAAAATGAGAGGTTAAATTTGTTAAAT 1057
Db 4166 TTTTGTGTAATGAAGAGATTAATTAATTAATAAAATGCTCATATTTTTCAAA 4107
Qy 1058 ACAGTTTACAGTGCACAAAGAAATAGCAGACATATTTGCAAAAGAAATGAAGATGAAGATA 1117
Db 4106 ACAGAAATACAGCAATTTGACAAATTTGTCAAAATATGCTAAAAATATATCATCTTAATTTT 4047
Qy 1118 TTTAAGATATTTATAGAGAGAAATGCCAAAATCTGTATCATATA 1159
Db 4046 TACACAAATTAATTAATTAATGAATCCCAACATAATAACACA 4005

RESULT 25
US-08-998-416-288/c
; Sequence 288, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jergen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Reibschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPPII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 288:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 837 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE: PAG1241RP
; ORGANISM: US-08-998-416-288

Query Match 3.1%; Score 47.2; DB 3; Length 837;
Best Local Similarity 45.4%; Pred. No. 0.18;

Matches 169; Conservative 0; Mismatches 203; Indels 0; Gaps 0;
Qy 790 TAAATAAATACTAGGCAAGCTTCTCTACGAAAAAATAATAGGCAACATGATGTTTCTAA 849
Db 635 TTATAAGTATTTTAACTACATCTTTTATAATATTTTATTAATTAATTAATGATAA 576
Qy 850 AGCCCATCGTAAAAATTCAGGATTTTGTAAAGGAATCAACTAATGATCAATTTGTAATTT 909
Db 575 AATATTAATTAATAATTAATTTAAATTTAAATAAATAAATAAATAAATAAATAAATAAATTT 516
Qy 910 AGTCATATAACAAATAATAAATAATTTGATGCTACTGCTAAAGCTTTTCAATATCTGTTTA 969
Db 515 ATTAATAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 456
Qy 970 CAGTTTGTAGTAAACATACAGACCTTTTATCTGATATTGAGGGGCAAGAGAAATACAGGA 1029
Db 455 TCTTATAAAGATTAATAATAATAATCAACATAATAATTTTATAAATAATAGTATTATAA 396
Qy 1030 AAAAAATGGAGAGGTAAATTTGTTTAAATPACAGTTTACAGTGCAACAAAGATAGCAGACA 1089
Db 395 TAAAAATAATAATTTTACAATATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATA 336
Qy 1090 TATTGCAAAAGAAATGAAGATGAAGATATTTAAAGATATTTATAGAGAGAAATGCCAAAAT 1149
Db 335 TTTTAATAAACAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATTTAT 276
Qy 1150 CTGTATCATATAAT 1161
Db 275 AAAGAAAAATAAT 264

RESULT 26
US-09-710-279-2057
; Sequence 2057, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2057
; LENGTH: 2163
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-2057

Query Match 3.0%; Score 46.8; DB 3; Length 2163;
Best Local Similarity 43.5%; Pred. No. 0.34;
Matches 213; Conservative 0; Mismatches 277; Indels 0; Gaps 0;
Qy 644 ACAGAACTACAAATGCGCTTGAATAAAGAGGTAAATTAAGGATGTAAGGATTTGTTCA 703
Db 31 AAAGAAATTAATCTAAAGAGTAAAGAGATTATAGATGAGTTAAAAAGATATGAATGTTGAA 90
Qy 704 GCAGTTCCGGCATTTGGGATCGAAACAGAAAGCATGTCATGTGTCCAAGGAATGATTT 763
Db 91 GTGTCAAAATCATATGCAAGCTTTAGAGAAAGAAACAAATCAAAAGCATTAGATATAAATAATTT 150
Qy 764 GCATATTTTAGTAAACCCCTAATGGCAGTAAATAAACTACTAGGCAAGCTTTCTCTACGAAA 823
Db 151 AAAGCCTCTCAAGCGAAGACACTAATAACAAATACTCAAAATAATACCCAAAATCT 210
Qy 824 AAAATTAGGGAACATGATGTTTCTAAAGCCCATGTTAAAGTAAATTCAGGATTTGTTAAAGGAA 883
Db 211 AATAATAAACAAATAATTTCTAAACGATAAAGAAAAACAAAGTAAGTAATAATAGTAAACCA 270

Qy 884 TCAACTAATGATCAATTTGTAAATTAGTCATATAACAAATAATAATAAATATATGATGCT 943
Db 271 ACGAAGAAAAAGAAACAAACAAAGGAAAAACAGCAAAATAAATAAATAAATAAATAAAT 330
Qy 944 ACTGTAAAGTTTTCAATCTGTTTACAGTTTAGTAAACATACAGACCTTTTATCTGAT 1003
Db 331 AAGAATCAAAAAACAATAAAAAATAAAGAATAATAAATAAATAAATAAATAAATAAATGAG 390
Qy 1004 ATTGAGGGGCAAGAGAAATTACAGGAAAAAATAATGGAGAGGTAAATTTGTTTAAATACACGT 1063
Db 391 GTACAGAAACAAAGAAATGCCCTCTTAATCACTTATCAAGAGGCATAAATCTGTCGGT 450
Qy 1064 TACAGTCAACAAGATAGCAGAAACATATTGCAAAAAGAAATGAAGATGAATTTAAG 1123
Db 451 GAGTTAGCTGAAAAGCTAAATGTAGAATCAGCTGGTATTATTAAAAAATTTGTTCTACTA 510
Qy 1124 AATATTATAG 1133
Db 511 GGTATTATGG 520

RESULT 27

US-09-134-001C-2131
; Sequence 2131, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2131
; LENGTH: 2187
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2131

Query Match 3.0%; Score 46.8; DB 3; Length 2187;
Best Local Similarity 43.5%; Pred. No. 0.35;
Matches 213; Conservative 0; Mismatches 277; Indels 0; Gaps 0;

Qy 644 ACAGAACATACAAATGCGCTTGAATTAAGAAGAGTAAATTAGGATGTAGGATTTGTTCA 703
Db 55 AAGAATTTAAATCTAAAGAGTAAAGAGATTATAGATGAGTTTAAAAAGTATGAATGTTGAA 114
Qy 704 GCAGTTGCGCATTTGGGATCGAAAGCAGAAAGCATGTCCATGTGTCCAGGAATGATTT 763
Db 115 GTGTCAATCATATGCAAGCTTTAGAGAGAGCAATCAAGCATTAGATAAATAATTT 174
Qy 764 GCATATTTAGTAACCCCTTAATGGCAGTAAATAAACTACTAGGCGAGCTTCTCTACGAAA 823
Db 175 AAGCCTCTCAAGCGAAGACACTAATAAACAATACTCAAAATAATCACCAAAATCT 234
Qy 824 AAAATTAGGGAACATGATGTTTCTTAAGCCCATCGTAAATTCAGGATTTGTTAAAGGAA 883
Db 235 AATAATAACAAAATTTCTAACGATAAAGAAAAACAACAAAGTAAGAATAATAGTAAACCA 294
Qy 884 TCACTAATGATTCATTTGTTAAATTTAGTCATAAACAATAATAAATAATTTATGATGCT 943
Db 295 ACGAAGAAAAAAGAAACAAACAAAGGAAAAACAGCAAAATAAATAAATAAATAAATAAAT 354
Qy 944 ACTGTAAAGTTTTCAATCTGTTTACAGTTTAGTAAACATACAGACCTTTTATCTGAT 1003
Db 355 AAGAATCAAAAAACAATAAAAAATAAAGAATAATAAATAAATAAATAAATAAATAAATGAG 414
Qy 1004 ATTGAGGGGCAAGAGAAATTACAGGAAAAAATAATGGAGAGGTAAATTTGTTTAAATACACGT 1063

Db 415 GTAGCAGAAACAAAGAAATGCCCTCTAAATCATCTTATCAAGAGGCATTAATCTGCGGT 474
Qy 1064 TACAGTGCACAAGAAATAGCAGAAACATATTGCAAAAAGAAATGAAGATGAAGATATTAAAG 1123
Db 475 GAGTTAGCTGAAAAGCTAAATGTAGAATCAGCTGGTATTATTAAAAAATTTGTTCTACTA 534
Qy 1124 AATATTATAG 1133
Db 535 GGTATTATGG 544

RESULT 28

US-09-710-279-3962/c
; Sequence 3962, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P034800S
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3962
; LENGTH: 3898
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3962

Query Match 3.0%; Score 46.8; DB 3; Length 3898;
Best Local Similarity 43.5%; Pred. No. 0.45;
Matches 213; Conservative 0; Mismatches 277; Indels 0; Gaps 0;

Qy 644 ACAGAACATACAAATGCGCTTGAATTAAGAAGAGTAAATTAGGATGTAGGATTTGTTCA 703
Db 915 AAGAATTTAAATCTAAAGAGTAAAGAGATTATAGATGAGTTTAAAAAGTATGAATGTTGAA 856
Qy 704 GCAGTTGCGCATTTGGGATCGAAAGCAGAAAGCATGTCCATGTGTCCAGGAATGATTT 763
Db 855 GTGTCAATCATATGCAAGCTTTTAGAAGAGAAACAAATCAAGCATTAGATAAATAATTT 796
Qy 764 GCATATTTAGTAACCCCTTAATGGCAGTAAATAAACTACTAGGCAAGCTTCTCTACGAAA 823
Db 795 AAGCCTCTCAAGCGAAGACACTAATAAACAATACTCAAAATAATCAACCAAAATCT 736
Qy 824 AAAATTAGGGAACATGATGTTTCTTAAGCCCATGGTAAATTCAGGATTTGTTAAAGGAA 883
Db 735 AATAATAACAAAATTTCTAACGATAAAGAAAAACAACAAAGTAAGAATAATAGTAAACCA 676
Qy 884 TCACTAATGATTCATTTGTTAAATTTAGTCATAAACAATAATAAATAATTTATGATGCT 943
Db 675 ACGAAGAAAAAAGAAACAAACAAAGGAAAAACAGCAAAATAAATAAATAAATAAATAAAT 616
Qy 944 ACTGTAAAGTTTTCAATCTGTTTACAGTTTAGTAAACAATAACAGACCTTTATCTGAT 1003
Db 615 AAGAATCAAAAAACAATAAAAAATAAAGAATAATAAATAAATAAATAAATAAATAAATGAG 556
Qy 1004 ATTGAGGGGCAAGAGAAATTACAGGAAAAAATAATGGAGAGGTAAATTTGTTTAAATACACGT 1063
Db 555 GTAGCAGAAACAAAGAAATGCCCTCTTAAATCACTTATCAAGAGGCATAAATCTGTCGGT 496
Qy 1064 TACAGTGCACAAGATAGCAGAAACATATTGCAAAAAGAAATGAAGATGAAGATATTAAAG 1123
Db 495 GAGTTAGCTGAAAAGCTAAATGTAGAATCAGCTGGTATTATTAAAAAATTTGTTCTACTA 436
Qy 1124 AATATTATAG 1133

Db 435 GGTATTATGG 426

RESULT 29
US-09-662-254B-23
; Sequence 23, Application US/09662254B
; Patent No. 6933145
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Li, Yi
; APPLICANT: Bawden, Alison Louise
; TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous
; FILE REFERENCE: UP-221C1X1
; CURRENT APPLICATION NUMBER: US/09/662,254B
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 09/086,651
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/224,479
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 50000
; TYPE: DNA
; ORGANISM: Amsacta moorei entomopoxvirus
US-09-662-254B-23

Query Match 3.0%; Score 46.8; DB 3; Length 50000;
Best Local Similarity 44.3%; Pred. No. 1.4;
Matches 235; Conservative 0; Mismatches 292; Indels 3; Gaps 1;

QY 664 TGAATATAAGAGGTAATTAAGGATGTAAGGATGTTTCAGCAGTTCGCGATTCGGATC 723
Db 26146 TCAAAACAAAGGAGATATAAGATGAAATGTAATAAATAAATACTGTTGTTATGTACC 26205

QY 724 GAACGAGAAAGCATGTCATGTCGCAAGGAATGGATGTCATATTTAGTAACCCCTAA 783
Db 26206 CAAGAAGTCATTTAGATATATCGTCTGGATATCTGTAGAAATTTATTTAAATGTAA 26265

QY 784 TGGCAGTATAAACTACTAGGCAAGCTTCTTACCAAAAAAATTTAGGGAACATGATGT 843
Db 26266 TGACATAATTTAATATTATTAATTAATCTGAATTTAAATCTTTGCTGAAAAAGAAATTA 26325

QY 844 TTCTAAAGCCCATGGTA---AAATTCAGGATTTGTTAAAGGAATCAACTAATGATTCAT 900
Db 26326 TAATAAATTTAAAGAAATAGAAAAATAATATATATTTAGTAGAAGATAAAGAAATTAGA 26385

QY 901 TTGTAATTTAGTGCATAAAACAAATAATAAATAATTTGATGCTACTGTAAAAAGTTTCAA 960
Db 26386 AATTAAATGATTTAAATAAAAAATTTAAGTGATTTAATCAATCAAAATAATAAGATATTAGA 26445

QY 961 TACTGTTTACAGTTTGTATTAACATAACAGACCTTTTATCTGATATTGAGGGGCGAAGAGA 1020
Db 26446 ATCTAATAAACTTTAGAAAATCAAAATAAATAAATTTACTTAAGTTAGCAGAGAAACAAA 26505

QY 1021 ATTACAGGAAAAATGGAGAGTAAATTTGTTTAAATACAGCTTACAGTGCACAGAAAT 1080
Db 26506 CATAAATTTAGTGAATAGGAGATGAATTAGATGAACCAAAATTTTAAATTTAGATACAT 26565

QY 1081 ACCAGACATATTGCAAAAGAAATGAAGATGAAGATTTTAAAGATATTATATAGAGAGAA 1140
Db 26566 AACTCAACAGTTTGAAGAAAAATATATTACCTGATGAATAATATATACCTTAAGAGCTTAA 26625

QY 1141 TGCCAAAATCTGTATCATTAATTTGATGAGGCATCTCAGTTTCAAAGAAAA 1190
Db 26626 TCTAAACATATTTAGTAAATTTATATAAATAATAACGAATTAAGATTA 26675

RESULT 30
US-08-998-416-186/c
; Sequence 186, Application US/08998416
; Patent No. 6239264

GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Reibschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 615 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1074RP
US-08-998-416-186

Query Match 3.0%; Score 46.2; DB 3; Length 615;
Best Local Similarity 46.0%; Pred. No. 0.28;
Matches 234; Conservative 0; Mismatches 268; Indels 7; Gaps 2;

QY 883 ATCAACTAATGATTCGAATTTGTAATTTAGTCGATTAACAAAATAATAAAATATTGATGC 942
Db 577 ATAAATATTAAATAAATAAATTTAATTTAAATAAATAAATAAATAAATAAATAAATAA 518

QY 943 TACTGTAAGGTTTCAATGCTGTTTACAGTTTGTAGTAAACATAACAGACCTTTTCTCGA 1002
Db 517 TTTATTAATAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 462

QY 1003 TATTGAGGGGCAAGAGAAATTAACAGAAAAAATGAGAGGTAATTTGTTAAATACACG 1062
Db 461 TAATAATTTCTATAAAGAGTTAAATAATAATAATAATAATAATAATAATAATAATAATA 402

QY 1063 TTACAGTGCACAAAGAAATAGCAGAACATATTGCAAAAGAAA---TGAAGATCAAGATATT 1119
Db 401 TTATAATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 342

QY 1120 TAAGAAATATTATAGAGAGAAATGCCAAATCTGTATCATTAATTTGATGAGGCATCTACAG 1179
Db 341 ATATTATTTTAAATAAACAATTAATAATAATAATAATAATAATAATAATAATAATAATA 282

QY 1180 TTCAAAAGAAAACCCCTAGTATTATCTCCAGTGCACAAATTCAGTCAGCTCCTGCACC 1239

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Db      281 TTTATTAAAGAAAATAATAATATCTAATAATAATTTTAACTAACTAATTTAAAAATTGAACA 222
Qy      1240 TGTATATGTTATTTTGTGGCTTTAAAGAATTGGTGTCTCAACTATAGCAGAGTGTATTTGTCAA 1299
Db      221 TAGCTAAATAGTATTTCATATTAAATATTTTATAAATATATATAAATATTAATGA 162
Qy      1300 TACATTATGACTACTTTTAAATGATTGTGGTTTTACAAATGAATATTTGAAAGCAAATTT 1359
Db      161 TGAATTAAGTAAATATATAATAATTAATAAATAAGTATTAAATAATCAAATAATTAATTT 102
Qy      1360 AATTGCATTTTGTTCCTGATGGTGCTAATA 1388
Db      101 ATTAATAATGATAATAATAAGTTTAAATA 73
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Job time : 316.691 secs

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OM nucleic - nucleic search, using sw model
Run on: December 3, 2005, 09:21:06 ; Search time 6415.89 Seconds
(without alignment)
11201.085 Million cell updates/sec

Title: US-10-757-745-5
Perfect score: 1536
Sequence: 1 agagaaagagctcgaggga.....attaatcatttaamntataa 1536

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_est3:
4: gb_hc:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_est7:
9: gb_gsa1:
10: gb_gsa2:
11: gb_gsa3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	ID	Description
1	1131.6	73.7	2214	11	DQ051955 Homo sapi
2	1111.2	72.3	2214	11	DQ051956 Pan trogl
3	854.8	55.7	858	8	CX164545 HESC2 18
4	834.4	54.3	1006	3	BQ230874 AGENCOURT
5	698.8	45.5	818	5	BU945621 AGENCOURT
6	671.6	43.7	691	2	BG777259 602664490
7	660	43.0	682	8	DN999300 TC121030
8	646.8	42.1	701	3	BI465045 603206445
9	645.8	42.0	741	2	BG286553 602382555
10	642.6	41.8	790	5	BU747241 CH3#010.D
11	633.6	41.2	645	7	CN359916 170005977
12	613.8	40.0	627	3	BM352924 ig69a09.Y
13	609.6	39.7	616	2	BG944466 ax50g10.X
14	602.6	39.2	768	2	BF667883 602122117
15	581.8	37.9	586	2	BG942992 ax32c07.X
16	574.8	37.4	581	3	BM352621 ig69a09.X
17	574.8	37.4	582	3	BI438747 1c26b08.X
18	572.8	37.3	576	3	BI439068 1c26b08.Y
19	571.8	37.2	588	7	CK821916 ig69a09.Y
20	570	37.1	615	2	BE614069 601503803
21	567.4	36.9	975	2	BG028983 602295120
22	562.4	36.6	581	3	BM972376 UI-CF-EC1

96	135.8	12.7	702	7	C0738423	C0738423	SILE04C20	169	75.8	4.9	1299	8	DN705619	DN705619	CLJ60-P02	
97	133.2	12.6	752	2	BE613457	BE613457	601504223	170	75.8	4.9	1459	8	DN726869	DN726869	CNB32-G02	
c	183.6	12.0	1992	4	BC035337	BC035337	Homo sapi	171	75.8	4.9	1727	10	CL118815	CL118815	ISB1-7205	
98	180.6	11.8	760	7	CN314848	CN314848	170005318	c	172	75.8	4.9	1811	10	CG753732	CG753732	P048-4-G0
100	176.8	11.5	267	8	T85912	T85912	Y959C02.r1	173	75.6	4.9	1043	6	CD385012	AGENCOURT	AGENCOURT	
101	175	11.4	258	1	AW501502	AW501502	UI-HF-RP0	c	174	75.6	4.9	1193	10	CG746298	P039-3-A0	CG746298
102	165.2	10.8	630	7	CV024153	CV024153	1345 Full1	c	175	75.2	4.9	1243	10	CL016663	CH216-1A2	CH216-1A2
103	162	10.5	162	7	CN277087	CN277087	170006001	176	75	4.9	1101	10	CNS0183Y	AL108856	Drosophila	
104	162	10.5	878	8	DN933911	DN933911	AGENCOURT	c	177	75	4.9	1151	8	DN582125	DN582125	92292027
105	161.4	10.5	578	7	CK357744	CK357744	AGENCOURT	c	178	75	4.9	1195	8	DR146887	DR146887	49090846
106	158	10.3	388	5	BY094255	BY094255	BY094255	c	179	75	4.9	1608	10	CL118721	ISB1-7208	CL118721
107	158	10.3	644	2	BB657575	BB657575	BB657575	c	180	74.8	4.9	1147	10	AG278327	Mus muscu	AG278327
108	158	10.3	715	5	BY715342	BY715342	BY715342	c	181	74.6	4.9	1362	10	CG757918	P053-2-A0	P053-2-A0
109	158	10.3	1750	4	AK015797	AK015797	Mus muscu	c	182	74.4	4.8	1559	10	CL646206	CH213-110	CL646206
110	157.4	10.2	738	8	DN538184	DN538184	1383868 M	c	183	74.2	4.8	1531	10	CG748014	P041-4-B0	P041-4-B0
111	156.8	10.2	653	2	BB626942	BB626942	BB626942	c	184	74	4.8	1187	9	CC217975	CC217975	CH261-119
112	156.8	10.2	929	5	B0886508	B0886508	AGENCOURT	c	185	74	4.8	1224	10	CL077121	CH216-143	CH216-143
113	155.8	10.1	362	5	BY064671	BY064671	BY064671	c	186	74	4.8	1386	10	AG442161	Mus muscu	AG442161
114	155.6	10.1	362	5	BY300743	BY300743	BY300743	c	187	73.8	4.8	650	10	AG066236	Pan trogl	AG066236
115	155	10.1	378	5	BY307103	BY307103	BY307103	c	188	73.6	4.8	1394	10	AG29511	Mus muscu	AG29511
116	153.8	10.0	553	2	BE750927	BE750927	202601 MA	c	189	73.6	4.8	1484	10	CL078073	CH216-147	CH216-147
117	153.4	10.0	671	5	BY307104	BY307104	BY307104	c	190	73.4	4.8	1256	10	CL119201	ISB1-76J1	ISB1-76J1
118	152.8	9.9	378	2	BB616798	BB616798	BB616798	c	191	73.4	4.8	1522	10	CL128484	ISB1-9411	ISB1-9411
119	152.8	9.9	3651	4	AK030088	AK030088	Mus muscu	c	192	73.4	4.8	1594	10	CL110653	ISB1-53P2	ISB1-53P2
120	152.6	9.9	366	5	BY230029	BY230029	BY230029	c	193	73.2	4.8	590	6	CF105429	ma192407	ma192407
121	150.6	9.8	406	6	CB808042	CB808042	AMGNNUC:N	c	194	73.2	4.8	634	2	BB615389	BB615389	BB615389
122	150.4	9.8	398	5	BY019311	BY019311	BY019311	c	195	73	4.8	1071	1	AJ926320	AJ926320	AJ926320
123	149.6	9.7	496	8	DR768918	DR768918	ILLUMIGEN	c	196	73	4.8	1114	8	DN656077	CEC21-A11	CEC21-A11
124	148.8	9.7	796	5	B0769546	B0769546	UI-M-F10-	c	197	73	4.8	1153	1	AJ928889	AJ928889	AJ928889
125	147.8	9.6	914	5	B0952426	B0952426	AGENCOURT	c	198	73	4.8	1253	10	CG748514	P042-2-G0	P042-2-G0
126	147.6	9.6	381	5	BY011101	BY011101	BY011101	c	199	73	4.8	1344	10	AG382142	Mus muscu	AG382142
127	146.8	9.6	353	5	BY210989	BY210989	BY210989	c	200	73	4.8	1364	8	DN693282	CGX87-B03	CGX87-B03
128	144.2	9.4	377	5	BY028275	BY028275	BY028275	c	201	73	4.8	1533	10	CL040854	CH216-50P	CH216-50P
129	144	9.4	339	5	BY138987	BY138987	BY138987	c	202	72.8	4.7	1145	10	AG364464	Mus muscu	AG364464
130	142	9.2	368	5	BY009270	BY009270	BY009270	c	203	72.8	4.7	1146	10	CL649333	CH213-227	CH213-227
131	139	9.0	443	6	CS789225	CS789225	AMGNNUC:M	c	204	72.8	4.7	1981	10	CL082000	CH216-165	CH216-165
132	138	9.0	392	5	BY024214	BY024214	BY024214	c	205	72.6	4.7	1288	10	CG744915	P037-3-F0	P037-3-F0
133	136.2	8.9	343	2	BB854831	BB854831	BB854831	c	206	72.6	4.7	1312	10	CL082693	CH216-169	CH216-169
134	132.8	8.6	827	3	B1836404	B1836404	603082932	c	207	72.6	4.7	1359	10	CG748855	P042-4-E1	P042-4-E1
135	132.4	8.6	562	7	CN314849	CN314849	170006000	c	208	72.4	4.7	1385	10	CL076799	CH216-140	CH216-140
136	131.2	8.5	814	2	BF178444	BF178444	601807896	c	209	72.4	4.7	1447	8	DN698671	CLJ18-H11	CLJ18-H11
137	130.2	8.5	337	7	C4633663	C4633663	CG748514	c	210	72.2	4.7	1205	10	CL143963	ISB1-1230	ISB1-1230
138	128.6	8.4	655	2	BB659280	BB659280	BB659280	c	211	72.2	4.7	1305	10	CG744200	P036-3-H0	P036-3-H0
139	126.4	8.2	410	4	AK210231	AK210231	Mus muscu	c	212	72.2	4.7	1566	10	CG757757	P053-1-D0	P053-1-D0
140	126.4	8.2	411	5	BY208338	BY208338	BY208338	c	213	72.2	4.7	1632	10	CL082569	CH216-167	CH216-167
c	141	122.2	8.0	444	9	AQ372518	AQ372518	RPC111-11	214	72.2	4.7	1739	10	CL136004	ISB1-107F	ISB1-107F
142	121.8	7.9	411	10	CG496856	CG496856	OST37152	c	215	72	4.7	886	8	DN567115	93902841	93902841
143	121.2	7.9	619	3	BP352609	BP352609	BP352609	c	216	72	4.7	959	10	CNS00655	Drosophila	Drosophila
144	117.6	7.7	339	5	BY184757	BY184757	BY184757	c	217	72	4.7	1594	10	CL078613	CH216-151	CH216-151
145	116	7.6	884	2	BG296904	BG296904	602394719	c	218	72	4.7	2172	10	CL078016	CH216-147	CH216-147
c	146	115	7.5	688	3	BF764731	BF764731	603051071	219	71.8	4.7	639	10	CNS0170D	Drosophila	Drosophila
147	106	6.9	350	5	BY220310	BY220310	BY220310	c	220	71.8	4.7	1220	10	CL641847	CH213-19H	CH213-19H
148	105.6	6.9	396	5	BY002237	BY002237	BY002237	c	221	71.8	4.7	1282	10	CG744668	P037-2-D0	P037-2-D0
c	149	104.6	6.8	621	9	A0441033	A0441033	HS 5109 A	222	71.8	4.7	1362	10	AG340853	Mus muscu	AG340853
150	104.2	6.8	343	5	BY502765	BY502765	DKFZP790	c	223	71.6	4.7	1253	10	CG749622	P043-4-F0	P043-4-F0
151	100.4	6.5	673	2	BB657355	BB657355	BB657355	c	224	71.6	4.7	1353	10	CG744812	P037-3-B0	P037-3-B0
152	92.8	6.0	1098	3	BF461462	BF461462	603206337	c	225	71.6	4.7	1393	10	AG387281	Mus muscu	AG387281
c	153	88	5.7	1391	10	CL646766	CL646766	CH213-123	226	71.6	4.7	1416	8	DN711652	CH216-512	CH216-512
154	84	5.5	657	8	CX831155	CX831155	ACAC-aaa2	c	227	71.6	4.7	1491	10	CG753221	P048-2-A0	P048-2-A0
c	155	82.4	5.4	1221	9	CG301561	CG301561	CH261-13K	228	71.6	4.7	1542	10	AG430573	Mus muscu	AG430573
156	80.8	5.3	1135	11	CNS033GQ	CNS033GQ	CH261-13K	c	229	71.6	4.7	1594	10	CL038406	CH216-46A	CH216-46A
157	79.4	5.2	1626	6	CF238805	CF238805	AGENCOURT	c	230	71.6	4.7	1797	10	CL066150	CH216-108	CH216-108
158	78.4	5.1	1599	10	CL083840	CL083840	ISB1-2H14	c	231	71.6	4.7	1843	10	AG435185	Mus muscu	AG435185
159	77	5.0	1493	10	CL078589	CL078589	CH216-151	c	232	71.4	4.6	1235	10	CG750878	P045-2-F0	P045-2-F0
c	160	77	5.0	1508	10	AG429777	AG429777	Mus muscu	233	71.4	4.6	1300	3	BM468018	BM468018	BM468018
161	76.8	5.0	1193	8	DN656299	DN656299	CEC2-C11	c	234	71.4	4.6	1376	10	CG747831	P041-3-B0	P041-3-B0
c	162	76.6	5.0	1276	10	CG754010	CG754010	P049-2-C0	235	71.4	4.6	1826	5	BU960792	AGENCOURT	AGENCOURT
163	76.6	5.0	1296	10	CG744840	CG744840	P037-3-C0	c	236	71.2	4.6	1975	5	CNS0039G	Drosophila	Drosophila
164	76.4	5.0	1178	10	CL491661	CL491661	SAIRL 559	c	237	71.2	4.6	1101	10	CG758413	P053-4-F0	P053-4-F0
165	76.4	5.0	1217	10	CL062848	CL062848	CH216-98N	c	238	71.2	4.6	1316	10	AG346348	Mus muscu	AG346348
166	76.2	5.0	319	8	L19145	L19145	WALMRNAM Ta	c	239	71.2	4.6	1355	10	AG595634	Mus muscu	AG595634
c	167	76.2	5.0	1242	8	DN695208	DN695208	CGX98-F10	240	71	4.6	878	10	CG749445	P043-3-G0	P043-3-G0
168	76.2	5.0	1288	10	CL082001	CL082001	CH216-165	c	241	71	4.6	1269	10	CG749445	P043-3-G0	P043-3-G0

C 242	71	4.6	1482	10	AG332292	Mus muscu	C 315	69.2	4.5	1434	10	AJ592058	Arabidops
C 243	71	4.6	1738	8	DR141924	49190649	316	69.2	4.5	1457	10	CL082658	CH216-169
C 244	71	4.6	1983	8	DR142277	49191190	317	69.2	4.5	1744	10	CL066409	CH216-108
C 245	70.8	4.6	1250	9	CC279901	CH261-24B	C 318	69	4.5	508	9	AQ455673	HS_5068_B
C 246	70.8	4.6	1315	10	CG754061	P049-3-E0	C 319	69	4.5	902	10	AG478273	Mus muscu
C 247	70.8	4.6	1380	10	CG744815	P037-3-B0	320	69	4.5	1075	11	CR028500	Forward 8
C 248	70.8	4.6	1573	6	DR124188	49179725	C 321	69	4.5	1155	1	AJ928993	AJ928993
C 249	70.6	4.6	1005	6	CB207771	AGENCOURT	C 322	69	4.5	1287	10	AG429705	Mus muscu
C 250	70.6	4.6	1101	10	CNS008VL	Drosophil	C 323	69	4.5	1295	10	AG288769	Mus muscu
C 251	70.6	4.6	1204	8	DN432684	LIB42117-0	C 324	69	4.5	1348	8	DN721897	CNB140-H1
C 252	70.6	4.6	1333	10	AG310863	Mus muscu	C 325	69	4.5	1373	10	CG750869	P045-2-E1
C 253	70.6	4.6	1378	10	AG350209	Mus muscu	326	69	4.5	1596	10	CL081967	CH216-165
C 254	70.6	4.6	1533	10	CL081968	CH216-165	C 327	69	4.5	1928	10	CL073845	CH216-130
C 255	70.4	4.6	1105	1	AJ929052	AJ929052	C 328	68.8	4.5	787	11	CR118377	Forward 8
C 256	70.4	4.6	1201	10	CG754932	P050-3-B0	C 329	68.8	4.5	1058	10	CL077132	CH216-143
C 257	70.4	4.6	1401	10	AG346504	Mus muscu	330	68.8	4.5	1162	10	CL073944	CH216-131
C 258	70.4	4.6	1507	10	AG346189	Mus muscu	331	68.8	4.5	1199	8	DN707481	CH216-143
C 259	70.4	4.6	1528	10	CG753854	P049-1-D0	C 332	68.8	4.5	1248	8	DN808090	CH216-143
C 260	70.4	4.6	1563	10	CL077268	CH216-143	C 333	68.8	4.5	1260	10	CG751608	CH216-143
C 261	70.4	4.6	1758	10	CL0509408	SATL 811	C 334	68.8	4.5	1298	10	CG756607	CGX08-H06
C 262	70.2	4.6	1142	1	AJ928301	AJ928301	C 335	68.8	4.5	1330	8	DN679922	CGX08-H06
C 263	70.2	4.6	1217	10	CL641230	CH213-7M0	C 336	68.8	4.5	1395	10	AG346313	Mus muscu
C 264	70.2	4.6	1231	10	CG755650	P051-1-G0	C 337	68.8	4.5	1484	10	AG371414	Mus muscu
C 265	70.2	4.6	1299	8	DN709204	CLJ81-H10	C 338	68.8	4.5	1519	10	AG386893	Mus muscu
C 266	70.2	4.6	1310	10	CL641510	CH213-13C	C 339	68.8	4.5	1583	10	CL075415	CH216-136
C 267	70.2	4.6	1324	10	CG746828	P040-1-G1	340	68.8	4.5	1165	11	CR007727	Reverse 8
C 268	70.2	4.6	1331	10	CG749578	P043-4-D1	341	68.6	4.5	1254	10	CG748584	P042-3-B0
C 269	70.2	4.6	1331	10	CL081265	CH216-161	C 342	68.6	4.5	1260	10	CG744622	P037-2-B0
C 270	70.2	4.6	1394	8	DN810217	77064084	C 343	68.6	4.5	1270	8	DN713071	CH216-44E
C 271	70.2	4.6	1416	10	CL49036	SAIL 662	344	68.6	4.5	1312	10	CL037916	Mus muscu
C 272	70.2	4.6	1433	10	CG745119	P037-4-G0	345	68.6	4.5	1498	10	AG332242	Mus muscu
C 273	70.2	4.6	1454	10	CG747614	P041-2-A0	C 346	68.6	4.5	1512	10	AG332242	Mus muscu
C 274	70.2	4.6	1512	10	CL082685	CH216-169	C 347	68.4	4.5	1092	8	DN585373	CH216-145
C 275	70	4.6	1074	9	BZ696936	SP_Ba009	C 348	68.4	4.5	1112	10	CL077397	CH216-145
C 276	70	4.6	1152	8	DN692538	CGX82-F11	C 349	68.4	4.5	1225	10	CG745927	P039-1-A0
C 277	70	4.6	1211	10	CG747324	P040-4-D1	C 350	68.4	4.5	1313	10	CG745713	P038-3-H0
C 278	70	4.6	1231	9	CC295583	CH261-64G	C 351	68.4	4.5	1344	10	CG748432	P042-2-C1
C 279	70	4.6	1285	10	CL648517	CH213-182	C 352	68.4	4.5	1392	10	CG757503	P052-4-C0
C 280	70	4.6	1289	10	AG383034	Mus muscu	C 353	68.4	4.5	1407	10	AJ592026	Arabidops
C 281	70	4.6	1334	10	AG341525	Mus muscu	354	68.4	4.5	1626	10	CL081997	CH216-165
C 282	70	4.6	1340	10	AG280360	Mus muscu	355	68.4	4.5	1680	10	CL079033	CH216-154
C 283	70	4.6	1453	10	AJ591978	Arabidops	356	68.4	4.5	2003	10	CL081999	CH216-165
C 284	70	4.6	1536	10	CL078538	CH216-151	357	68.2	4.4	1163	10	CL081338	CH216-161
C 285	69.8	4.5	1310	10	AJ592180	Arabidops	C 358	68.2	4.4	1293	10	AG429866	Mus muscu
C 286	69.8	4.5	1028	8	DN564006	9085017	C 359	68.2	4.4	1321	10	CG746535	P039-4-C0
C 287	69.8	4.5	1046	8	DN783952	90161936	C 360	68.2	4.4	1351	10	AG347205	Mus muscu
C 288	69.8	4.5	1223	10	CG750277	P044-4-B1	C 361	68.2	4.4	1352	9	CC268594	CH261-67F
C 289	69.8	4.5	1242	10	CG745315	P038-1-G0	C 362	68.2	4.4	1389	10	CG747695	P041-2-D0
C 290	69.8	4.5	1321	10	AG360584	Mus muscu	C 363	68.2	4.4	1489	10	CL078612	CH216-151
C 291	69.8	4.5	1330	8	DN705530	CLJ50-A10	364	68.2	4.4	1717	10	CL140478	ISB1-115J
C 292	69.8	4.5	1372	10	CG746616	P039-4-F0	C 365	68.2	4.4	1784	10	CL081992	CH216-165
C 293	69.6	4.5	1038	10	CL032098	CH216-33P	366	68.2	4.4	1824	10	CL081234	CH216-161
C 294	69.6	4.5	1167	1	AJ926512	AJ926512	C 367	68	4.4	948	6	CA465606	AGENCOURT
C 295	69.6	4.5	1314	10	CL077082	CH216-143	368	68	4.4	1099	1	AJ928262	AJ928262
C 296	69.6	4.5	1370	10	AG430078	Mus muscu	C 369	68	4.4	1223	9	B12981	ISB1-115J
C 297	69.6	4.5	1581	10	AG430645	Mus muscu	C 370	68	4.4	1266	10	AJ859745	Brassicica
C 298	69.4	4.5	759	6	CF255838	mdvnl32_f	C 371	68	4.4	1297	10	CG758143	P053-3-B1
C 299	69.4	4.5	1091	8	AJ927100	AJ927100	C 372	68	4.4	1400	10	AG430154	Mus muscu
C 300	69.4	4.5	1219	8	DR146428	49089533	373	68	4.4	2033	10	CL081977	CH216-165
C 301	69.4	4.5	1615	10	AG311072	Mus muscu	374	68	4.4	2071	8	DR147304	49027161
C 302	69.4	4.5	1616	10	CL081995	CH216-165	C 375	67.8	4.4	622	9	AZ526127	251PDH11
C 303	69.2	4.5	1047	9	CC266341	CH261-12K	C 376	67.8	4.4	1126	10	CL084090	ISB1-2N19
C 304	69.2	4.5	1113	8	DN683062	CGX27-G08	C 377	67.8	4.4	1259	11	CR004722	Forward 8
C 305	69.2	4.5	1228	10	CG749404	P043-3-E0	C 378	67.8	4.4	1317	10	AG360968	Mus muscu
C 306	69.2	4.5	1263	10	CL079431	CH216-155	379	67.8	4.4	1362	9	CC270526	CH261-119
C 307	69.2	4.5	1274	10	CL082683	CH216-169	C 380	67.8	4.4	1377	10	CG749971	P044-2-E0
C 308	69.2	4.5	1282	10	CL077120	CH216-143	C 381	67.8	4.4	1401	10	CL040987	CH216-51G
C 309	69.2	4.5	1286	10	CL081247	CH216-161	C 382	67.8	4.4	1571	10	CL066123	CH216-107
C 310	69.2	4.5	1334	10	AG288824	Mus muscu	383	67.6	4.4	614	10	CNS0152H	Drosophil
C 311	69.2	4.5	1334	10	CL647352	CH213-136	C 384	67.6	4.4	737	10	CNS0808U	AL051476
C 312	69.2	4.5	1335	10	AG280061	Mus muscu	C 385	67.6	4.4	1050	10	CL2965760	Drosophil
C 313	69.2	4.5	1355	10	AG361139	Mus muscu	C 386	67.6	4.4	1053	5	BUS08694	CZ565760
C 314	69.2	4.5	1378	10	AG280595	Mus muscu	C 387	67.6	4.4	1132	9	CC248307	CH261-88I

C 388	67.6	4.4	1133	10	CL147548	CL147548	ISB1-234N	461	66.6	4.3	1459	10	CL040025	CL040025	CH216-49A
C 389	67.6	4.4	1170	1	AJ925688	AJ925688	AJ925688	462	66.4	4.3	1073	1	AJ925652	AJ925652	AJ925652
C 390	67.6	4.4	1170	10	CG749508	CG749508	P043-4-A1	C 463	66.4	4.3	1128	10	CG753708	CG753708	P048-4-F0
C 391	67.6	4.4	1284	10	AG341125	AG341125	Mus muscu	C 464	66.4	4.3	1311	10	AG346751	AG346751	Mus muscu
C 392	67.6	4.4	1301	10	CL646303	CL646303	CH213-112	C 465	66.4	4.3	1383	10	AG341030	AG341030	Mus muscu
C 393	67.6	4.4	1306	10	CL078566	CL078566	CH216-151	C 466	66.4	4.3	1472	10	AG350118	AG350118	Mus muscu
C 394	67.6	4.4	1426	9	CC231597	CC231597	CH261-36A	467	66.4	4.3	1547	10	CL066420	CL066420	CH216-108
C 395	67.6	4.4	1436	10	CL057761	CL057761	CH216-860	C 468	66.4	4.3	1547	10	CL081966	CL081966	CH216-165
C 396	67.6	4.4	1438	10	CL078561	CL078561	CH216-151	C 469	66.2	4.3	1059	10	CNS0042B	CNS0042B	Drosophill
C 397	67.6	4.4	1631	10	CL062994	CL062994	CH216-99D	C 470	66.2	4.3	1101	10	CNS001FB	CNS001FB	CH216-158
C 398	67.6	4.4	1721	8	DR145459	DR145459	49056454	C 471	66.2	4.3	1137	10	CL080345	CL080345	CH216-158
C 399	67.6	4.4	1773	10	CL077987	CL077987	CH216-147	472	66.2	4.3	1232	9	CC281707	CC281707	CH261-37P
C 400	67.6	4.4	1808	8	DR125630	DR125630	49096520	C 473	66.2	4.3	1256	10	AG430074	AG430074	Mus muscu
C 401	67.6	4.4	1885	2	BE420745	BE420745	HMW002.B0	C 474	66.2	4.3	1307	10	CL647351	CL647351	CH213-136
C 402	67.6	4.4	2103	10	CL041093	CL041093	CH216-51M	C 475	66.2	4.3	1325	10	AG341551	AG341551	Mus muscu
C 403	67.4	4.4	884	7	CO881817	CO881817	BoVgen.10	476	66.2	4.3	1377	10	CL077307	CL077307	CH216-144
C 404	67.4	4.4	942	10	CNS018GS	AL109318	Drosophill	477	66.2	4.3	1461	10	CL081232	CL081232	CH216-161
C 405	67.4	4.4	1104	1	AJ925669	AJ925669	AJ925669	478	66.2	4.3	1475	10	CL082662	CL082662	CH216-169
C 406	67.4	4.4	1107	10	CL048339	CL048339	CH216-67M	479	66.2	4.3	1596	9	CC293489	CC293489	CH261-62N
C 407	67.4	4.4	1145	10	CL077970	CL077970	CH216-147	480	66.2	4.3	1842	10	CL044158	CL044158	CH216-59P
C 408	67.4	4.4	1156	10	CL103217	CL103217	ISB1-41D5	C 481	66.2	4.3	1896	10	CG753083	CG753083	P048-1-C0
C 409	67.4	4.4	1158	10	CL078712	CL078712	CH216-152	482	66.2	4.3	2001	10	CL118787	CL118787	ISB1-72M2
C 410	67.4	4.4	1175	10	CL073834	CL073834	CH216-130	483	66	4.3	945	10	CL107121	CL107121	ISB1-47N1
C 411	67.4	4.4	1224	1	AJ928740	AJ928740	AJ928740	C 484	66	4.3	1023	10	CL102986	CL102986	ISB1-40N1
C 412	67.4	4.4	1262	10	AG387122	AG387122	Mus muscu	C 485	66	4.3	1085	10	AG075009	AG075009	Pan trogl
C 413	67.4	4.4	1317	1	AJ926430	AJ926430	AJ926430	C 486	66	4.3	1174	10	CG746305	CG746305	P039-3-30
C 414	67.4	4.4	1338	10	AG429453	AG429453	Mus muscu	C 487	66	4.3	1176	10	CG749040	CG749040	P043-1-E1
C 415	67.4	4.4	1379	10	CL058765	CL058765	CH216-88M	C 488	66	4.3	1224	10	CG757393	CG757393	P052-3-G0
C 416	67.4	4.4	1641	10	CL078595	CL078595	CH216-151	489	66	4.3	1329	10	CL078715	CL078715	CH216-152
C 417	67.4	4.4	1690	10	CL078351	CL078351	CH216-149	490	66	4.3	1407	8	DN698856	DN698856	CLJ20-A09
C 418	67.4	4.4	1856	10	CL081986	CL081986	CH216-165	491	66	4.3	1428	10	CL081978	CL081978	CH216-165
C 419	67.2	4.4	907	10	CNS021J4	AL176953	Tetradodon	C 492	66	4.3	1441	10	AG396166	AG396166	Mus muscu
C 420	67.2	4.4	1104	6	CF264382	CF264382	AGENCOURT	493	66	4.3	1598	10	CL082702	CL082702	CH216-169
C 421	67.2	4.4	1249	9	BZ566650	BZ566650	pac82-164	494	65.8	4.3	912	8	DN567335	DN567335	OP20766 M
C 422	67.2	4.4	1271	10	CG744446	CG744446	P037-1-B0	C 495	65.8	4.3	966	3	BM415686	BM415686	90159753
C 423	67.2	4.4	1283	10	AG429716	AG429716	Mus muscu	496	65.8	4.3	1020	6	CD050222	CD050222	AGENCOURT
C 424	67.2	4.4	1361	10	CG744327	CG744327	P036-4-E0	C 497	65.8	4.3	1115	10	CL114095	CL114095	ISB1-59J1
C 425	67.2	4.4	1376	10	CG746561	CG746561	P039-4-D0	C 498	65.8	4.3	1165	10	AG341247	AG341247	Mus muscu
C 426	67.2	4.4	1380	1	AJ928744	AJ928744	AJ928744	C 499	65.8	4.3	1203	10	CL078699	CL078699	CH216-152
C 427	67.2	4.4	1386	8	DN661111	DN661111	CEC50-F07	C 500	65.8	4.3	1228	10	AJ592059	AJ592059	Arabidops
C 428	67.2	4.4	1452	10	CL125503	CL125503	ISB1-87B2								
C 429	67.2	4.4	1473	10	AG349809	AG349809	Mus muscu								
C 430	67.2	4.4	1756	10	CL078846	CL078846	CH216-153								
C 431	67	4.4	793	5	BU209730	BU209730	603952971								
C 432	67	4.4	879	10	CNS01JRG	AL147405	Anopheles								
C 433	67	4.4	1035	5	BU521025	BU521025	AGENCOURT								
C 434	67	4.4	1129	5	BU384961	BU384961	603582531								
C 435	67	4.4	1269	10	CG757211	CG757211	P052-2-G0								
C 436	67	4.4	1280	10	AG347131	AG347131	Mus muscu								
C 437	67	4.4	1313	10	CG751144	CG751144	P045-3-E0								
C 438	67	4.4	1394	10	AG365955	AG365955	Mus muscu								
C 439	67	4.4	1625	10	AG280005	AG280005	Mus muscu								
C 440	66.8	4.3	692	1	AJ929812	AJ929812	AJ929812								
C 441	66.8	4.3	811	1	AL514901	AL514901	AL514901								
C 442	66.8	4.3	1025	10	CNS014J2	AL104216	Drosophill								
C 443	66.8	4.3	1069	10	CL144571	CL144571	ISB1-144K								
C 444	66.8	4.3	1083	10	CL120068	CL120068	ISB1-78G7								
C 445	66.8	4.3	1154	10	CL078248	CL078248	CH216-148								
C 446	66.8	4.3	1223	10	CG745583	CG745583	P038-3-B1								
C 447	66.8	4.3	1275	10	CL647839	CL647839	CH213-152								
C 448	66.8	4.3	1276	10	AG346223	AG346223	Mus muscu								
C 449	66.8	4.3	1402	10	CL078552	CL078552	CH216-151								
C 450	66.8	4.3	1720	10	CL019799	CL019799	CH216-5P1								
C 451	66.6	4.3	983	1	AJ926697	AJ926697	AJ926697								
C 452	66.6	4.3	1005	10	CL077409	CL077409	CH216-145								
C 453	66.6	4.3	1052	9	CC243335	CC243335	CH261-120								
C 454	66.6	4.3	1060	10	CW937448	CW937448	TsB16.2.H								
C 455	66.6	4.3	1221	9	CC264768	CC264768	CH261-163								
C 456	66.6	4.3	1281	10	AG349913	AG349913	Mus muscu								
C 457	66.6	4.3	1289	10	AG347097	AG347097	Mus muscu								
C 458	66.6	4.3	1362	10	AG429915	AG429915	Mus muscu								
C 459	66.6	4.3	1419	10	AG371158	AG371158	Mus muscu								
C 460	66.6	4.3	1436	10	CL082687	CL082687	CH216-169								

ALIGNMENTS

2214 bp DNA linear

GSS 02-JUN-2005

DO051955 Homo sapiens HCl9996 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

DO051955 QD051955.1 GI:66905368

DO051955 GSS.

DO051955 Homo sapiens (human)

DO051955 Homo sapiens

DO051955 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

DO051955 1 (bases 1 to 2214)

DO051955 Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fedel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

DO051955 A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees

DO051955 (er) PLOS Biol. 3 (6), E170 (2005)

DO051955 15869325

DO051955 2 (bases 1 to 2214)

DO051955 Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fedel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

DO051955 Direct Submission

DO051955 Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

FEATURES

source Location/Qualifiers
1. .2214
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
<1..>2214
/locus_tag="HC19996"

gene

ORIGIN

Query Match 73.7%; Score 1131.6; DB 11; Length 2214;
Best Local Similarity 99.6%; Pred No. 3.1e-247; Indels 0; Gaps 0;
Matches 1134; Conservative 0; Mismatches 5;

Qy 391 TCATATCTGTTCTCTAAATGCCAAACGACAGGGTGAATTTTGCATTTTAAATAT 450
Db 33 TCAGATTCTGTTCTCTAAATGCCAAACGACAGGGTGAATTTTGCATTTTAAATGT 92

Qy 451 GAAGAAGTGAACACAGACAGAAAATAATGAAGTGAACAAAATCACTGCAGATTGTC 510
Db 93 GAAGAAGTGAACACAGACAGAAAATAATGAAGTGAACAAAATCACTGCAGATTGTC 152

Qy 511 TAAGCAAGGACACACATTTTCGATATATAGAACCAACCAATCATTTGAAGAAAAGCCATC 570
Db 153 TAAGCAAGGACACACATTTTCGATATATAGAACCAACCAATCATTTGAAGAAAAGCCATC 212

Qy 571 ACTTTCATCAAGAAAGAAATAGATAATCTTGTGCTTCCAGATTGTTGGAATGAAAACA 630
Db 213 ACTTTCATCAAGAAAGAAATAGATAATCTTGTGCTTCCAGATTGTTGGAATGAAAACA 272

Qy 631 AGCATTTATGTTACAGAACCAATCAAAATGCTTGAATAAAGAGTAAATTAGGATG 690
Db 273 AGCATTTATGTTACAGAACCAATCAAAATGCTTGAATAAAGAGTAAATTAGGATG 332

Qy 691 TAAGGATTTTCAGCAGTTCCGATTTCCGATTCGAAGCAGAAAGCATGTCCTATGTC 750
Db 333 TAAGGATTTTCAGCAGTTCCGATTTCCGATTCGAAGCAGAAAGCATGTCCTATGTC 392

Qy 751 CAAGAAATGGATTGATATTTAGTAACCCCTAATGGCAGTAAATAAACTACTAGGCAAGC 810
Db 393 CAAGAAATGGATTGATATTTAGTAACCCCTAATGGCAGTAAATAAACTACTAGGCAAGC 452

Qy 811 TTCTCTAGAAAAAATTTAGGGAACATGATTTTCTAAGCCCATGTTAAATTCAGGA 870
Db 453 TTCTCTAGAAAAAATTTAGGGAACATGATTTTCTAAGCCCATGTTAAATTCAGGA 512

Qy 871 TTGTGTAAGGATCACTAATGATTCATTTGTAATTTAGTGCATTAACAAAATAATAA 930
Db 513 TTGTGTAAGGATCACTAATGATTCATTTGTAATTTAGTGCATTAACAAAATAATAA 572

Qy 931 AAATATTGATGCTACTGTAAGAGTTTCAATCTGTTTACAGTTTGTAGTAAACATAACAG 990
Db 573 AAATATTGATGCTACTGTAAGAGTTTCAATCTGTTTACAGTTTGTAGTAAACATAACAG 632

Qy 991 ACCTTTATCTGATATTGAGGGGCGCAAGAGAAATTAACGAAAAAATGAGAGGTTAAATG 1050
Db 633 ACCTTTATCTGATATTGAGGGGCGCAAGAGAAATTAACGAAAAAATGAGAGGTTAAATG 692

Qy 1051 TTTAAATACAGTTTACAGTGCACAGAAATAGCAGACATATTTGCAAAAGAAATCAAGAT 1110
Db 693 TTTAAATACAGTTTACAGTGCACAGAAATAGCAGACATATTTGCAAAAGAAATCAAGAT 752

Qy 1111 GAAGATATTTAAGATATTTATAGAGAGAAATGCCAAATCTGTATCAATAATTGATGAGC 1170
Db 753 GAAGATATTTAAGATATTTATAGAGAGAAATGCCAAATCTGTATCAATAATTGATGAGC 812

Qy 1171 ATCTACAGTTTCAAGAAACCAACCCCTAGTGTATTTATCTCCAGTGCACAAATTCAGTCAGC 1230
Db 813 ATCTACAGTTTCAAGAAACCAACCCCTAGTGTATTTATCTCCAGTGCACAAATTCAGTCAGC 872

Qy 1231 TCCTGCACCTGTTATGTTATTTGTCCTTTTAAAGAAATGGTGTCAACTATAGCAGAGTG 1290
Db 873 TCCTGCACCTGTTATGTTATTTGTCCTTTTAAAGAAATGGTGTCAACTATAGCAGAGTG 932

Qy 1291 TATTGTCAATACATTATTGACTACTTTAAATGATTTGGTTTAAATGAATATTTGAA 1350
Db 933 TATTGTCAATACATTATTGACTACTTTAAATGATTTGGTTTAAATGAATATTTGAA 992

Qy 1351 AGCAAAATTTAAATGCAATTTTCTGATGTCGCTTAATACAACTCTGGAGAAAGTCTGG 1410
Db 993 AGCAAAATTTAAATGCAATTTTCTGATGTCGCTTAATACAACTCTGGAGAAAGTCTGG 1052

Qy 1411 AGTAGCTACAAAATTTGTAGAAAATTTCTCGAAAATCATCATTTGGAACTGTTAAATCA 1470
Db 1053 AGTAGCTACAAAATTTGTAGAAAATTTCTCGAAAATCATCATTTGGAACTGTTAAATCA 1112

Qy 1471 TCGATTCAATTTGTCATTTGATGATTTCTATATCGAAATAAAACAAATTAATCATTTAA 1529
Db 1113 TCGATTCAATTTGTCATTTGATGATTTCTATATCGAAATAAAACAAATTAATCATTTAA 1171

RESULT 2
DQ051956 2214 bp DNA linear GSS 02-JUN-2005
LOCUS Pan troglodytes HC19996 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION DQ051956
VERSION DQ051956.1 GI:66905369
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
REFERENCE 1. (bases 1 to 2214)
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fedel-Alon, A., Tanenbaum, D.M., Civeillo, D.,
White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(er) PLoS Biol. 3 (6), E170 (2005) X
JOURNAL PLoS Biol. 3 (6), E170 (2005) X
PUBMED 15869325
REFERENCE 2. (bases 1 to 2214)
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fedel-Alon, A., Tanenbaum, D.M., Civeillo, D.,
White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA X
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
FEATURES Location/Qualifiers
source 1. .2214
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>2214
/locus_tag="HC19996"

gene
ORIGIN

Query Match 72.3%; Score 1111.2; DB 11; Length 2214;
Best Local Similarity 98.0%; Pred No. 1.4e-242;
Matches 1116; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 391 TCATATCTGTTCTCTAAATGCCAAACGACAGGGTGAATTTTGCATTTTAAATAT 450
Db 33 TCAGATTCTGTTCTCTAAATGCCAAACGACAGGGTGAATTTTGCATTTTAAATAT 92

Qy 451 GAAGAAGTGAACACAGACAGAAAATAATGAAGTGAACAAAATCACTGCAGATTGTC 510
Db 93 GAAGAAGTGAACACAGACAGAAAATAATGAAGTGAACAAAATCACTGCAGATTGTC 152

Qy	511	TAAGGCAAGAACCAATTTTCAGTATATAGAACCAATCATTTGAGAAAAGCCATC	570
Db	153	TANGGCAAGGAACCAATTTTCAGTATATAGAACCAATCATTTGAGAAAAGCCATC	212
Qy	571	ACTTTTCATCAAGAAAGAAATAGATAATCTTGTGCTTCCAGATTGTTGGAATGAAAACA	630
Db	213	ACTTTTCATCAAGAAAGAAATAGATAATCTTGTGCTTCCAGATTGTTGGAATGAAAACA	272
Qy	631	AGCAATTTATGTTTACAGAACAAATCAAAATGCTTGAATAAAAAGAGTAAATTAGGATG	690
Db	273	AGCAATTTATGTTTACAGAACAAATCAAAATGCTTGAATAAAAAGAGTAAATTAGGATG	332
Qy	691	TAAGGATTTTCAGCAGTTTCGGCATTTGGGATCGAAAGCAGAAAAGCATGTCATGTGTC	750
Db	333	TAAGGATTTTCAGCAGTTTCGGCATTTGGGATTTGAAAGCAGAAAAGCATGTCATGTGTC	392
Qy	751	CAAGGAATGGATTCATATTTAGTAACCCCTAATGGCAGTAATAAATACTACTAGGCAAGC	810
Db	393	CAAGGAATGGATTCATATTTAGTAACCCCTAATGGCAGTAATAAATACTACTAGGCAAGC	452
Qy	811	TTCTCTACGAAAAAATAATAGGGAACATGATGTTTCTTAAAGCCCATGTTAAATTCAGGA	870
Db	453	TTCTCTACGAAAAAATAATAGGGAACATGATGTTTCTTAAAGCCCATGTTAAATTCAGGA	512
Qy	871	TTTGTTPAAGGAATCAACTAATGATTCATTTGTAATTTAGTGCATATAACAAATATAAA	930
Db	513	TTTGTTPAAGGAATCAACTAATGATTCATTTGTAATTTAGTGCATATAACAAATATAAA	572
Qy	931	AAATATTGATGCTACTGTAAAAGTTTTCATACACTGTTTACAGTTTGTAGTAAACCAATACAG	990
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Qy	991	ACCTTTATCTGATATTCAGGGGGCAAGAGAATTAACAGAAAAAATGAGAGGTAAATTG	1050
Db	632	ACCTTTATCTGATATTCAGGGGGCAAGAGAATTAACAGAAAAAATGAGAGGTAAATTG	692
Qy	1051	TTTAAATACAGTTTACAGTGCACAAAGATAGCAGAACATATTCGCAAAAGAAATGAAGAT	1110
Db	693	TTTAAATACAGTTTACAGTGCACAAAGATAGCAGAACATATTCGCAAAAGAAATGAAGAT	752
Qy	1111	GAAGATATTTAAGAAATATTATAGAGAGAGATGCAAAATCTGTATCATATTTGATGAGGC	1170
Db	753	GAAGATATTTAAGAAATATTATAGAGAGAGATGCAAAATCTGTATCATATTTGATGAGGC	812
Qy	1171	ATCTACAGTTTCAAGAAAAACCCCTAGTGAATTTATCTCCAGTGCAATTTAGTCAGC	1230
Db	813	ATCTACAGTTTCAAGAAAAACCCCTAGTGAATTTATCTCCAGTGCAATTTAGTCAGC	872
Qy	1231	TCCTGCACCTGTTATGTTATTTGTTGCTTTAAAAGAAATTTGGTGTCAACTATAGCAGATG	1290
Db	873	TCCTGCACCTGTTATGTTATTTGTTGCTTTAAAAGAAATTTGGTGTCAACTATAGCAGATG	932
Qy	1291	TATTGTCAATACATATTGACTACTTTAAATGATTGTTTAAATCAATGAATATTTGAA	1350
Db	933	TATTGTCAATACATATTGACTACTTTAAATGATTGTTTAAATCAATGAATATTTGAA	992
Qy	1351	AGCAAAATTTAATTCGATTTGTTCTGATGTTGCTTAATAACAACTGGGAGAAAGTCTGG	1410
Db	993	AGCAAAATTTAATTCGATTTGTTCTGATGTTGTTAATAACAACTGGGAGAAAGTCTGG	1052
Qy	1411	AGTAGCTACAAAATTTGTAGAAAATTTTCCTGAAATCATATTTGGAACCTGTTAAATCA	1470
Db	1053	AGTAGCTACAAAATTTGTAGAAAATTTTCCTGAAATCGTCAATTTTGGAACTGTTTAAATCA	1112
Qy	1471	TCGATTACAAATTTGTCACCTTGATGATTCATATCCGAAATAAAACAAATTAATCATTTAA	1529
Db	1113	TCGATTACAAATTTGTCACCTTGATGATTCATATCCGAAATAAAACAAATTAATCATTTAA	1171

RESULT 3
CX164545
LOCUS
DEFINITION HES2_18_A02_g1_A035 NIH_MGC_258 Homo sapiens cDNA clone

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

IMAGE:7467918 5', mRNA sequence.
CX164545
GI:56794625
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini,
Hominidae; Homo.
1 (bases 1 to 858)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-x@mail.nih.gov
Tissue Procurement: BresaGen, Inc.
cDNA Library Preparation: Express Genomics, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Laboratory for Genomics and Bioinformatics,
University of Georgia
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM15766 row: a column: 04
Seq primer: JENREV (CAGGAACAGCTATGACC)
High quality sequence stop: 858.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7467918"
/sex="male"
/tissue_type="human embryonic stem cells differentiated to
an early endodermal cell type"
/cell_type="human embryonic stem cells"
/cell_line="BG01"
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/clone_lib="NIH_MGC_258"
/notes="Vector: pExpress-1; Site 1: NotI; Site 2: EcoRV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos and
differentiated to an early endodermal cell type. Cell line
id and NIH Registry designation is BG01. Positive for
GATA4, MixL1, Mx1, HNF4alpha expression; negative for AFP
expression. Passage number 40. cDNA primed using oligo-dT
primer: 5'-pGACTAGTCTAGATCGGCGGCCCTTT25-3' and
cloned into the EcoRV/NotI sites of pExpress-1. This
primary library is non-normalized (normalized primary
library is NIH_MGC_259). It was constructed by Express
Genomics (Frederick, MD). Sequence ends have been trimmed
to exclude vector and regions below phred quality 16.
Three-prime sequences are presented as their reverse
complement and have been trimmed to exclude polyA. Note:
this is a Mammalian Gene Collection library."

ORIGIN

Query Match 55.7%; Score 854.8; DB 8; Length 858;
Best Local Similarity 99.8%; Pred. No. 4.2e-184;
Matches 856; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 155 TCGCGCAGTAGGACAGCAGGAGCAGTGCTGCTCAGCGCGCGCTCGGAGACATGGGA 214
Db 1 TCGCGCAGTAGGACAGCAGGAGCAGTGCTGCTCAGCGCGCGCTCGGAGACATGGGA 60
Qy 215 GACCCGGGGTCGGAATAATAGATATCTCCCTCAGCTGGCCCTGAGGCATCTGAGTCA 274
Db 61 GACCCGGGGTCGGAATAATAGATATCTCCCTCAGCTGGCCCTGAGGCATCTGAGTCA 120
Qy 275 AACACGATGAAATGAAGACGACATTCAGTTTCTCAGTGAAGGACCATCGAGACCTGTT 334

Db	121	ACACCGGATGAAATGAAGACGACATTCAGTTTGTCACTGAAGGACCATCGAGACCTGTT	180
Qy	335	CTTGAATACATCGATCTGGTCTGGTGATGATGAAGAACCCCTAGCGCTATATATAGTGAT	394
Db	181	CTTGAATACATCGATCTGGTCTGGTGATGATGAAGAACCCCTAGCGCTATATATAGTGAT	240
Qy	395	ATTCTGTTTCTTAAATGCCAAACGACAGGGGTGATTTTTCATATTTTAAATATGAAG	454
Db	241	ATTCTGTTTCTTAAATGCCAAACGACAGGGGTGATTTTTCATATTTTAAATATGAAG	300
Qy	455	AAGGTGAAACAGACACAGAAATATGAAGTGAGCAAAATCACTGCAGATTTGTCTAAG	514
Db	301	AAGGTGAAACAGACACAGAAATATGAAGTGAGCAAAATCACTGCAGATTTGTCTAAG	360
Qy	515	GCAAGGACACATTTCCGATGATATAGACACCAATCACTTGAAGAAAGCCATCACTT	574
Db	361	GCAAGGACACATTTCCGATGATATAGACACCAATCACTTGAAGAAAGCCATCACTT	420
Qy	575	TCATCAAGAAAGAAATAGATATCTTGTCTTCCAGATTTGTGAATGAAACCAAGCA	634
Db	421	TCATCAAGAAAGAAATAGATATCTTGTCTTCCAGATTTGTGAATGAAACCAAGCA	480
Qy	635	TTTATGTTTACAGAACATACAAATGGCTTTGAAATGAAAGAGGTAAATTAGGATGTAAG	694
Db	481	TTTATGTTTACAGAACATACAAATGGCTTTGAAATGAAAGAGGTAAATTAGGATGTAAG	540
Qy	695	GATGTTTCAGAGTTGCGGATTTGGATCGAAAGCAGAAACATGTCATGTGCCAAG	754
Db	541	GATGTTTCAGAGTTGCGGATTTGGATCGAAAGCAGAAACATGTCATGTGCCAAG	600
Qy	755	GATGATGTCATATTTAGTACCCCTAATGCGCAGTAAATAAACTACTAGGCAAGCTTCT	814
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Qy	815	CTACGAAAGAAATAGGGAACATGATGTTTCTTAAAGCCCATGTTAAATTCAGGATTTG	874
Db	661	CTACGAAAGAAATAGGGAACATGATGTTTCTTAAAGCCCATGTTAAATTCAGGATTTG	720
Qy	875	TTAAAGGAATCAACTAATGATTCATTTGTAATTTAGTGCATAAACAAATTAATAAAT	934
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Qy	935	ATTGATGCTACTGTAAGGTTTCAATGTTTCAATGTTTCAATGTTTCAATGTTTCAATG	994
Db	781	ATTGATGCTACTGTAAGGTTTCAATGTTTCAATGTTTCAATGTTTCAATGTTTCAATG	840
Qy	995	TTATCTGATATTGAGGGG 1012	
Db	841	TTATCTGATATTGAGGGG 858	

RESULT 4
BO230874
LOCUS BO230874 1006 bp mRNA linear EST 02-MAY-2002
DEFINITION AGENCOURT_7260801 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5785266
5', mRNA sequence.
ACCESSION BO230874
VERSION BO230874.1 GI:20412274
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1006)
NIH-MGC <http://mgc.ncl.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LHAM12872 row: b column: 19
High quality sequence stop: 647.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5785266"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site: 1; NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.1 kb."

ORIGIN	Query Match	54.3%	Score 834.4;	DB 3;	Length 1006;
	Best Local Similarity	95.9%	Pred. No. 1.9e-179;		
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Qy	41	TGCCCCCTCTTTTGAAGCGGTTTTCGTCTCTCTTCCGCCAGTGGCCTCCAGAGCTCAGCGAGG	100		
Db	1	TGCCCCCTCTTTTGAAGCGGTTTTCGTCTCTCTTCCGCCAGTGGCCTCCAGAGCTCAGCGAGG	60		
Qy	101	GGCGGGTCCCAGTAGCGAGCGGTGAGGGCGGGAAGGGGAGTGGTGGCGGCTCGCGC	160		
Db	61	GGCGGGTCCCAGTAGCGAGCGGTGAGGGCGGGAAGGGGAGTGGTGGCGGCTCGCGC	120		
Qy	161	AGTAGGGACAGCAGCAGCAGTGGTCTCTCAGCGCGCGCTCGGAGACATCGGAGACCCG	220		
Db	121	AGTAGGGACAGCAGCAGCAGTGGTCTCTCAGCGCGCGCTCGGAGACATCGGAGACCCG	180		
Qy	221	GGGTCCGAAATTAATAAGAACTCTGCTCCCTCAGCTGGCCCTCGAGGCATCTGAGTCAACAACG	280		
Db	181	GGGTCCGAAATTAATAAGAACTCTGCTCCCTCAGCTGGCCCTCGAGGCATCTGAGTCAACAACG	240		
Qy	281	GATGAAATTAAGACGACATTCAGTTTGTCTAGTGAAGACCAATCGAGACCTGTTCTTGA	340		
Db	241	GATGAAATTAAGACGACATTCAGTTTGTCTAGTGAAGACCAATCGAGACCTGTTCTTGA	300		
Qy	341	TACATCGATCTGCTGTTGATGATGAAACCCCTAGCGCTATATATAGTATATCTG	400		
Db	301	TACATCGATCTGCTGTTGATGATGAAACCCCTAGCGCTATATATAGTATATCTG	360		
Qy	401	TTTCTCTAAATGCGCAAAACGACAGGGTGATTTTTCATATTTTAAATATGAAGAGGTG	460		
Db	361	TTTCTCTAAATGCGCAAAACGACAGGGTGATTTTTCATATTTTAAATATGAAGAGGTG	420		
Qy	461	AAAAACAGACACAGAAATAATGAAGTGAAGCAAAATCACTGCAGATTTGCTAAGCAAG	520		
Db	421	AAAAACAGACACAGAAATAATGAAGTGAAGCAAAATCACTGCAGATTTGCTAAGCAAG	480		
Qy	521	GAACACATTTTCAGTATATAGAAACCAATCATTTGAAGAAAGCCATCATCTTCATCA	580		
Db	481	GAACACATTTTCAGTATATATGAACCAATCATTTGAAGAAAGCCATCATCTTCATCA	540		
Qy	581	AGAAAGAAATAGATAATCTTCTGCTCCAGATTTGTTGAATGAAATGAAACCAAGCATTTATG	640		
Db	541	AGAAAGAAATAGATAATCTTCTGCTCCAGATTTGTTGAATGAAATGAAACCAAGCATTTATG	600		
Qy	641	TTTACAGAAACATACAAATGGCTTGAAATTAAGAAAGGTAAATAGGATGTAAGGATTTG	700		
Db	601	TTTACAGAAACATACAAATGGCTTGAAATTAAGAAAGGTAAATAGGATGTAAGGATTTG	660		
Qy	701	TCAGAGTTTCGGCATTTGGATTCGAAAGCAGAAAGCATGTCATGTTGTCGAAGGATG	760		
Db	661	TCAGAGTTTCGGCATTTGGATTCGAAAGCAGAAAGCATGTCATGTTGTCGAAGGATG	720		


```
REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC#1664 row: d column: 24
High quality sequence stop: 691.
FEATURES
source
1..691
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:4809575"
/tissue_type="mucoepidermoid carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 59"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcgcc); Site_2: SfiI (ggccattggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGGCGCATATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGGCGGCGGCGCATG-dt(30)BN-3'
(where B = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."
ORIGIN
Query Match 43.7%; Score 671.6; DB 2; Length 691;
Best Local Similarity 99.3%; Pred. No. 2.7e-142;
Matches 685; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 175 GAGCAGTGTGTCTGTCAGCGCGGCGTGGAGACATGGAGACCGGGTGGGAATAT 234
DB 1 GAGCAGTGTGTCTGTCAGCGCGGCGTGGAGACATGGAGACCGGGTGGGAATAT 60
QY 235 AGAATCTGCTCCAGTGGCCCTGAGGCATCTGATCAACACGGATGAAATGAAGA 294
DB 61 AGAATCTGCTCCAGTGGCCCTGAGGCATCTGATCAACACGGATGAAATGAAGA 120
QY 295 CGACATTCAGTTTGTTCAGTGAAGGACCAATCGAGACCTGTTTGAATACATCTGG 353
DB 121 CGACATTCAGTTTGTTCAGTGAAGGACCAATCGAGACCTGTTTGAATACATCTGG 180
QY 354 TCTGTGGTATGATGAAGAACCTTAGCCCTATTATAGTATATCTGTTCTTAAATGC 413
DB 181 TCTGTGGTATGATGAAGAACCTTAGCCCTATTATAGTATATCTGTTCTTAAATGC 240
QY 414 CAAACAGCAGCGGTGATTTTGTGCAATTTTAAATGAAGGTGAAACAGACACAG 473
DB 241 CAAACAGCAGCGGTGATTTTGTGCAATTTTAAATGAAGGTGAAACAGACACAG 300
QY 474 AAAATAATGAAGTGAACAAAATCACTGAGATTTGTCTAAGCAAGGAACCAATTCG 533
DB 301 AAAATAATGAAGTGAACAAAATCACTGAGATTTGTCTAAGCAAGGAACCAATTCG 360
QY 534 AGTATATAGAACCAACCAATCATTGAAGAAAGCCATCATCTTCATCAAGAAAGAAATAG 593
DB 361 AGTATATAGAACCAACCAATCATTGAAGAAAGCCATCATCTTCATCAAGAAAGAAATAG 420
QY 594 ATAATCTCTGCTCCAGATTTGTGAATGAAGAAACCAAGCATTTATGTTTACAGAACAT 653
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Db 421 ATAAATCTGTGCTTCCAGATTGTTGGAATGAAAAACAAGCATTTATGTTTACAGAACAT 480
QY 654 ACAAATGCTTGAATTAATAAGAAAGTAAATTTAGGATGTAAGGATTTGTTTACAGATTCGGC 713
Db 481 ACAAATGCTTGAATTAATAAGAAAGTAAATTTAGGATGTAAGGATTTGTTTACAGATTCGGC 540
QY 714 ATTTGGGATCGAAAGCAGAAAGCATGTCCATGTGTCCAGGAATGGATTCATATTTAG 773
Db 541 ATTTGGGATCGAAAGCAGAAAGCATGTCCATGTGTCCAGGAATGGATTCATATTTAG 600
QY 774 TAACCCCTAATGGCAGTAATAAACTACTAGGCAAGCTTCTTACGAAAAAATTTAGGG 833
Db 601 TAACCCCTAATGGCAGTAATAAACTACTAGGCAAGCTTCTTACGAAAAAATTTAGGG 660
QY 834 AACATGATGTTTCTAAAGCCCATGTAATA 863
Db 661 AACATGATGTTTCTAAAGCCCATGTAATA 690

RESULT 7
DN999300
LOCUS DN999300
DEFINITION DN999300 682 bp mRNA linear EST 17-MAY-2005
TCT121030 Human endothelial cells, large insert, pCMV expression
library Homo sapiens cDNA clone TCT121030 5' similar to PREDICTED:
Homo sapiens KIAA1586 (KIAA1586), mRNA sequence.
ACCESSION DN999300 GI:66259127
VERSION DN999300.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 682)
Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L.,
Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M.,
Zhang,X., Jay,G. and He,W.
High-throughput cloning of full-length human cDNAs directly from
cDNA libraries optimized for large and rare transcripts
Unpublished (2005)
Contact: Kovacs, KF
High throughput cDNA Cloning
Origene Technologies, Inc. ( www.origene.com )
6 Taft Court, Suite 100, Rockville, MD 20850, USA
Tel: 301 340 3188
Fax: 301 340 8606
Email: cdna@origene.com
This EST submission is part of an on-going human full-length
cloning project at Origene Technologies, Inc.
Please contact Origene for access.
Origene Technologies, Inc.
6 Taft Ct. Suite 100
Rockville, MD 20850
Tel: (301) 340-3188
http://www.origene.com
Seq primer: pCMV6 Sprime forward vector primer, Origene
Technologies Inc.
Location/Qualifiers
1..682
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TCT121030"
/cell_type="Endothelial cells"
/clone_lib="Human endothelial cells, large insert, pCMV
expression library"
/note="Vector: pCMV6-XL6; Site 1: EcoRI; Site 2: XhoI/Sall
compatible end ligatio; Oligo-dT primed reverse
transcription optimized for large and GC rich mRNA
transcripts, cDNA size selection, optimized ligation for
large inserts into mammalian expression vector, random
clones selected for end sequence verification of
full-length genes"
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ORIGIN

Query Match 43.0%; Score 660; DB 8; Length 682;
Best Local Similarity 99.3%; Pred. No. 1.2e-139;
Matches 663; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 129 AGGCGGGAAGGAGTGGTGGCGGCTGGCGGAGTGGGACAGCAGGAGCAGTGGTCTG 188
Db 8 AGGCGGGAAGGAGTGGTGGCGGCTGGCGGAGTGGGACAGCAGGAGCAGTGGTCTG 67
Qy 189 TCAGCGCGGCTCGGAGACATGGGAGACCGGGTCCGGAATAATAGATCTGTCCCTC 248
Db 68 TCAGCGCGGCTCGGAGACATGGGAGACCGGGTCCGGAATAATAGATCTGTCCCTC 127
Qy 249 CAGTGGCCCTGAGGCATCTGAGTCAACAACGGATGAAATGAAGACGACATTCAGTTTG 308
Db 128 CAGTGGCCCTGAGGCATCTGAGTCAACAACGGATGAAATGAAGACGACATTCAGTTTG 187
Qy 309 TCAGTGAAGGACCATCAGACCTGTTCTTGAATACATCGATCTGCTGTGGTGAATG 368
Db 188 TCAGTGAAGGACCATCAGACCTGTTCTTGAATACATCGATCTGCTGTGGTGAATG 247
Qy 369 AARACCTAGCGCTATTATAGTATCTGTTCTTAAATGCCAAACGACAGGCTG 428
Db 248 AARACCTAGCGCTATTATAGTATCTGTTCTTAAATGCCAAACGACAGGCTG 307
Qy 429 ATTTTTCGCAATTTTAAATATGAAGAGGTGAAACACAGACACAGAAATAATGAAGTGA 488
Db 308 ATTTTTCGCAATTTTAAATATGAAGAGGTGAAACACAGACACAGAAATAATGAAGTGA 367
Qy 489 GCAAAATCACTGAGATTTGTGTAAGGCAAGGACACACATTCGAGTATATGAACAAC 548
Db 368 GCAAAATCACTGAGATTTGTGTAAGGCAAGGACACACATTCGAGTATATGAACAAC 427
Qy 549 CAATCATTTGAAGAAAGCCATCACTTTTCATCAAGAAAGAAATAGATAATCTTGCTTC 608
Db 428 CAATCATTTGAAGAAAGCCATCACTTTTCATCAAGAAAGAAATAGATAATCTTGCTTC 487
Qy 609 CAGATTGTGGAATGAAACCAAGCATTTATGTTTACAGAACCAATACAAATGGCTTGA 668
Db 488 CAGATTGTGGAATGAAACCAAGCATTTATGTTTACAGAACCAATACAAATGGCTTGA 547
Qy 669 TAAAGAGGTAAATAGGATGTAAGGATGTTTCAGCAGATTCGGCATTTGGATCGAAG 728
Db 548 TAAAGAGCGTAAATAGGATGTAAGGATGTTTCAGCAGATTCGGCATTTGGATCGAAG 607
Qy 729 CAGAAAGCATGTCATGTTGCCAAGGATGATGATATTTAGTAAACCCCTAATGGCA 788
Db 608 CAGAAAGCATGTCATGTTGCCAAGGATGATGATATTTAGTAAACCCCTAATGGCA 667
Qy 789 GTAATAAA 796
Db 668 GTAATAAA 675

RESULT 8
BI465045
LOCUS 603206445F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5272042 5',
DEFINITION mRNA sequence.
ACCESSION BI465045
VERSION BI465045.1 GI:15255701
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 701)
NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11686 row: j column: 11
High quality sequence stop: 700.

FEATURES
source

1..701
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5272042"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/notes="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTN-3', size-selected for average
insert size 2.2 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN

Query Match 42.1%; Score 646.8; DB 3; Length 701;
Best Local Similarity 99.1%; Pred. No. 1.2e-136;
Matches 692; Conservative 0; Mismatches 2; Indels 4; Gaps 4;

Qy 2 GAGAAAGAGGCTCCGGGAGATAGCGACCCAGTGAGGGCTGCCCTCTTTTGAAGCGGTT 61
Db 8 GAGAAAGAGGCTCCGGGAGATAGCGACCCAGTGAGGGCTGCCCTCTTTTGAAGCGGTT 67
Qy 62 TTCGTCTCTTTCCGCCAGTGGCTCCAGCTCAACGAGGGCGGGTCCCGTAGCGCGAG 121
Db 68 TTCGTCTCTTTCCGCCAGTGGCTCCAGCTCAACGAGGGCGGGTCCCGTAGCGCGAG 127
Qy 122 GCGGTGACAGGCGGGAAGGGAGTGTGGCGCTGGCGCAGTAGGACACAGCAGGAGCAGT 181
Db 128 GCGGTGACAGGCGGGAAGGGAGTGTGGCGCTGGCGCAGTAGGACACAGCAGGAGCAGT 187
Qy 182 GGTGCTGTGACGCGCGCGCTCGGAGACATGGGAGACCCCGGGTCCGGAATAATAGAACTCT 241
Db 188 GGTGCTGTGACGCGCGCGCTCGGAGACATGGGAGACCCCGGGTCCGGAATAATAGAACTCT 246
Qy 242 GTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACACCGATGAAATGAAGACGACATT 301
Db 247 GTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACACCGATGAAATGAAGACGACATT 306
Qy 302 CAGTTTGTGACGAGACCATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGGT 361
Db 307 CAGTTTGTGACGAGACCATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGGT 366
Qy 362 GATGATGAAACCCCTAGCGCTATTATAGTGATATCTGTTTCTTAAATGCCAAACGA 421
Db 367 GATGATGAAACCCCTAGCGCTATTATAGTGATATCTGTTTCTTAAATGCCAAACGA 426
Qy 422 CAGGCTGATTTTTTGCATTTTTTAAATATGAAGAGGTGAAACACAGACAGAAAAATAAT 481
Db 427 CAGGCTGATTTTTTGCATTTTTTAAATATGAAGAGGTGAAACACAGACAGAAAAATAAT 486
Qy 482 GAAGTGAAGAAAAATCACTGAGATTTGCTTAAGGCAAGGACACACATTTTCGAGTATATA 541
Db 487 GAAGTGAAGAAAAATCACTGAGATTTGCTTAAGGCAAGGACACACATTTTCGAGTATATA 546
Qy 542 GAACACCAATCATTTGAAGAAAGCCATCACTTTTCATCAAGAAAGAAATAGATAATCTTT 601

QY 610 AGATTGTTGGAAATGAAACCAAGCAATTTATGTTTACAGAACAAATACAAATGGCTTGAAT 669
DB 424 AGATTGTTGGAAATGAAACCAAGCAATTTATGTTTACAGAACAAATACAAATGGCTTGAAT 483
QY 670 AAAAGAAGGTAAATAGGATTAAGGATGTTTTCAGAGTTTCGGCAATTTGGGATCGAAAGC 729
DB 484 AAAAGAAGGTAAATAGGATTAAGGATGTTTTCAGAGTTTCGGCAATTTGGGATCGAAAGC 543
QY 730 AGAAAGCATGTCATGTTGTCACAGGATGGAATTCATATTTAGTAACCCCTTAATGGCAG 789
DB 544 AGAAAGCATGTCATGTTGTCACAGGATGGAATTCATATTTAGTAACCCCTTAATGGCAG 603
QY 790 TAATAAACTACTAGGCAAGCTTCTCTACGAAAAAAATTT 829
DB 604 TAATAAACTACTAGGCAAGCTTCTCTACGAAAAAAATTT 643

RESULT 12
BM352924
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM352924 627 bp mRNA linear EST 07-JAN-2002
ig69a09.y1 HR85 islet Homo sapiens cDNA 5' similar to TR:Q9Y4E5
Q9Y4E5 KIAA0576 PROTEIN ;, mRNA sequence.
BM352924
BM352924.1 GI:18085282
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 627)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Bliscain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, Y., McCann, R., Cole, R., Teagareishvili, R.,
Williams, T., Jackson, M., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: ig69a09.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Glibco
High quality sequence stop: 481.
Location/Qualifiers
1. .627
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="Purified pancreatic islet"
/lab_host="PH108"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size: selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

FEATURES
source

RESULT 13
BG944466
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BG944466 616 bp mRNA linear EST 15-JAN-2003
ax50g10.x2 Hembase; Erythroid Progenitor Cells (LCB:ax library)
Homo sapiens cDNA clone ax50g10 random, mRNA sequence.
BG944466
BG944466.1 GI:14343838
EST.
Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

1 (bases 1 to 616)
Gubin, A.N., Njorge, J.M., Bouffard, G.G. and Miller, J.L.
Gene expression in proliferating human erythroid cells
Genomics 59 (2), 168-177 (1999)
10409428
Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
20892, USA
Tel: 301 402 2373

Query Match 40.0%; Score 613.8; DB 3; Length 627;
Best Local Similarity 99.7%; Pred. No. 4.1e-129;
Matches 615; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 217 CCCGGGTGCGAAATATAGAAATCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAAC 276
DB 11 CCCGGGTGCGAAATATAGAAATCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAAC 70
QY 277 AACGSGATGAAATGAAGACGACATTCAGTTGTGTGAGTGAAGAACCCCTGAGGCATCTGAGTCAAC 336
DB 71 AACGSGATGAAATGAAGACGACATTCAGTTGTGTGAGTGAAGAACCCCTGAGGCATCTGAGTCAAC 130
QY 337 TGAATACATCGATCTGTGTCGTGATGATGAAGAACCCCTGAGGCATCTGAGTCAAC 396
DB 131 TGAATACATCGATCTGTGTCGTGATGATGAAGAACCCCTGAGGCATCTGAGTCAAC 190
QY 397 TCTGTTTCTTAAATGCCAAACGACAGGGTGATTTTTTGCATTTTTTAAATATGAAGAA 456
DB 191 TCTGTTTCTTAAATGCCAAACGACAGGGTGATTTTTTGCATTTTTTAAATATGAAGAA 250
QY 457 GGTGAAACACACACAGACAGAAATATGAAGTGCAGCAAAATCACTGCAGATTTGTCTAAGGC 516
DB 251 GGTGAAACACACACAGACAGAAATATGAAGTGCAGCAAAATCACTGCAGATTTGTCTAAGGC 310
QY 517 AAAGGAACACATTTTCGAGTATATAGAAACACCAATCATTTGAAGAAAGCCATCTTTC 576
DB 311 AAAGGAACACATTTTCGAGTATATGAAGAACCAATCATTTGAAGAAAGCCATCTTTC 370
QY 577 ATCAAGAAAGAAATAGATTAATCTTGTGCTTCCAGATTTGTTGGAATGAAAGCAAGCAT 636
DB 371 ATCAAGAAAGAAATAGATTAATCTTGTGCTTCCAGATTTGTTGGAATGAAAGCAAGCAT 430
QY 637 TATGTTTACAGCAACAATCAAAATGCTTGAATTAAGAAAGCAAGTAAATTAGGATGTAAGCA 696
DB 431 TATGTTTACAGCAACAATCAAAATGCTTGAATTAAGAAAGCAAGTAAATTAGGATGTAAGCA 490
QY 697 TTGTTTACAGCAGTTTCGGCATTTGGGATCGAAAGCAAGCAAGCATGTCATGTTCCAAAGCA 756
DB 491 TTGTTTACAGCAGTTTCGGCATTTGGGATCGAAAGCAAGCAAGCATGTCATGTTCCAAAGCA 550
QY 757 ATGAGTTTCATATTTAGTAACCCCTTAATGCGAGTAAATAAACTACTAGGCAGCTTCTCT 816
DB 551 ATGAGTTTCATATTTAGTAACCCCTTAATGCGAGTAAATAAACTACTAGGCAGCTTCTCT 610
QY 817 ACGAAAAAATTTAGGG 833
DB 611 ACGAAAAAATTTAGGG 627

ORIGIN

Fax: 301 435 5148
 Email: jmf@nih.gov
 DNA Sequencing and analyses by National Institutes of Health
 Intramural Sequencing Center (NISC).
 Plate: 50 row: 9 column: 10
 Seq primer: -21M13 forward primer (ABI).
 Location/Qualifiers
 1. .616
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="ax50gl0"
 /sex="unknown"
 /tissue_type="blood"
 /cell_type="Erythroid Cells"
 /cell_line="Primary Culture of Peripheral Blood Mononuclear Cells"
 /dev_stage="Progenitor; EPO responsive CD71++++"
 /lab_host="SOLR"
 /clone_lib="Hembase; Erythroid Progenitor Cells (LCB:ax library)"
 /note="Organ: blood; Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: EcoRI; 65,000 proliferating erythroid cells from the Buffy coat of a blood donation were obtained by flow cytometric separation after a 5-day culture period in the presence of erythropoietin. Total RNA was purified from the sorted cell population using Trizol reagent. RNA (0.3 ug) was converted into double stranded cDNA using Clontech's CapFinder cDNA Library Construction Kit (Clontech) according to the manufacturer's protocol and cloned into EcoRI digested Lambda Zap II vector (Stratagene). The phage library was amplified once prior to in vivo excision in SOLR cells. Individual colonies were grown, and the cDNA inserts were sequenced in high throughput (NIH intramural sequencing center http://www.nisc.nih.gov/)."

ORIGIN

Query Match 39.7%; Score 609.6; DB 2; Length 616;
 Best Local Similarity 99.4%; Pred. No. 3.7e-128;
 Matches 612; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

300 TTCAAGTTGTCAGTGAAGGACCATCGAGACCTGTTCTTGATATCATCGATCGTCTGTG 359
 1 TTCAAGTTGTCAGTGAAGGACCATCGAGACCTGTTCTTGATATCATCGATCGTCTGTG 60

360 GTGATGATGAAAAACCCCTAGCGCCCTATTATAGTGATATTCCTTTCTTAAATGCCAAAC 419
 61 GTGATGATGAAAAACCCCTAGCGCCCTATTATAGTGATATTCCTTTCTTAAATGCCAAAC 120

420 GACAGGGTGATTTTTTGCATTTTTTAAATATGAAAGAGTGAAACGACACAGAAATA 479
 121 GACAGGGTGATTTTTTGCATTTTTTAAATATGAAAGAGTGAAACGACACAGAAATA 180

480 ATGAAGTGACAAAAATCACATGCGATGTTCTAGGCAAGGACCAATTCAGATATA 539
 181 ATGAAGTGACAAAAATCACATGCGATGTTCTAGGCAAGGACCAATTCAGATATA 240

540 TAGAACACCAATCATTTGAAGAAAGCCATCACATTTTCATCAAGAAAGAAATAGATAATC 599
 241 TTGAACACCAATCATTTGAAGAAAGCCATCACATTTTCATCAAGAAAGAAATAGATAATC 300

600 TTGTCCTTCCAGATTGTTGGAATGAAAAACAAGCATTTATGTTTACAGAAACAATACAAAT 659
 301 TTGTCCTTCCAGATTGTTGGAATGAAAAACAAGCATTTATGTTTACAGAAACAATACAAAT 360

660 GGCTTGAATTAAGAAGGTAAATAGGATCTAGGATTTGTTTCAGCAGTTCGGCATTTGG 719
 361 GGCTTGAATTAAGAAGGTAAATAGGATCTAGGATTTGTTTCAGCAGTTCGGCATTTGG 420

720 GATCAAAAGCAGAAAGCATGTCCATGTGTCCAGGAATGGATTTGATATTTAGTAACCC 779
 421 GATCAAAAGCAGAAAGCATGTCCATGTGTCCAGGAATGGATTTGATATTTAGTAACCC 480

Qy 780 CTAATGGCAGTAATAAACTACTAGCAAGCTTCTTACGAAAAAAATTTAGGACATG 839
 Db 481 CTAATGGCAGTAATAAACTACTAGCAAGCTTCTTACGAAAAAAATTTAGGACATG 540
 Qy 840 ATGTTTCTAAAGCCCATGGTAAATTCAGGATTTGTTAAAGGAATCAACTAATGATTCAA 899
 Db 541 ATGTTTCTAAAGCCCATGGTAAATTCAGGATTTGTTAAAGGAATCAACTAATGATTCAA 600
 Qy 900 TTTGTAATTTAGTGCA 915
 Db 601 TTTGTAATTTAGTGCA 616

RESULT 14

BF667883
 LOCUS 602122117F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4279180 5',
 DEFINITION mRNA sequence.

ACCESSION BF667883.1 GI:11941778

VERSION BF667883

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1 (bases 1 to 768)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LICM1104 row: a column: 05

High quality sequence stop: 678.

FEATURES

source

1. .768
 /location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4279180"
 /tissue_type="primitive neuroectoderm"
 /lab_host="DH10B (Ti phage-resistant)"
 /clone_lib="NIH_MGC_56"
 /notes="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
 SfiI (ggcgctcgcc); Site_2: SfiI (ggccattatggcc);
 Double-stranded cDNA was prepared from cell line RNA.
 5' and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGCCATTATGCGC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dT(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 39.2%; Score 602.6; DB 2; Length 768;
 Best Local Similarity 92.7%; Pred. No. 1.5e-126;
 Matches 665; Conservative 0; Mismatches 49; Indels 3; Gaps 3;

Qy 149 GCGCGCTCGGCAGTAGGACAGCAGCAGCAGTGTGCTGTCTGTCAGCGCGCGTGGAGAC 208
 Db 1 GCGCGCTCGGCAGTAGGACAGCAGCAGCAGTGTGCTGTCTGTCAGCGCGCGTGGAGAC 60
 Qy 209 ATGGGAGACCGGGGTCCGAAATAATAGAATCTGTCCCTCCA-GCTGGCCCTGAGGCATC 267

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Db      61  ATGGGAGACCGGGTCGGAATAATAGAAATCTGCTCCCTCCAGGCTGGCCCTGAGGCATC 120
Qy      268  TGAGTCAACACGAGTGAATAATGAAGACGACATTCAGTTTGTCTAGTGAAGGACCATCGAG 327
Db      121  TGAGTCAACACGAGTGAATAATGAAGACGACATTCAGTTTGTCTAGTGAAGGACCATCGAG 180
Qy      328  ACCTGTTCTTGAATACATCGATCTGCTGCTGCTGATGATGATGATGATGATGATGATGAT 387
Db      181  ACCTGTTCTTGAATACATCGATCTGCTGCTGCTGATGATGATGATGATGATGATGATGAT 240
Qy      388  TAGTGATATTTCTGTTTCTTAAATGCAAAACGACAGGCTGATTTTTTGCATTTTTTAAA 447
Db      241  TAGTGATATTTCTGTTTCTTAAATGCAAAACGACAGGCTGATTTTTTGCATTTTTTAAA 300
Qy      448  TATGAAGAGGTGAACACAGACACAGACAAATATGAAGTGACAAAATCACTGCAGATT 507
Db      301  TGTGAAGAGGTGAACACAGACACAGACAAATATGAAGTGACAAAATCACTGCAGATT 360
Qy      508  GTCTAAGGCAAGGAACCACTTTGAGTATATAGAACCAACCAATCATTTGAAGAAAGCC 567
Db      361  GTCTAAGGCAAGGAACCACTTTGAGTATATATGAACCAACCAATCATTTGAAGAAAGCC 420
Qy      568  ATCACTTTTCATCAAGAAAGAAATAGATAATCTTGTCTTCAGATTTGTTGGAATCAAAA 627
Db      421  ATCACTTTTCATCAAGAAAGAAATAGATAATCTTGTCTTCAGATTTGTTGGAATCAAAA 480
Qy      628  ACAAGCATTTATGTTTACAGACATACAAATGGCTTGAATTAAGAAAGGTAAATTAGG 687
Db      481  ACAAGCATTTATGTTTACAGACATACAAATGGCTTGAATTAAGAAAGGTAAATTAGG 540
Qy      688  ATGTAAGGATTTCTCAGCAGTTTCGGCATTTGGGATCGAAGCAGACAAAGCATGTCATGT 747
Db      541  ATGTAAGGATTTCTCAGCAGTTTCGGCATTTGGGATCGAAGCAGACAAAGCATGTCATGT 600
Qy      748  GT-CCAAGGAATGGATTGCATATTTAGTAACCCC-TAATGGCAGTAATAAAACTACTAGG 805
Db      601  GTCCCAAGGAATGGATTGCATATTTAGTAACCCC-TAATGGCAGTAATAAAACTACTAA 660
Qy      806  CAAAGCTTCTCAGAAAAAAATTTAGGGAAACATGATGTTTCTTAAAGCCCATGGTAAA 862
Db      661  GCAAGTTCTCTACGAAAAAAATTTGCGACCTGATGTTTCTTAAAGCCCATGGTAAA 717
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RESULT 15
BG942992
LOCUS      586 bp mRNA linear EST 15-JAN-2003
DEFINITION Homo sapiens cDNA clone ax32c07 random, mRNA sequence.
ACCESSION BG942992
VERSION   BG942992.1 GI:14342364
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Homnidae; Homo.
REFERENCE 1 (bases 1 to 586)
AUTHORS   Gubin,A.N., Njoroge,J.M., Bouffard,G.G. and Miller,J.L.
TITLE     Gene expression in proliferating human erythroid cells
JOURNAL   Genomics 59 (2), 168-177 (1999)
PUBMED    10409428
```

```
COMMENT   Contact: Jeffery L. Miller
           Laboratory of Chemical Biology
           National Institute of Diabetes and Digestive and Kidney Diseases
           Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
           20892, USA
           Tel: 301 402 2373
           Fax: 301 435 5148
           Email: jml7@nih.gov
           DNA Sequencing and analyses by National Institutes of Health
           Intramural Sequencing Center (NISC).
           Plate: 32 row: c column: 07
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Seq primer: -21M13 forward primer (ABI).
FEATURES             Location/Qualifiers
     source            1..586
     organism="Homo sapiens"
     mol_type="mRNA"
     db_xref="taxon:9606"
     clone="ax32c07"
     sex="unknown"
     tissue_type="blood"
     cell_type="Erythroid Cells"
     cell_lines="Primary Culture of Peripheral Blood Mononuclear Cells"
     dev_stage="Progenitor; EPO responsive CD71++++"
     lab_host="SOLR"
     clone_lib="Hembase; Erythroid Progenitor Cells (LCB:ax library)"
     note="Organ: blood; Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: EcoRI; 65,000 proliferating erythroid cells from the buffy coat of a blood donation were obtained by flow cytometric separation after a 5-day culture period in the presence of erythropoietin. Total RNA was purified from the sorted cell population using TRIzol reagent. RNA (0.3 ug) was converted into double stranded cDNA using Clontech's CapFinder cDNA Library Construction Kit (Clontech) according to the manufacturer's protocol and cloned into EcoRI digested Lambda Zap II vector (Stratagene). The phage library was amplified once prior to in vivo excision in SOLR cells. Individual colonies were grown, and the cDNA inserts were sequenced in high throughput (NIH intramural sequencing center http://www.nisc.nih.gov/)."
ORIGIN
Query Match      37.9%; Score 581.8; DB 2; Length 586;
Best Local Similarity 99.7%; Pred. No. 8.2e-12;
Matches 583; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      164  AGGGACACGAGCAGTGCTGTCTCAGCGCGCGCTCGGAGACATGGGAGACCCGGGG 223
Db      2    AGGGACACGAGCAGTGCTGTCTCAGCGCGCGCTCGGAGACATGGGAGACCCGGGG 61
Qy      224  TCGGAAATTAATAGAAATCTGTCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACACGGAT 283
Db      62  TCGGAAATTAATAGAAATCTGTCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACACGGAT 121
Qy      284  GAAATGAAGACGACATTCAGTTTGTCTAGTGAAGACCATCGAGACCTGTTCTTGAATAC 343
Db      122  GAAATGAAGACGACATTCAGTTTGTCTAGTGAAGACCATCGAGACCTGTTCTTGAATAC 181
Qy      344  ATCGATCTGCTGTGTGTGATGATGAAACCCCTAGCGCTATTATAGTGATATTCTGTTT 403
Db      182  ATCGATCTGCTGTGTGTGATGATGAAACCCCTAGCGCTATTATAGTGATATTCTGTTT 241
Qy      404  CCTAAATGCCAAAACGACAGGCTGATTTTTTGGCATTTTTTAAATATGAAGAGGTGAAA 463
Db      242  CCTAAATGCCAAAACGACAGGCTGATTTTTTGGCATTTTTTAAATATGAAGAGGTGAAA 301
Qy      464  ACAGACACAGAAAATAATGAAGTGAGCAAAAATCACTCAGAGTTCTTAAGGCAAGGAA 523
Db      302  ACAGACACAGAAAATAATGAAGTGAGCAAAAATCACTCAGAGTTCTTAAGGCAAGGAA 361
Qy      524  CCACATTTTCGAGTATATAGAACCAACCAATCATTTGAAGAAAGCCATCACTTTCATCAAG 583
Db      362  CCACATTTTCGAGTATATAGAACCAACCAATCATTTGAAGAAAGCCATCACTTTCATCAAG 421
Qy      584  AAAAGAAATAGATAAATCTTTGTGCTTCCAGATTTGGAATGAAAAACAAGCATTTATGTTT 643
Db      422  AAAAGAAATAGATAAATCTTTGTGCTTCCAGATTTGGAATGAAAAACAAGCATTTATGTTT 481
Qy      644  ACAGAACCAATACAAATGGCTTGAATAAAGAGGTAAATTAGGATGTAGGATTTGTTTCA 703
Db      482  ACAGAACCAATACAAATGGCTTGAATAAAGAGGTAAATTAGGATGTAGGATTTGTTTCA 541
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/lab host="DH10B"
/clone lib="HR85 islet"
/organism="Pancras; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
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ORIGIN
Query Match 37.4%; Score 574.8; DB 3; Length 582;
Best Local Similarity 99.1%; Pred. No. 3.2e-120;
Matches 576; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 956 TTCAATCTGTTTACAGTTTGTAGTAAACATACAGACCTTTTCTGTATTTGAGGGGCA 1015
Db 582 TTCATCTGTTTACAGTTTGTAGTAAACATACAGACCTTTTCTGTATTTGAGGGGCA 523

Qy 1016 AGAGAAATTACAGGAAAAAATGGAGAGTAAATGTTTAAATACACGTTACGTGCAACA 1075
Db 522 AGAGAAATTACAGGAAAAAATGGAGAGTAAATGTTTAAATACACGTTACGTGCAACA 463

Qy 1076 AGAATAGCAGACATATTGCAAAAGAAATGAAGATGAAGATATTAAAGATATTATAGAA 1135
Db 462 AGAATAGCAGACATATTGCAAAAGAAATGAAGATGAAGATATTAAAGATATTATAGAA 403

Qy 1136 GAGAAATGCCAAATCTGTATCATATTTGATGAGGATCTACAGTTTCAAGAAAAACCACC 1195
Db 402 GAGAAATGCCAAATCTGTATCATATTTGATGAGGATCTACAGTTTCAAGAAAAACCACC 343

Qy 1196 CTAGTGATTTATCTCAGTGCAATTCAGTCAGTCTCTGCACTCTGTATGTTATTTGTG 1255
Db 342 CTAGTGATTTATCTCAGTGCAATTCAGTCAGTCTCTGCACTCTGTATGTTATTTGTG 283

Qy 1256 GCTTTAAAGAAATGGTGTCACTATAGCAGAGTGTATGTCATACATTTTGTGACTACT 1315
Db 282 GCTTTAAAGAAATGGTGTCACTATAGCAGAGTGTATGTCATACATTTTGTGACTACT 223

Qy 1316 TTAATATGATTTGGTTTACAAATGAATATTTGAAAGCAATTTAAATGCAATTTGTCT 1375
Db 222 TTAATATGATTTGGTTTACAAATGAATATTTGAAAGCAATTTAAATGCAATTTGTCT 163

Qy 1376 GATGGTGCTTAATACAACTCTGGAGAGAAAGTCTGGAGTAGCTACAAATTTGTAGAAAT 1435
Db 162 GATGGTGCTTAATACAACTCTGGAGAGAAAGTCTGGAGTAGCTACAAATTTGTAGAAAT 103

Qy 1436 TTTCCTGAAATCATCATTTTGGAACTGTTTAAATCATCGATTACAAATTTGCTGATGAT 1495
Db 102 TTTCCTGAAATCATCATTTTGGAACTGTTTAAATCATCGATTACAAATTTGCTGATGAT 43

Qy 1496 TCTATATCCGAATTAACAAATTAATCATTTAAANNATAA 1536
Db 42 TCTATATCCGAATTAACAAATTAATCATTTAAANAAAAA 2
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RESULT 18
BI439068
LOCUS
DEFINITION
ic26b08.y3 HR85 islet Homo sapiens cDNA 5' similar to TR:Q9Y4E5
Q9Y4E5 KIAA0576 PROTEIN ; mRNA sequence.
ACCESSION
BI439068
VERSION
BI439068.1 GI:15263758
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 576)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
```

Lenishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Thelsing, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: ic26b08.x3
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@bioh.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
High quality sequence stop: 433.

FEATURES

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/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="Purified pancreatic islet"
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/note="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:
NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

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Query Match 37.3%; Score 572.8; DB 3; Length 576;
Best Local Similarity 99.7%; Pred. No. 9.3e-120;
Matches 574; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 253 TGGCCCTCAGCATCTGAGTCAACACCGATGAAATCAAGACGACATTCAGTTGTCTAG 312
Db 1 TGGCCCTCAGCATCTGAGTCAACACCGATGAAATCAAGACGACATTCAGTTGTCTAG 60

Qy 313 TGAAGGACCATCGAGACCTGTTCTTGAATACATCGATCTGGTCTCTGGTGATGATGAAA 372
Db 61 TGAAGGACCATCGAGACCTGTTCTTGAATACATCGATCTGGTCTCTGGTGATGATGAAA 120

Qy 373 CCCTAGCGCCTATTATAGTATTTCTGTTTCTTAAATGCCAAACGACAGGGTGATTT 432
Db 121 CCCTAGCGCCTATTATAGTATTTCTGTTTCTTAAATGCCAAACGACAGGGTGATTT 180

Qy 433 TTTCATTTTTTAAATATGAAGAGTGAAGACACACAGACAGAAATATGAATGAGCA 492
Db 181 TTTCATTTTTTAAATATGAAGAGTGAAGACACACAGACAGAAATATGAATGAGCA 240

Qy 493 AAATCAGTCAGATTTCTTAAGGCAAGAACCAATTCGAGTATATAGAACCAACCAAT 552
Db 241 AAATCAGTCAGATTTCTTAAGGCAAGAACCAATTCGAGTATATAGAACCAACCAAT 300

Qy 553 CATTGAAGAAAGCCATCATTCTTCAACAAAGAAAGAAATAGATAATCTTGTCTCTCCAGA 612
Db 301 CATTGAAGAAAGCCATCATTCTTCAACAAAGAAAGAAATAGATAATCTTGTCTCTCCAGA 360

Qy 613 TTGTGGAAATGAAGAAACAGCAATTTATGTTTACAGAACCAATACCAATGCTTGAATATA 672
Db 361 TTGTGGAAATGAAGAAACAGCAATTTATGTTTACAGAACCAATACCAATGCTTGAATATA 420

Qy 673 AGAAGGTAAATTAGGATGAAGATTTGTTTCAGCAGTTCGGCATTTGGGATTCGAAAGCAGA 732
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Db 421 AGAAGGTAATAGGATGTAAGGATTTCCAGAGTTCCGGATTTGGGATCGAAGCAGA 480
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Db 481 AAAGCATGTCATGTGCCAAGGAATGGATTGCATATTTAGTAACCCCTAATGGCAGTAA 540
Qy 793 TAAACTACTAGGCAAGCTTCTCTACGAAAAAAT 828
Db 541 TAAACTACTAGGCAAGCTTCTCTACGAAAAAAT 576

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DEFINITION mRNA sequence.
ACCESSION CK821916
VERSION CK821916.1 GI:44838841
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 588)
AUTHORS Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D.,
Wyllie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B.,
Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M.,
McCann,R., Cole,R., Tsagarishvili,R., Williams,T., Jackson,Y. and
Bowers,Y.
WashU-Harvard Pancreas EST Project
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
This read is a 5' RESEQUENCE of a previously sequenced pancreas
clone
Good hit to opposite strand read. . . wrong orientation BUT PASSED FOR
MOUSE-PANCREAS VERIFICATION
Seq primer: -40UP from Gibco.

FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
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/clone="IMAGE:5596336"
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/lab_host="DH10B"
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/note="Organ: Pancreas; Vector: pBluescript SK(-); Site:1:
NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN
Query Match 37.2%; Score 571.8; DB 7; Length 588;
Best Local Similarity 99.1%; Pred. No. 1.6e-119;
Matches 573; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 959 AATAGTGTTCAGTTAGTAAACATACAGACCTTTATCTGATATTGAGGGGGCAGA 1018
Db 588 AATAGTGTTCAGTTAGTAAACATACAGACCTTTATCTGATATTGAGGGGGCAGA 529
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Qy 1019 GAATTCAGGAAAAAATCGAGAGGTAAATTTGTTTAAATACACGTTACAGTGAACAAGA 1078
Db 528 GAATTCAGGAAAAAATCGAGAGGTAAATTTGTTTAAATACACGTTACAGTGAACAAGA 469
Qy 1079 ATAGCAGACATATTCGAAAGAAATGAAGATCAAGATATTTTAAGAATATTTATAGAAGAG 1138
Db 468 ATAGCAGACATATTCGAAAGAAATGAAGATCAAGATATTTTAAGAATATTTATAGAAGAG 409
Qy 1139 AATGCCAAAATCTGTATCATTAATTTGATGAGGCATCTACAGTTTCAAAGAAAAACCCCTA 1198
Db 408 AATGCCAAAATCTGTATCATTAATTTGATGAGGCATCTACAGTTTCAAAGAAAAACCCCTA 349
Qy 1199 GTGATTTATCTCCAGTGCACAATTCAGTCAGCTCCCTGCACCTGTTATGTTTGTGGCT 1258
Db 348 GTGATTTATCTCCAGTGCACAATTCAGTCAGCTCCCTGCACCTGTTATGTTTGTGGCT 289
Qy 1259 TTAAGAAGATTGGTGCACTATAGCAGAGTGATTGTCAATACATTTATTGACTACTTTA 1318
Db 288 TTAAGAAGATTGGTGCACTATAGCAGAGTGATTGTCAATACATTTATTGACTACTTTA 229
Qy 1319 AATGATTTGGTTTTCAAAATGAATATTTGAAAAGCAAAATTTAATTCGATTTGTTCTGAT 1378
Db 228 AATGATTTGGTTTTCAAAATGAATATTTGAAAAGCAAAATTTAATTCGATTTGTTCTGAT 169
Qy 1379 GGTGCTAATACAACCTCGGAAGAAAGCTCTGGAGTAGCTACAAAATTTGTAGAAAATTT 1438
Db 168 GGTGCTAATACAACCTCGGAAGAAAGCTCTGGAGTAGCTACAAAATTTGTAGAAAATTT 109
Qy 1439 CCTGAAATCATCATTTGGAACTGTTTAAATCATCGATTACAATTTGTCACTTGATGATCT 1498
Db 108 CCTGAAATCATCATTTGGAACTGTTTAAATCATCGATTACAATTTGTCACTTGATGATCT 49
Qy 1499 ATATCCGAATAAACAATAATTAATCAATTTAANNATATAA 1536
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DEFINITION mRNA sequence.
ACCESSION BB614069
VERSION BB614069.1 GI:9895666
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 615)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rga@nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9713 row: e column: 01
High quality sequence stop: 615.
Location/Qualifiers
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."

ORIGIN

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Query Match      37.1%; Score 570; DB 2; Length 615;
Best Local Similarity 99.2%; Pred. No. 4.1e-119; Indels 4; Gaps 4;
Matches 614; Conservative 0; Mismatches 1;

QY 793 TAAACTACTAGGCAAGCTTCTCTACGAAAAAATAATAGGGAACAATGATTTCTTAAAGC 852
DB 1 TAAACTACTAGGCAAGCTTCTCTACGAAAAAATAATAGGGAACAATGATTTCTTAAAGC 60

QY 853 CCATGTTAAATTCAGGATTTGTTAAAGGAATCAACTAATGATTTCAATTTGTAATTTAGT 912
DB 61 CCATGTTAAATTCAGGA-TTGTTAAAGGAATCAACTAATGATTTCAATTTGTAATTTAGT 119

QY 913 GCATAAACAAATAATATAAAATATTGATGCTACTGTAAAGTTTTCATATCTGTTTACAG 972
DB 120 GCATAAACAAATAATATAAAATATTGATGCTACTGTAAAGTTTTCATATCTGTTTACAG 179

QY 973 TTTAGTAAACATAACACAGACCTTTTATCTGATATTGAGGGGGCAAGAGAAATTAACAGAAAA 1032
DB 180 TTTAGTAAACATAACACAGACCTTTTATCTGATATTGAGGGGGCAAGAGAAATTAACAGAAAA 239

QY 1033 AAATGAGAGGTAATTTGTTTAAATACAGCTTTACAGTGCAACAAGATAGCAACATAT 1092
DB 240 AAATGAGAGGTAATA-TGTTTAAATACAGCTTTACAGTGCAACAAGATAGCAACATAT 298

QY 1093 TCCAAAGAAATCGAGATCAAGATATTTAAGATATTTAGAGAGAAATGCCAAATCTG 1152
DB 299 TCCAAAGAAATCGAGATCAAGATATTTAAGATATTTAGAGAGAAATGCCAAATCTG 358

QY 1153 TATCATAAATTTGATGAGGCAATCTACAGTTTCAAGAAAAACCCCTAGTGATTTATCTCCA 1212
DB 359 TATCATAAATTTGATGAGGCAATCTACAGTTTCAAGAAAAACCCCTAGTGATTTATCTCCA 418

QY 1213 GTGCAAAATTCAGTCAGCTCCGACCTGTTATGTTTATTTGCTGCTTTAAAGAAATGGT 1272
DB 419 GTGCAAAATTCAGTCAGCTCCGACCTGTTATGTTTATTTGCTGCTTTAAAGAAATGGT 478

QY 1273 GTCAACTATAGCAGAGTGATTTGTCATACATATTGACTACTTTAAATGATTTGGTTT 1332
DB 479 GTCAACTATAGCAGAGTGATTTGTCATACATATTGACTACTTTAAATGATTTGGTTT 537

QY 1333 TACAAATGAATATTTGAAAGCAAAATTTAAATTTGCAATTTTCTGATGGTGCTAATACAA 1392
DB 538 TACAAATGAATATTTGAAAGCAAAATTTAAATTTGCA-TTCTGCTGATGGTGCTAATACAA 596

QY 1393 CTGCGAAGAAAGTCTGGA 1411
DB 597 CTGCGAAGAAAGTCTGGA 615
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RESULT 21

BG028983
LOCUS 602295120F1 NIH_MGC_86 Homo sapiens cdna clone IMAGE:4389916 5',
DEFINITION mRNA sequence.

ACCESSION BG028983

VERSION BG028983.1 GI:12418078

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1 (bases 1 to 975)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM10078 Row: g Column: 05
High quality sequence stop: 586.

FEATURES

source

1. 975
/location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4389916"
/tissue_type="osteosarcoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_86"
/note="Organ: bone; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.533 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

```
Query Match      36.9%; Score 567.4; DB 2; Length 975;
Best Local Similarity 91.4%; Pred. No. 1.7e-118; Indels 17; Gaps 7;
Matches 682; Conservative 0; Mismatches 47;

QY 250 AGCTGGCCCTGAGGCATCTGAGTCAACCAACGGATGAAATGAAGACGACATTCAGTTGT 309
DB 32 AACTGGCCCTGAGGCATCTGAGTCAACCAACGGATGAAATGAAGACGACATTCAGTTGT 91

QY 310 CAGTGAAGGACCATCGAGACCTGTTCTTGAATATACATCGATCTGCTGTGGTGATGATGA 369
DB 92 CAGTGAAGGACCATCGAGACCTGTTCTTGAATATACATCGATCTGCTGTGGTGATGATGA 151

QY 370 AAACCCCTAGCGCTTATATAGTATATCTGTTCTTCTTAAATGCCAAACGACAGGTCGA 429
DB 152 AAACCCCTAGCGCTTATATAGTATATCTGTTCTTCTTAAATGCCAAACGACAGGTCGA 211

QY 430 TTTTGTGCAATTTTAAATATGAAGAGGTGAAAAACAGACACAGAAAAATAATGAAGTGAG 489
DB 212 TTTTGTGCAATTTTAAATATGAAGAGGTGAAAAACAGACACAGAAAAATAATGAAGTGAG 271

QY 490 CAAAAATCACTGCAGATTTGTTAAGGCAAAAGAACCAATTTTCGAGTATATAGAACCAAC 549
DB 272 CAAAAATCACTGCAGATTTGTTAAGGCAAAAGAACCAATTTTCGAGTATATAGAACCAAC 331

QY 550 AATCATTTGAAGAAAGCCATCACTTTTCATCAAGAAAGAAATAGATATAATTTGTGCTTCC 609
DB 332 AATCATTTGAAGAAAGCCATCACTTTTCATCAAGAAAGAAATAGATATAATTTGTGCTTCC 391

QY 610 AGATTGTTGGAAATGAAAAACAAGCATTTATGTTTACAGAAACAATACAAATGCTTGAAT 669
DB 392 AGATTGTTGGAAATGAAAAACAAGCATTTATGTTTACAGAAACAATACAAATGCTTGAAT 451

QY 670 AAAAGAAGGTAAATTTAGGATGTAAGATTTGTTACAGAGTTTCGGCATTTGGGATTCGAAAGC 729
DB 452 AAAAGAAGGTAAATTTAGGATGTAAGATTTGTTACAGAGTTTCGGCATTTGGGATTCGAAAGC 511

QY 730 AGAAAAAGCATGTCCATGTGTCCAA-GGAATGATTTGCATATTTTAGTACCCCTTAATGGCA 788
DB 512 AGAAAAAGCATGTGTCCATGTGTCCAAAGGAATGGAATTTAGTAAACCCCTTAATGGCA 571

QY 789 GTAATAAACTACTAGGCAAGCTTCTCTACGAAAAAATAATAGGGAACAATGATGTTTCTTA 848
DB 572 GTAATAAACTACTAGGCAAGCTTCTCTACGAAAAAATAATAGGGAACAATGATGTTTCTTA 629

QY 849 AAGCCCATGTTGTAATTCAGGATTTGTTTAAAGGAATCAACTAATGATCAATTTGTAATTT 908
```



```
Db 630 AAG-CCATGGTAAATTCGGATTGTT-----AAGGATCACTTATGATCAATTGTTT 682
Qy 909 TAGTGCATAACAAATAATAAATAATATGATGCTACTGTAAAGTTTTCATACTGTTT 968
Db 683 TAGTGCCTAAACAAA-----TAATAAATAATTTGGGTACTGTACAAAGTTT--ACTACCGTTA 735
Qy 969 ACAGTTTAAATAACATAACAGCCT 994
Db 736 CCGGTTTCAGTAACTACAACCTATCT 761

RESULT 22
BM972376/c
LOCUS
DEFINITION
  UI-CF-EC1-abq-i-22-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
  UI-CF-EC1-abq-i-22-0-UI 3', mRNA sequence.
ACCESSION
  BM972376
VERSION
  BM972376.1 GI:19589967
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homiidae; Homo.
REFERENCE
  1 (bases 1 to 581)
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
889548
Contact: McCray, PB
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.reagen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 1-41, >AT rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
  1..581
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="UI-CF-EC1-abq-i-22-0-UI"
  /tissue_type="Lung"
  /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
  /dev_stage="Adult and Fetal"
  /clone_lib="UI-CF-EC1"
  /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
  modified polylinker; Site 1: EcoR I; Site 2: Not I;
  UI-CF-EC1 is a normalized cDNA library containing the
  following tissue(s): Normal lung from adult and from fetal
  day 64, day 87, week 19 and week 42. The library was
  constructed according to Bonaldo, Lennon and Soares,
  Genome Research, 6:791-806, 1996. First strand cDNA
  synthesis was primed with an oligo-dT primer containing a
  Not I site. Double stranded cDNA was ligated to an EcoR I
  adaptor, digested with Not I, and cloned directionally
  into pT73-Pac vector. The oligonucleotide used to prime
  the synthesis of first-strand cDNA contains a library tag
  sequence that is located between the Not I site and the
  (dT)18 tail. The sequence tag for this library is
  AAGTGTCTAC.
```

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TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
and 380-383
TAG_LIB=UI-CF-EC1
TAG_SEQ=AAGTGTCTAC"

ORIGIN

Query Match      36.6%; Score 562.4; DB 3; Length 581;
Best Local Similarity 99.0%; Pred. No. 2.2e-117; Indels 0; Gaps 0;
Matches 566; Conservative 0; Mismatches 17;

Qy 381 CCTATTATAGTGATATTCTGTTTCCCTAAATGCAAAACGACAGGGTGATTTTTTGCATT 440
Db 581 CCTATTATAGTGATATTCTGTTTCCCTAAATGCAAAACGACAGGGTGATTTTTTGCATT 522
Qy 441 TTTTAAATATGAAGAAGGTGAAACAGACACAGAAAATATATGAATGAGCGAGCAAAATCATT 500
Db 521 TTTTAAATGTAAGAAGGTGAAACAGACACAGAAAATATATGAATGAGCGAGCAAAATCATT 462
Qy 501 GCAGATTGCTTAAGGCAAGGACCACTTTCCAGTATATAGAACCAACCAATCATTTGAAG 560
Db 461 GCAGATTGCTTAAGGCAAGGACCACTTTCCAGTATATATGAACCAACCAATCATTTGAAG 402
Qy 561 AAAAGCCATCACCTTTTCATCAAGAAAGAAATAGATAATCTTTGCTTCCAGATTGTTGGA 620
Db 401 AAAAGCCATCACCTTTTCATCAAGAAAGAAATAGATAATCTTTGCTTCCAGATTGTTGGA 342
Qy 621 ATGAAAAACAAGCATTTATGTTTACAGAACATACAAAATGGCTTGAATTAAGAGAGGTA 680
Db 341 ATGAAAAACAAGCATTTATGTTTACAGAACATACAAAATGGCTTGAATTAAGAGAGGTA 282
Qy 681 AATTAGGATGAAGGATTGTTTCAGCAGTTTCGGCATTCGAAAGCAAGAAAGCATG 740
Db 281 AATTAGGATGAAGGATTGTTTCAGCAGTTTCGGCATTCGAAAGCAAGAAAGCATG 222
Qy 741 TCCATGTGTCCTCAAGGAATGATTGCATATTTAGTAAACCCCTAATGCGAGTAAATAAACTA 800
Db 221 TCCATGTGTCCTCAAGGAATGATTGCATATTTAGTAAACCCCTAATGCGAGTAAATAAACTA 162
Qy 801 CTAGGCAAGCTTCTCTACGAAAAAAATATAGGAAACATGATGTTTCTAAAGCCCATGTA 860
Db 161 CTAGGCAAGCTTCTCTACGAAAAAAATATAGGAAACATGATGTTTCTAAAGCCCATGTA 102
Qy 861 AATTTCAGGATTTGTTTAAAGGAATCACTAATGATTCATCAATTTGTAATTTAGTCATAAAC 920
Db 101 AATTTCAGGATTTGTTTAAAGGAATCACTAATGATTCATCAATTTGTAATTTAGTCATAAAC 42
Qy 921 AAAATAATAAAAAATATTGATGCTACTGTAAAA 952
Db 41 AAAATAATAAAAAATATTGATGCTAAAAAAA 10

RESULT 23
BF687541
LOCUS
DEFINITION
  602066646F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065922 5',
  mRNA sequence.
ACCESSION
  BF687541
VERSION
  BF687541.1 GI:11972949
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homiidae; Homo.
REFERENCE
  1 (bases 1 to 831)
  NIH-MGC http://mgs.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgabs-remail.nih.gov
  Tissue Procurement: ATCC
  cDNA Library Preparation: CLONETECH Laboratories, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
```


DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCN902 row: k column: 11
High quality sequence stop: 652.

FEATURES
Source

1. 831
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4065922"
/tissue_type="glioblastoma"
/lab_host="PH108 (T1 phase-resistant)"
/clone_lib="NIH MGC 57"
/note="Organ: Brain; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccctcgccg); Site_2: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 36.3%; Score 557.8; DB 2; Length 831;
Best Local Similarity 92.8%; Pred. No. 2.6e-116;
Matches 684; Conservative 0; Mismatches 42; Indels 11; Gaps 9;

QY 170 AGCAGAGCAGTGTCTGTCTGACGCGCGCGCTCGGAGACATGGAGACCCGGGTCGGA 229
DB 2 AGCAGAGCAGTGTCTGTCTGACGCGCGCGCTCGGAGACATGGAGACCCGGGTCGGA 60

QY 230 ATAATAGATCTGTCCCTCCAGCTGCGCTGAGGCACTGAGTCAACACGATGAAAT 289
DB 61 ATAATAGATCTGTCCCTCCAGCTGCGCTGAGGCACTGAGTCAACACGATGAAAT 120

QY 290 GAAGACGACATTCAGTTTGTCTGAGTGAAGACCATCGAGACCTGTTCTTGAATACATCGAT 349
DB 121 GAAGACGACATTCAGTTTGTCTGAGTGAAGACCATCGAGACCTGTTCTTGAATACATCGAT 180

QY 350 CTGGTCTGTGTGATGATGAACACCTAGCGCTATTATAGTATATCTGTTCTCTAAA 409
DB 181 CTGGTCTGTGTGATGATGAACACCTAGCGCTATTATAGTATATCTGTTCTCTAAA 240

QY 410 ATGCCAAACGACAGGTCATTTTGTGCAATTTTAAATATGAAGAGGTGAACACAGAC 469
DB 241 ATGCCAAACGACAGGTCATTTTGTGCAATTTTAAATATGAAGAGGTGAACACAGAC 298

QY 470 ACAGAAATAATGAAGTGAACAAATCACTGCGAT-TGTCTAAGGCAAGGAAACCA 528
DB 299 ACAGAAATAATGAAGTGAACAAATCACTGCGATGCTCTAAGGCAAGGAAACCA 358

QY 529 TTTTCAGTATATAGAACAAATCACTGAAGAAAGCCATCACTTTTCATCAAGAAAGA 588
DB 359 TTTTCAGTATATAGAACAAATCACTGAAGAAAGCCATCACTTTTCATCAAGAAAGA 418

QY 589 AATAGATATCTGTGCTTCCAGATTTGGATGAACAAACAGCATTTATGTTTACAGA 648
DB 419 AATAGATATCTGTGCTTCCAGATTTGGATGAACAAACAGCATTTATGTTTACAGA 478

QY 649 ACAATCAATGCTTTGAATAAAGAGTAAATTTAGGATGTAAGGATTTGTTTCAGCAT 708
DB 479 ACAATCAATGCTTTGAATAAAGAGTAAATTTAGGATGTAAGGATTTGTTTCAGCAT 537

QY 709 TCGGCATTTGGGATCGAAAGCAGAAAGCATGTCATGTCGCAAGGATGGA-TTGCAT 767
DB 538 TCGGCATTTGGGATCGAAAGCAGAAAGCATGTCATGTCGCAAGGATGGA-TTGCAT 597

QY 768 ATTTAGTACCCCTAATGGCAGTAAATAAACTACTAGGCAAGCTTCTCTACGAAAAA 827

|||||
598 ATTTAGTAACCCCTAATGGAGTAAT-AAACTACTAGGCAAG-TTCTCTACGAAAAACA 655
QY 828 TTAGGACATGATGTTTCTAAAGCCCATGTGTAATTTTAAAGGAATCAA 887
DB 656 TTGGCGGAC---TGATGTTCTTAAGCCCATGTGTAATCAGGATTTCTGACGATCCTTA 712
QY 888 CTAATGATTCATTTGT 904
DB 713 TGATCCATGATGTTGT 729

RESULT 24
DN371450

LOCUS DN371450 764 bp mRNA linear EST 07-MAR-2005
DEFINITION LIB3733-028-A1-K1-A12 LIB3733 Canis familiaris cdNA clone
CLN12919601, mRNA sequence.
ACCESSION DN371450
VERSION DN371450.1 GI:60552398
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE 1 (bases 1 to 764)
AUTHORS Staton,N.R.
TITLE Direct Submission (Staton,N.R.)
JOURNAL Unpublished (2005)
COMMENT Contact: Nick Staton
Tel: 636 247 6855
Email: nicholas.r.staton@pfizer.com.

FEATURES
source
1. 764
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="beagle"
/db_xref="taxon:9615"
/clone="CLN12919601"
/tissue_type="brain"
/lab_host="BHK"
/clone_lib="LIB3733"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; brain
- dog"

ORIGIN

Query Match 36.1%; Score 554.8; DB 8; Length 764;
Best Local Similarity 86.6%; Pred. No. 1.2e-115;
Matches 634; Conservative 0; Mismatches 94; Indels 4; Gaps 2;

QY 131 GCGCGGAAGGGAGTGTGGCGCTGCGGACAGCAGGACGAGCAGTGGTCTGTC 190
DB 29 GCGCGGGCGGACGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTCTGTC 88

QY 191 AGCGCGCGCGTGGAGACATGGGAGACCGCGGGTGGGAAATATAGAATCTGTCCCTCCA 250
DB 89 AGTAGGCGGTGGAGAAATGGGACCGCGGGTGGAGATGATAGAATCTGTCCCTCCA 148

QY 251 GCTGCCCTGAGGCATCTGAGTCAACACGAGTGAATAAAGAGACGACATTCAGTTTGT 310
DB 149 GCTGGCGCGGAGCGCTCTGAGGCAACGACGATGAACGAAAGATGACATTCAGTTTGT 208

QY 311 AGTGAAGACCATCGAGACCTGTTCTTGAATACATCGATCTGCTGTGATGATGAA 370
DB 209 AGCGAAGGACCATCAAAATGTTCTTGAATCAATATCTAGTCTGTAGTATGAA 268

QY 371 AACCCCTAGCGCTATTATAGTATGATTTCTGTTTCTTAAATGCCAAACGACAGGTGAT 430
DB 269 AGCCCTAGCACCTGTCAATATGATTTCTGTTTCTTAAATGCCAAACGCGAGGAT 328

QY 431 TTTTTCGATTTTTTAAATATGAAGAGGTGAAACACGACACAGAAATATAGTGTGAC 490
DB 329 TTTTTCGTTTTTAAATATGAAGAGGTGAAACACGACACAGAAATAGTAA---TAAC 385

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Qy 491 AAAAATCAGTCGAGATTGTTCTAAGGCAAGGAACCAACATTTTCGAGTATATAGAACACCA 550
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 386 AAAAGTCAATGTGAATTTGTTCTAAGTCAAAGGAACCGAATTTCAAATACGTTGAACGCCA 445

Qy 551 ATCAATTGAAGAAAGCCATCCTTTTCATCAAGAAAGAAATAGNATATCTTGTCCTCCA 610
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 446 ATCACTGAAGAAATCCATCATCTGTTTCATCAAGGAAGAAACAGATAATCTTGTCCTCCA 505

Qy 611 GATTGTTGGATGAAACCAAGCAGCTTTATGTTTACAGAACAAATACAAATGGCTTGAATA 670
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 506 GATTGTTGGATGAAACCAAGCAGCTTTATGTTTACAGAACAAATACAAATGGCTTGAATA 565

Qy 671 AAAGAAGTAAATAGGATGTAAGGATGTTTCAGCAGTTCGGCATTTGGGATCGAAAGCA 730
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 566 AAAGAAGTAAATAGGATGTAAGGATGTTTCAGCAGTTCGGCATTTGGGATCGAAAGCA 625

Qy 731 GAAAAGCATGTCATGTCGCAAGGAATGGATTGCATATTTAGTAACCCCTTAATGGCAGT 790
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 626 GAAAAGCATGTCATGTCGCAAGGAATGGATTGCATATTTAGTAACCCCTTAATGGCAGT 685

Qy 791 AATAAACTACTAGGCAAGCTTCTCTACGAAAAAAATTAGGGAACATGATGTTTCTAAA 850
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 686 AATAAACTACTANGACAGCTTCTCTCGGGAGAAANA-TAGGGAACATGATGTTTCTAAA 744

Qy 851 GCCCATGGTAAA 862
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 745 GCCATGGTAAA 756
```

```
RESULT 25
LOCUS BM478749 1169 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOURT 6457663 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5575470
5' mRNA sequence.
ACCESSION BM478749
VERSION BM478749.1 GI:18527791
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1169)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12325 row: m column: 07
High quality sequence stop: 462.
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FEATURES
    source
        1..1169
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:5575470"
            /tissue_type="embryonal carcinoma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_92"
            /note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
            Average insert size 2.5 kb. Library enriched for
            full-length clones and constructed by Life Technologies.
            Note: this is a NIH_MGC Library."
```

ORIGIN

```
Query Match 35.9%; Score 551.2; DB 3; Length 1169;
Best Local Similarity 96.5%; Pred. No. 8.7e-115;
Matches 574; Conservative 0; Mismatches 19; Indels 2; Gaps 1;

Qy 846 CTAAAGCCCATGCTAAAAATTCAGGATTTGTAAAGGAATCAACTAATGATTTCAATTTGTA 905
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 22 CTAAAGCCCATGCT--AAATTCAGGATTTGTAAAGGAATCAACTAATGATTTCAATTTGTA 79

Qy 906 ATTTAGTGCATAAACCAAAATAATAAATAATTTGATGCTACTGTAAAGTTTTCATCACTG 965
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 ATTTAGTGCATAAACCAAAATAATAAATAATTTGATGCTACTGTAAAGTTTTCATCACTG 139

Qy 966 TTTACAGTTTTAGTAAACATAACAGACCTTTATCTGATATTGAGGGGGCAAGAAATTAC 1025
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 140 TTTACAGTTTTAGTAAACATAACAGACCTTTATCTGATATTGAGGGGGCAAGAAATTAC 199

Qy 1026 AGGAAAAAATGAGAGAGTAAATTTGTTAAATAACAGTTACAGTGCAACAAGAAATAGCAG 1085
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 200 AGGAAAAAATGAGAGAGTAAATTTGTTAAATAACAGTTACAGTGCAACAAGAAATAGCAG 259

Qy 1086 AACATATTGCAAAAGAAATGAAGATGAAGATATTTAAGAAATATTTAGAGAGAATGCCA 1145
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 260 AACATATTGCAAAAGAAATGAAGATGAAGATATTTAAGAAATATTTAGAGAGAATGCCA 319

Qy 1146 AAATCTGTATCATTAATTTGATGAGGCATCTACAGTTTCAAGAAAAACCCCTAGTGNATT 1205
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 320 AAATCTGTATCATTAATTTGATGAGGCATCTACAGTTTCAAGAAAAACCCCTAGTGNATT 379

Qy 1206 ATCTCAGTGACAAATTCAGTCAGCTCCGACCTGTATTGTTATTGTCGGCTTTAAAG 1265
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 380 ATCTCAGTGACAAATTCAGTCAGCTCCGACCTGTATTGTTATTGTCGGCTTTAAAG 439

Qy 1266 AATTGGTGTCAACTATAGCAGAGTGATTGTCATACATTATTTGACTACTTTAAATGATT 1325
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 440 AATTGGTGTCAACTATAGCAGAGTGATTGTCATACATTATTTGACTACTTTAAATGAG 499

Qy 1326 GTGGTTTTACAATGAATATTTGAAAGCAAAATTTAATTCGATTTGTCATGGTGCTA 1385
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 500 GTGGCTTTTACAATGAATATTTGAAAGCAAAATTTAATTCGATTTGTCATGGTGCTC 559

Qy 1386 ATACAAACCTGGGAAGAAAGTCTGGAGTAGCTACAAAATTTGTAGAAAAATTTTCC 1440
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 560 ATACAACTCTGGGAAGAAAGTCTGGAGTAGCTACAAAATTCGGCTACAAAATCTTCC 614
```

```
RESULT 26
LOCUS AW977782/c 571 bp mRNA linear EST 02-JUN-2000
DEFINITION AW977782 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
ACCESSION AW977782
VERSION AW977782.1 GI:8168932
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 571)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,
Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
Quackenbush, J.
REFERENCE 1
AUTHORS Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 382
Seq primer: Forward.
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FEATURES
source

Location/Qualifiers
1..571
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGE"
/note="Vector: pBluescriptSKm"

ORIGIN

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Query Match      35.6%; Score 546.8; DB 1; Length 571;
Best Local Similarity 98.4%; Pred. No. 8-114;
Matches 562; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 957 TCAATCTCTTTTACAGTTTGTAGTAAACATAACAGAG-CCTTTATCTGATATTGAGGGGCA 1015
DB 571 TCAATCCGGTTTCCAGTTTGTAGTAAACATAACAGAGCCCTTTTCTGATATTGAGGGGCA 512

QY 1016 AGAGAAATTACAGAGAAAAAATGGAGAGTAAATTTGTTTAAATACACGTTTACAGTCAACA 1075
DB 511 AAAGAAATCCAGGAAAAAATGGAGAGTAAATTTGTTTAAATACACGTTTACAGTCAACA 452

QY 1076 AGAATAGCAGACATATTCCAAAGAAATGAAGATGAAGATATTTAAGATATTATAGAA 1135
DB 451 AGAATAGCAGACATATTCCAAAGAAATGAAGATGAAGATATTTAAGATATTATAGAA 392

QY 1136 GAGATGCCAAATCTGTATCATATTTGATGAGGCATCTACAGTTTCAAGAAACACC 1195
DB 391 GAGATGCCAAATCTGTATCATATTTGATGAGGCATCTACAGTTTCAAGAAACACC 332

QY 1196 CTAGTGATTTATCTCCAGTGCAATTTCACTGAGCTCTCGACCTGTTATGTTTGTG 1255
DB 331 CTAGTGATTTATCTCCAGTGCAATTTCACTGAGCTCTCGACCTGTTATGTTTGTG 272

QY 1256 GCTTTAAAGAAATGGTGCAACTATAGCAGAGTGATTTGTCAATCATTTATGACTACT 1315
DB 271 GCTTTAAAGAAATGGTGCAACTATAGCAGAGTGATTTGTCAATCATTTATGACTACT 212

QY 1316 TTAAATGATTTGGTTTACAAATGAATTTTGAAGCAAAATTTAATGCAATTTGTTCT 1375
DB 211 TTAAATGATTTGGTTTACAAATGAATTTTGAAGCAAAATTTAATGCAATTTGTTCT 152

QY 1376 GATGGTGCTAAATACAACTGGGAGAAAGTCTGGAGTAGCTACAAAATTTGTAGAAAT 1435
DB 151 GATGGTGCTAAATACAACTGGGAGAAAGTCTGGAGTAGCTACAAAATTTGTAGAAAT 92

QY 1436 TTTCTGAAATCATCAATTTGGAACTGTTTAAATCATCGAATTAATTTGCACTTGATGAT 1495
DB 91 TTTCTGAAATCATCAATTTGGAACTGTTTAAATCATCGAATTAATTTGCACTTGATGAT 32

QY 1496 TCTATATCCGAATAAAACAAATTAATCATTT 1526
DB 31 TCTATATCCGAATAAAACAAATTAATCATTT 1
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RESULT 27

CX598356 627 bp mRNA linear EST 13-JAN-2005
LOCUS
DEFINITION
CX598356 Equus caballus Articular Cartilage cDNA Library Equus
caballus cDNA clone CT020020B10H08, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

EST.
Equus caballus (horse)
Equus caballus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
1 (bases 1 to 627)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Expressed sequence tags from a normalized equine articular
cartilage cDNA library
Unpublished (2005)
Contact: MacLeod JN
Department of Veterinary Science

University of Kentucky
Gluck Equine Research Center, Lexington, KY 40546-0099, USA
Tel.: 859.257.4757
Fax: 859.257.8542
Email: jhmacleod@uky.edu
High quality sequence stop: 627.
Location/Qualifiers
1..627
/organism="Equus caballus"
/mol_type="mRNA"
/strain="Thoroughbred"
/db_xref="taxon:9796"
/clone_lib="CT020020B10H08"
/sex="male"
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/dev stages="1.5 year old"
/lab_host="DH12S E. Coli cells (Invitrogen)"
/clone_lib="Equine Articular Cartilage cDNA Library"
/note="Vector: pGEM11zf(+)" (promega); Site_1: EcoRI;
Site_2: NotI"

FEATURES

source

ORIGIN

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Query Match      35.0%; Score 538; DB 8; Length 627;
Best Local Similarity 91.9%; Pred. No. 8.2e-112;
Matches 568; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 375 CTAGCGCTATTATAGTGCATATCTGTTTCTAAATGCCAAACGACAGGGTGATTTT 434
DB 10 CTAGCATTACTATAGTGACATTTCTTCCCTAAATGCCAAACGACAGGGTGATTTT 69

QY 435 TGCATTTTAAATATGAAGAGGTGAAGAAACAGACACAGAAATTAATGAAGTGAGCAAAA 494
DB 70 TGCATTTTAAATATGAAGAGGTGAAGAAACAGACACAGAAATTAATGAAGCAAAA 129

QY 495 ATCACTGCAGATTTGTCTAAGGCAAGGAAACACATTTTCGAGTATATAGAAACCAATCA 554
DB 130 ATCACTGCAGATTTGTCTAAGGCAAGGAAATCAATTTTCAATATATGTAACCAACGATCA 189

QY 555 TTGAAGAAAGCCATCACTTTTCATCAAGAAAGAAATAGATAATCTTGTGCTTCCAGATT 614
DB 190 TTGAAGAAAGCCATCACTTTTCATCAAGAAAGAAATAGATAATCTTGTGCTTCCAGATT 249

QY 615 GTTGAATGAAAAAACAAGCATTTATGTTTACAGAAACAATACAAATGGCTTGAATAAAAAG 674
DB 250 GTTGAATGAAAAAACAAGCATTTATGTTTACAGAGCAGTACAAATGGCTTGAATAAAAAG 309

QY 675 AAGTAAATTAGGATGTAAGGATTTTTCAGCAGTTTCGGCATTTGGATCGAAAGCAGAAA 734
DB 310 AAGTAAATTAGGATGTAAGGATTTCTCAACAGATTTGGCATTTGGATCGAAAGCAGAAA 369

QY 735 AGCATGTCCTGTCCTCAAGGAAATGATTTGATTAACCCCTAATGCGCAGTAATA 794
DB 370 AGCATGTCCTGTCCTCAAGGAAATGATTTGATTAACCCCTAATGCGCAGTAATA 429

QY 795 AAATCTACTAGGCAAGCTTCTCTACGAAAAAAAATTTAGGGAACAATGATGTTTCTTAAAGCCC 854
DB 430 AAATCTACTAGGCAAGCTTCTCTCGGAAAAAAAATTTAGGGAACAATGATGTTTCTTAAAGCCC 489

QY 855 ATGTGAAATTTACAGATTTGTTTAAAGGAATCAACTAATGATTTCAATTTGTAATTTAGTGC 914
DB 490 ATGTGAAATTTACAGATTTGTTTAAAGGAATCAAGTTAATGGCTCGATTTCTAATTTAGTGC 549

QY 915 ATAAACAAATTAATAAATATTTGATGCTACTGTAAGGTTTCTCAATCTGTTTACAGTT 974
DB 550 ATAAACAAATTAATAAATATTTGATGCTACTGTAAGGTTTCTCAATCTGTTTACAGTT 609

QY 975 TAGTAAACATTAACAGAC 992
DB 610 TAGTAAACATTAATAGAC 627
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RESULT 28
BF219459

LOCUS BF219459 1213 bp mRNA linear EST 06-NOV-2000
DEFINITION 601884253F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102765 5',
mRNA sequence.
ACCESSION BF219459
VERSION BF219459.1 GI:11113269
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1213)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LUCM976 row: j column: 14
High quality sequence stop: 599.
Features
1. 1213
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/clone="IMAGE:4102765"
/tissue type="glioblastoma"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NIH MGC 57"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgccctcgcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTATGGC-3' and 3' adaptor
sequence: 5'-ATTCTAGCGCCGAGCGCGCATG-dt(30)BN-3',
where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

ORIGIN
Query Match 35.0%; Score 537.4; DB 2; Length 1213;
Best Local Similarity 94.5%; Pred. No. 1.2e-111;
Matches 589; Conservative 0; Mismatches 31; Indels 3; Gaps 3;
QY 411 TGCCAAACGACGAGGTGATTTTGGCATTTTAAATATGCAAGGTGAAACAGACA 470
DB 1 TGCCAAACGACGAGGTGATTTTGGCATTTTAAATATGCAAGGTGAAACAGACA 60
QY 471 CAGAAATAATCAAGTGAACAAAATCACTGCAGATTGCTAAGCAAGCAACACATT 530
DB 61 CAGAAATAATCAAGTGAACAAAATCACTGCAGATTGCTAAGCAAGCAACACATT 119
QY 531 TCGAGTATATGAAACCAATCATTTGAAGAAAAGCCATCATCTTTCATCAAGAAAGAAA 590
DB 120 TCGAGTATATGAAACCAATCATTTGAAGAAAAGCCATCATCTTTCATCAAGAAAGAAA 179
QY 591 TAGATAATCTTGCTCCAGATTCTGCAATGAAATGAAACCAAGCATTTATGTTTACAGAC 650
DB 180 TAGATAATCTTGCTCCAGATTCTGCAATGAAATGAAACCAAGCATTTATGTTTACAGAC 239
QY 651 AATCAAAATGGCTTGAATAAAGAAAGGTAAATAGGATGTGAAGATTGTTTCAAGCTTC 710
DB 240 AATCAAAATGGCTTGAATAAAGAAAGGTAAATAGGATGTGAAGATTGTTTCAAGCTTC 299
QY 711 GGCATTTGGGATCGAAGCAGAAAGCATGTCCATGTGTCACGAAGATGGATTGCATATT 770

DB 300 GGCAATTTGGGATCGAAGCAGAAAGCATGTCCATGTGTCGAAGGATGGATGATATT 359
QY 771 TAGTAACCCCTAATGCGCAGTAATAAATACTAGGCAAGCTTCTTACGAAAAAAATTA 830
DB 360 TAGTAACCCCTAATGCGCAGTAATAAATACTAGGCAAGCTTCTTACGAAAAAAATTA 419
QY 831 GGAACATGATGTTTCTAAAGCCCATGTTAAATTCAGGATTTGTTAAAGGATCAACTA 890
DB 420 GGAACATGATGTTTCTAAAGCCCATGTTAAATTCAGGATTTGTTAAAGGATCAACTA 478
QY 891 ATGATTCAATTTGTTAAATTTAGTCATAATAACAAATAATAATAATATTGATCTACTGTAA 950
DB 479 ATGATTCAATTTGTTAAATTTAGTCATAATAATAATAATATTGATCTACTGTAA 537
QY 951 AAGTTTTCATCTACTGTTTACAGTTTATAGTAAACATAACAGACCTTATCTGATATTGAGG 1010
DB 538 AAGTTTTCATCTACTGTTTACAGTTTATAGTAAACATAACAGACCTTATCTGATATTGAGG 597
QY 1011 GGCACAGAGATTTACAGGAAAA 1033
DB 598 GGCACAGAGATTTCCGGAACAAA 620
RESULT 29
BE783754
LOCUS 601471158F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874119 5',
mRNA sequence.
ACCESSION BE783754
VERSION BE783754.1 GI:10204952
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 565)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM9631 row: c column: 16
High quality sequence stop: 562.
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1. 565
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/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 67"
/notes="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 34.9%; Score 536.2; DB 2; Length 565;
Best Local Similarity 99.1%; Pred. No. 2.1e-111;
Matches 560; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
QY 382 CTATTATAGTGATTTCTGTTTCTTAAATGCCAAAACGACAGGTGATTTTTCGATTT 441

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 06:13:56 ; Search time 944.215 Seconds
(without alignments)
10841.779 Million cell updates/sec

Title: US-10-757-745-5
Perfect score: 1536
Sequence: 1 agagaaaggctccggga.....attaatcatttaamtataa 1536

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : N_Geneseq_21.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1533	99.8	1536	3	Aaz47120 Human CD4
2	1488.2	96.9	2949	10	Adc30114 Human nov
3	1131.6	73.7	4061	10	Adf76786 Novel hum
4	580.2	37.8	632	4	Aai192516 Human pol
5	580.2	37.8	632	10	Adc32029 Human nov
6	317.6	20.7	4999	6	Abk12391 cDNA enco
7	317.6	20.7	4999	6	Abk12392 cDNA enco
8	317.6	20.7	4999	14	Adx07795 Cyclin-de
9	317.6	20.7	5143	6	Abk12407 cDNA #2 e
10	317.6	20.7	5144	6	Abk12394 cDNA #1 e
11	317.6	20.7	5144	6	Abk12393 cDNA #1 e
12	308	20.7	448	9	Ach40820 Human foe
13	301.6	19.6	5245	10	Adc32216 Human nov
14	301.4	19.6	3363	5	Aas81317 DNA encod
15	295.4	19.2	5089	10	Adc30333 Human nov
16	270.8	17.6	274	3	Aac01653 Human sec
17	208.2	13.6	4961	13	Adr52788 Drug ther
18	170	11.1	2039	5	Aas81318 DNA encod
19	165.2	10.8	3042	14	Adv43036 Human psy

20	165.2	10.8	3183	6	ABK12397	Abk12397 cDNA #2 e
21	164.8	10.7	394	5	AA81316	AA81316 DNA encod
22	164.8	10.7	394	5	AA879405	AA879405 DNA encod
23	83.8	5.5	121	4	AA191954	AA191954 Human pol
24	67.8	4.4	12237	6	ABL34358	ABL34358 Human imm
25	62.8	4.1	6292	4	AA846735	AA846735 Tumour su
26	62.8	4.1	7442	4	AA846686	AA846686 Tumour su
27	62.6	4.1	3683	8	ABZ10199	ABZ10199 Haematopo
28	62.4	4.1	6668	6	ABL33697	ABL33697 Human imm
29	60.8	4.0	2000	8	ADA71938	ADA71938 Rice gene
30	60.8	4.0	6644	2	AAx33181	AAx33181 Base sequ
31	60.8	4.0	7372	2	AAx33182	AAx33182 Base sequ
32	60.8	4.0	7797	2	AAx33180	AAx33180 Cowpox vi
33	60.8	4.0	7996	2	AAx33184	AAx33184 Base sequ
34	59.6	3.9	12142	6	ABL33673	ABL33673 Human imm
35	59.2	3.9	8056	8	ABZ10246	ABZ10246 Haematopo
36	59	3.8	6419	6	ABL32267	ABL32267 Human imm
37	59	3.8	7597	6	ABL33013	ABL33013 Human imm
38	58.8	3.8	7814	4	AA846530	AA846530 Tumour su
39	58.2	3.8	3683	8	ABZ10053	ABZ10053 Haematopo
40	58	3.8	461	5	ADL43834	ADL43834 Human ova
41	58	3.8	1000	12	ADQ62833	ADQ62833 Homopoly-
42	58	3.8	1000	12	ADQ62832	ADQ62832 Homopoly-
43	58	3.8	1300	12	ADP85917	ADP85917 Synthetic
44	58	3.8	34548	6	ABL70603	ABL70603 Chemical
45	57.8	3.8	3057	2	AAx99555	AAx99555 Nucleic a
46	57.6	3.8	6109	6	ABL32326	ABL32326 Human imm
47	57.6	3.8	6109	6	AA561077	AA561077 Human gen
48	57.6	3.8	6286	4	AA846591	AA846591 Tumour su
49	57.6	3.8	17674	6	ABL33344	ABL33344 Human imm
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51	57.4	3.7	6048	6	ABQ67002	ABQ67002 Human ang
52	56.6	3.7	50000	6	ABL56201	ABL56201 AmEPV gen
53	56.2	3.7	393	8	ABX39417	ABX39417 Bovine ES
54	56.2	3.7	396	6	ABL48812	ABL48812 Ovarian c
55	56.2	3.7	396	6	ABT03129	ABT03129 Human ova
56	56.2	3.7	396	11	ADM10722	ADM10722 Human ova
57	56.2	3.7	396	12	ADJ11052	ADJ11052 Represent
58	56.2	3.7	396	12	ADM43313	ADM43313 Human ova
59	56.2	3.7	7143	3	AAA70250	AAA70250 Plasmodiu
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61	55.4	3.6	8222	8	ACF62794	ACF62794 Colon can
62	55.4	3.6	8222	10	ADB54190	ADB54190 Pretreate
63	55.4	3.6	11222	10	ADB54318	ADB54318 Pretreate
64	55.4	3.6	13784	6	ABK40062	ABK40062 Human che
65	55.4	3.6	1524	14	ADZ70897	ADZ70897 Human mat
66	55.2	3.6	4660	14	ADZ70902	ADZ70902 Human mat
67	55.2	3.6	2000	11	ACL35887	ACL35887 Rice stre
68	54.8	3.6	14006	6	ABL33958	ABL33958 Human imm
69	54.8	3.6	3399	2	AA805868	AA805868 Chicken l
70	54.6	3.5	5989	4	AA846536	AA846536 Tumour su
71	54.4	3.5	9539	4	AA845347	AA845347 Chemical
72	54.2	3.5	9539	4	ABK28180	ABK28180 DNA trans
73	54.2	3.5	9539	6	ABK28180	ABK28180 DNA trans
74	54.2	3.5	14066	2	AAx99556	AAx99556 Nucleic a
75	54.2	3.5	14067	8	ACA52811	ACA52811 Prokaryot
76	53.8	3.5	969	6	ABQ39490	ABQ39490 Oligonucle
77	53.8	3.5	969	6	ABQ39491	ABQ39491 Oligonucle
78	53.8	3.5	6254	6	ABL33620	ABL33620 Human imm
79	53.6	3.5	1998	3	AAA70212	AAA70212 Plasmodiu
80	53.4	3.5	612	14	ACL64894	ACL64894 M. xanthu
81	53.4	3.5	2000	11	ACL33363	ACL33363 Rice stre
82	53.4	3.5	88208	14	ADZ13389	ADZ13389 Human can
83	53.4	3.5	88445	13	ABD33536	ABD33536 Human can
84	53.4	3.5	121434	12	ADN30326	ADN30326 Human Not
85	53.4	3.5	121434	14	AEA08528	AEA08528 Human Not
86	53.2	3.5	975	6	ABQ29508	ABQ29508 Oligonucle
87	53.2	3.5	975	6	ABQ29509	ABQ29509 Oligonucle
88	53.2	3.5	15548	6	ABL34155	ABL34155 Human imm
89	53.2	3.5	19124	2	AA72882	AA72882 Plasmodiu
90	53.2	3.5	19124	3	AA298287	AA298287 Plasmodiu
91	52.6	3.4	8056	8	ABZ10246	ABZ10246 Haematopo
92	52.4	3.4	19734	6	ABL33933	ABL33933 Human imm

93	52.4	3.4	158001	12	ADL17884	Adl17884 Human pho	c 166	49	3.2	8298	6	ABN80191	Abn80191 Human che
c 94	52.2	3.4	2000	8	ADA71938	Ada71938 Rice gene	c 167	49	3.2	8943	6	ABK39967	Abk39967 Human che
c 95	51.8	3.4	9964	4	ABL32098	AbL32098 Human imm	c 168	48.8	3.2	337	8	ABX41811	Abx41811 Bovine ES
c 96	51.8	3.4	13321	6	AAS46421	Aas46421 Tumour su	c 169	48.8	3.2	516	8	ABX40620	Abx40620 Bovine ES
c 97	51.8	3.4	19965	4	AAK73166	Aak73166 Human imm	c 170	48.8	3.2	1428	14	ADZ70899	Adz70899 Human mat
c 98	51.8	3.4	19965	6	ABK69932	Abk69932 Human sec	c 171	48.8	3.2	3931	9	ACC84661	Acc84661 P. falcip
c 99	51.6	3.4	1039	14	ACL64817	Acl64817 M. xanthu	c 172	48.8	3.2	4985	10	ABQ75107	Abq75107 Anopheles
c 100	51.6	3.4	5930	6	ABL32517	AbL32517 Human imm	c 173	48.8	3.2	4985	6	ACF79720	Acf79720 Mosquito
c 101	51.6	3.4	8771	6	ABL33825	AbL33825 Human imm	c 174	48.8	3.2	9510	4	AAS46437	Aas46437 Tumour su
c 102	51.4	3.3	2000	11	ACL37108	Acl37108 Rice stre	c 175	48.8	3.2	9510	6	ABL34562	AbL34562 Human met
c 103	51.2	3.3	446	8	ABX38235	Abx38235 Bovine ES	c 176	48.8	3.2	9510	7	ADZ99823	Adz99823 Bisulphit
c 104	51.2	3.3	731	2	AAQ31693	Aaq31693 RsaI rest	c 177	48.8	3.2	32392	6	ABL56203	AbL56203 AnePV gen
c 105	51	3.3	520	13	ACN52918	Acn52918 Cotton an	c 178	48.6	3.2	32392	6	ABK11431	Abk11431 Signal tr
c 106	51	3.3	1413	2	AXX99616	Axx99616 Nucleic a	c 179	48.6	3.2	6107	6	ABL70390	AbL70390 Chemicall
c 107	51	3.3	1413	8	ACA52631	Aca52631 Prokaryot	c 180	48.6	3.2	6107	6	AAS61342	Aas61342 Human gen
c 108	51	3.3	5689	4	AAS45384	Aas45384 Chemicall	c 181	48.6	3.2	6115	6	ABL33801	AbL33801 Human imm
c 109	51	3.3	5689	4	AAS46426	Aas46426 Tumour su	c 182	48.6	3.2	7544	4	AAS45300	Aas45300 Chemicall
c 110	51	3.3	5689	6	ABK28226	Abk28226 DNA trans	c 183	48.6	3.2	7544	6	ABK28139	Abk28139 DNA trans
c 111	51	3.3	8056	8	ABZ10100	Abz10100 Haematopo	c 184	48.6	3.2	188971	12	ADL08108	AdL08108 Human gen
c 112	51	3.3	11036	4	AAS45411	Aas45411 Chemicall	c 185	48.4	3.2	553	6	ABQ36150	Abq36150 Oligonuc1
c 113	51	3.3	11036	6	ABK28264	Abk28264 DNA trans	c 186	48.4	3.2	553	6	ABQ36151	Abq36151 Oligonuc1
c 114	51	3.3	20579	6	ABQ67073	Abq67073 Human ang	c 187	48.4	3.2	700	10	ACD92384	AcD92384 Human col
c 115	50.8	3.3	5493	13	ADS99675	AdS99675 Oligonuc1	c 188	48.4	3.2	2184	8	ACA46890	Aca46890 Prokaryot
c 116	50.6	3.3	5981	6	ABL33762	AbL33762 Human imm	c 189	48.4	3.2	4673	2	AAQ27189	Aaq27189 P. yoelii
c 117	50.6	3.3	6154	6	ABK31200	Abk31200 Signal tr	c 190	48.4	3.2	5886	6	ABL34212	AbL34212 Human imm
c 118	50.6	3.3	6154	6	ABL70167	AbL70167 Chemicall	c 191	48.4	3.2	16579	10	ADS54117	AdS54117 Pretreate
c 119	50.6	3.3	6154	6	AAS61112	Aas61112 Human gen	c 192	48.4	3.2	16579	10	ADE37762	Ade37762 Human che
c 120	50.6	3.3	6191	6	ABL33216	AbL33216 Human imm	c 193	48.4	3.2	16579	13	ADS89273	AdS89273 Oligonuc1
c 121	50.6	3.3	6191	6	ABK31306	Abk31306 Signal tr	c 194	48.4	3.2	16750	4	AAS46313	Aas46313 Tumour su
c 122	50.6	3.3	6191	6	ABL70281	AbL70281 Chemicall	c 195	48.4	3.2	16750	6	ABL32520	AbL32520 Human imm
c 123	50.6	3.3	6191	6	ABN80160	Abn80160 Human che	c 196	48.4	3.2	17869	6	ABK39921	Abk39921 Human che
c 124	50.6	3.3	78064	13	ADS17402	AdS17402 Nucleotid	c 197	48.4	3.2	17869	6	ABL32105	AbL32105 Human imm
c 125	50.4	3.3	500	3	AAC94279	Aac94279 cat filea	c 198	48.2	3.1	478	13	ACN51993	Acn51993 Cotton an
c 126	50.4	3.3	778	6	ABQ15588	Abq15588 Oligonuc1	c 199	48.2	3.1	1686	2	AAQ87587	Aaq87587 DNA encod
c 127	50.4	3.3	778	6	ABQ15589	Abq15589 Oligonuc1	c 200	48.2	3.1	6033	3	AAA70152	Aaa70152 Plasmodi
c 128	50.4	3.3	871	13	ADR60929	Adr60929 Cotton cD	c 201	48.2	3.1	12507	6	ABL32298	AbL32298 Human imm
c 129	50.4	3.3	9539	4	AAS45346	Aas45346 Chemicall	c 202	48.2	3.1	17538	6	ABL33157	AbL33157 Human imm
c 130	50.4	3.3	9539	6	ABK28179	Abk28179 DNA trans	c 203	48	3.1	556	6	ABQ36997	Abq36997 Oligonuc1
c 131	50.2	3.3	548	13	ACN61238	Acn61238 Cotton gy	c 204	48	3.1	556	6	ABQ36996	Abq36996 Oligonuc1
c 132	50.2	3.3	7011	6	ABK39940	Abk39940 Human che	c 205	48	3.1	875	4	AAI95044	Aai95044 Human neu
c 133	50.2	3.3	7011	6	ABL32546	AbL32546 Human imm	c 206	48	3.1	5795	6	ABL33769	AbL33769 Human imm
c 134	50.2	3.3	9741	6	ABL33323	AbL33323 Human imm	c 207	48	3.1	5795	6	ABN80233	Abn80233 Human che
c 135	50	3.3	3450	4	ABL19319	AbL19319 Drosophil	c 208	48	3.1	6155	6	ABK28361	Abk28361 DNA trans
c 136	50	3.3	11076	8	ACA47181	Aca47181 Prokaryot	c 209	48	3.1	6688	6	ABL33696	AbL33696 Human imm
c 137	50	3.3	11076	13	ADS20616	AdS20616 S. epide	c 210	48	3.1	12393	6	ABL3262	AbL3262 Human imm
c 138	50	3.3	11091	6	ABN92780	Abn92780 Staphyloc	c 211	47.8	3.1	3501	3	AAA70202	Aaa70202 Plasmodi
c 139	50	3.3	11091	13	ADS02875	AdS02875 Staphyloc	c 212	47.8	3.1	5750	4	AAS46708	Aas46708 Tumour su
c 140	50	3.3	11143	4	ABL12834	AbL12834 Drosophil	c 213	47.8	3.1	5750	6	ABL34008	AbL34008 Human imm
c 141	50	3.3	16579	10	ADB54245	AdB54245 Pretreate	c 214	47.6	3.1	13326	6	ABL33713	AbL33713 Human imm
c 142	50	3.3	16579	10	ADE37772	Ade37772 Human che	c 215	47.6	3.1	574	11	ACN79882	Acn79882 Breast ca
c 143	49.8	3.2	525	11	ACN80333	Acn80333 Breast ca	c 216	47.6	3.1	628	6	ABQ16733	Abq16733 Oligonuc1
c 144	49.8	3.2	525	11	ACN80333	Acn80333 Breast ca	c 217	47.6	3.1	628	6	ABQ16732	Abq16732 Oligonuc1
c 145	49.8	3.2	6352	8	ABL32905	AbL32905 Human imm	c 218	47.6	3.1	1533	8	ACA28672	Aca28672 Prokaryot
c 146	49.8	3.2	6352	8	ADA20359	Ada20359 Prostata	c 219	47.6	3.1	2943	3	AAA70229	Aaa70229 Plasmodi
c 147	49.8	3.2	6352	8	ADA84166	Ada84166 Human ren	c 220	47.6	3.1	6145	6	ABL32972	AbL32972 Human imm
c 148	49.8	3.2	7348	4	AAS46336	Aas46336 Tumour su	c 221	47.6	3.1	6337	6	ABL33310	AbL33310 Human imm
c 149	49.6	3.2	431	8	ABX40393	Abx40393 Bovine ES	c 222	47.6	3.1	6337	6	ABQ67154	AbQ67154 Human ang
c 150	49.4	3.2	768	4	AAH71272	Aah71272 Human cer	c 223	47.6	3.1	6729	6	ABQ67154	AbQ67154 Human ang
c 151	49.4	3.2	1035	3	AAA01936	Aaa01936 Human col	c 224	47.6	3.1	11155	6	ABL32604	AbL32604 Human imm
c 152	49.4	3.2	1515	3	AAA70162	Aaa70162 Plasmodi	c 225	47.6	3.1	11691	6	ABL34240	AbL34240 Human imm
c 153	49.4	3.2	1560	10	ADH83273	Adh83273 Enterococ	c 226	47.6	3.1	13420	6	ABL32917	AbL32917 Human imm
c 154	49.4	3.2	3996	6	AAD47004	Aad47004 Plasmodi	c 227	47.6	3.1	13511	6	ABL32280	AbL32280 Human imm
c 155	49.4	3.2	7657	2	AAI12970	Aai12970 Enterococ	c 228	47.6	3.1	16914	6	ABL70315	AbL70315 Chemicall
c 156	49.4	3.2	7657	6	ABS98765	AbS98765 Enterococ	c 229	47.6	3.1	16914	6	AAS61253	Aas61253 Human gen
c 157	49.2	3.2	419	8	ABX46069	Abx46069 Bovine ES	c 230	47.4	3.1	887	4	AAI94064	Aai94064 Human neu
c 158	49.2	3.2	526	6	ABQ39217	Abq39217 Oligonuc1	c 231	47.4	3.1	887	8	ABT42734	Abt42734 Human neu
c 159	49.2	3.2	526	6	ABQ39216	Abq39216 Oligonuc1	c 232	47.4	3.1	2000	11	ACL35887	Acl35887 Rice stre
c 160	49.2	3.2	6816	12	ADQ24856	Adq24856 Human sof	c 233	47.4	3.1	6025	4	AAS45339	Aas45339 Chemicall
c 161	49.2	3.2	8056	8	ABZ10100	Abz10100 Haematopo	c 234	47.4	3.1	6759	4	AAS46608	Aas46608 Tumour su
c 162	49.2	3.2	13449	6	ABL33385	AbL33385 Human imm	c 235	47.4	3.1	7659	6	ABL32188	AbL32188 Human imm
c 163	49.2	3.2	15387	6	ABL32184	AbL32184 Human imm	c 236	47.2	3.1	581	13	ADX09939	Adx09939 Plant ful
c 164	49	3.2	4551	3	AAA70129	Aaa70129 Plasmodi	c 237	47.2	3.1	837	2	ADR01596	Adr01596 A. gosseyp
c 165	49	3.2	6661	6	ABN80294	Abn80294 Human che	c 238	47.2	3.1	5181	6	ABL70444	AbL70444 Chemicall

C 239	47.2	3.1	5493	6	AA613387	AA613387 Human gen
C 240	47.2	3.1	6831	6	ABL33487	ABL33487 Human imm
C 241	47.2	3.1	8420	4	AA646557	AA646557 Tumour su
C 242	47.2	3.1	8420	4	ABL31324	ABL31324 Signal tr
C 243	47.2	3.1	8420	4	ABL31324	ABL31324 Signal tr
C 244	47.2	3.1	11745	6	ABK28332	ABK28332 DNA trans
C 245	47.2	3.1	17934	6	ABL33719	ABL33719 Human imm
C 246	47	3.1	6464	6	ABL32514	ABL32514 Human imm
C 247	47	3.1	7823	6	AA645490	AA645490 Chemical
C 248	47	3.1	7823	6	ABL34061	ABL34061 Human imm
C 249	47	3.1	7823	6	ABL31493	ABL31493 Signal tr
C 250	47	3.1	7823	6	ABK28418	ABK28418 DNA trans
C 251	47	3.1	13627	4	ABQ66975	ABQ66975 Tumour su
C 252	46.8	3.0	509	6	ABQ16729	ABQ16729 Oligonucle
C 253	46.8	3.0	509	6	ABQ16728	ABQ16728 Oligonucle
C 254	46.8	3.0	2163	4	AAH53332	AAH53332 S. epider
C 255	46.8	3.0	2187	6	ABN92668	ABN92668 Staphyloc
C 256	46.8	3.0	2187	13	AD801322	AD801322 Staphyloc
C 257	46.8	3.0	2501	10	ADB54116	ADB54116 Pretreat
C 258	46.8	3.0	2501	13	AD89272	AD89272 Oligonucle
C 259	46.8	3.0	3898	4	AAH54598	AAH54598 S. epider
C 260	46.8	3.0	6095	4	AA646310	AA646310 Tumour su
C 261	46.8	3.0	6095	6	ABL32361	ABL32361 Human imm
C 262	46.8	3.0	6095	6	ABL34475	ABL34475 Human met
C 263	46.8	3.0	6095	6	ABL70150	ABL70150 Chemical
C 264	46.8	3.0	6095	7	AD599736	AD599736 Complemen
C 265	46.8	3.0	6432	10	ADB54290	ADB54290 Pretreat
C 266	46.8	3.0	6432	10	ADB54290	ADB54290 Pretreat
C 267	46.8	3.0	6432	13	AD895950	AD895950 Human lym
C 268	46.8	3.0	6432	13	AD895950	AD895950 Human lym
C 269	46.8	3.0	7057	4	AA646601	AA646601 Tumour su
C 270	46.8	3.0	7057	6	ABL33848	ABL33848 Human imm
C 271	46.8	3.0	7057	6	ABL34594	ABL34594 Human met
C 272	46.8	3.0	7057	6	ABL70407	ABL70407 Chemical
C 273	46.8	3.0	7057	6	AA661354	AA661354 Human gen
C 274	46.8	3.0	8254	7	AD599855	AD599855 Bisulphit
C 275	46.8	3.0	8254	7	ABL32864	ABL32864 Human imm
C 276	46.8	3.0	9145	6	ABL32888	ABL32888 Human imm
C 277	46.8	3.0	15121	6	ABN80238	ABN80238 Human che
C 278	46.8	3.0	50000	6	ABL55643	ABL55643 AmEPV gen
C 279	46.6	3.0	6036	6	ABL33108	ABL33108 Human imm
C 280	46.6	3.0	6036	6	ABL31290	ABL31290 Signal tr
C 281	46.6	3.0	6036	6	ABL70267	ABL70267 Chemical
C 282	46.6	3.0	6036	6	AA661192	AA661192 Human gen
C 283	46.6	3.0	6898	6	ABN80222	ABN80222 Human che
C 284	46.6	3.0	11522	3	AA70187	AA70187 Plasmodi
C 285	46.6	3.0	47108	6	ABK31510	ABK31510 Signal tr
C 286	46.4	3.0	341	13	ACN45670	ACN45670 Cotton pr
C 287	46.4	3.0	413	14	AD270590	AD270590 Human chr
C 288	46.4	3.0	629	10	ABT21705	ABT21705 Breast ca
C 289	46.4	3.0	1524	3	AA70107	AA70107 Plasmodi
C 290	46.4	3.0	1524	8	ABZ23337	ABZ23337 Nucleotid
C 291	46.4	3.0	1527	3	AA70121	AA70121 Plasmodi
C 292	46.4	3.0	6160	6	ABL33533	ABL33533 Human imm
C 293	46.4	3.0	6247	6	ABK39923	ABK39923 Human che
C 294	46.4	3.0	7522	6	ABL32915	ABL32915 Human imm
C 295	46.4	3.0	15743	6	ABK28395	ABK28395 DNA trans
C 296	46.4	3.0	17594	6	ABL34026	ABL34026 Human imm
C 297	46.4	3.0	37515	6	ABQ66998	ABQ66998 Human ang
C 298	46.4	3.0	113515	6	ABL34174	ABL34174 Human imm
C 299	46.2	3.0	337	4	AA11578	AA11578 Human bre
C 300	46.2	3.0	385	8	ABK36574	ABK36574 Bovine ES
C 301	46.2	3.0	424	11	ACN81779	ACN81779 Breast ca
C 302	46.2	3.0	479	8	ABX47707	ABX47707 Bovine ES
C 303	46.2	3.0	615	2	AD801494	AD801494 A. gossyp
C 304	46.2	3.0	641	6	ABQ56694	ABQ56694 Human col
C 305	46.2	3.0	1104	12	ADK16582	ADK16582 Nanoparcha
C 306	46.2	3.0	5487	6	ABL33598	ABL33598 Human imm
C 307	46.2	3.0	5493	13	AD89401	AD89401 Oligonucle
C 308	46.2	3.0	7057	4	AA646602	AA646602 Tumour su
C 309	46.2	3.0	7057	6	ABL33849	ABL33849 Human imm
C 310	46.2	3.0	7057	6	ABL34595	ABL34595 Human met
C 311	46.2	3.0	7057	6	ABL70408	ABL70408 Chemical
C 312	46.2	3.0	7057	6	AA613355	AA613355 Human gen
C 313	46.2	3.0	7057	7	AD599856	AD599856 Complemen
C 314	46.2	3.0	8079	6	ABL92313	ABL92313 Chemical
C 315	46.2	3.0	10205	6	ABK31275	ABK31275 Signal tr
C 316	46.2	3.0	10205	6	ABL70236	ABL70236 Chemical
C 317	46.2	3.0	11631	10	ADL13897	ADL13897 Osteoarth
C 318	46.2	3.0	18154	6	ABL32255	ABL32255 Human imm
C 319	46.2	3.0	50000	6	ABL56202	ABL56202 AmEPV gen
C 320	46.2	3.0	110000	12	ADK16049_2	Continuation (3 of
C 321	46	3.0	494	5	ABV10021	ABV10021 Human pro
C 322	46	3.0	1498	3	AD000017	AD000017 Scorpion
C 323	46	3.0	1554	14	ADZ70999	ADZ70999 Human chr
C 324	46	3.0	3970	12	ADQ23340	ADQ23340 Human sof
C 325	46	3.0	5145	3	AAA70209	AAA70209 Plasmodi
C 326	46	3.0	5647	6	ABL33566	ABL33566 Human imm
C 327	46	3.0	5647	6	ABL70355	ABL70355 Chemical
C 328	46	3.0	5647	6	ABL61320	ABL61320 Human gen
C 329	46	3.0	5768	6	AAK31192	AAK31192 Signal tr
C 330	46	3.0	5768	6	ABL70517	ABL70517 Chemical
C 331	46	3.0	5768	6	AA611105	AA611105 Human gen
C 332	46	3.0	7459	6	ABK31382	ABK31382 Signal tr
C 333	46	3.0	7459	6	ABL32257	ABL32257 Human imm
C 334	46	3.0	7657	4	AA645477	AA645477 Chemical
C 335	46	3.0	7657	6	ABL34022	ABL34022 Human imm
C 336	46	3.0	11787	6	ABL92243	ABL92243 Chemical
C 337	46	3.0	11787	10	ADB54202	ADB54202 Pretreat
C 338	46	3.0	11787	10	ADB54330	ADB54330 Pretreat
C 339	46	3.0	17738	6	ABL33538	ABL33538 Human imm
C 340	46	3.0	33734	13	ABD32715	ABD32715 Human can
C 341	45.8	3.0	402	13	ACN58883	ACN58883 Cotton gy
C 342	45.8	3.0	627	13	ACN54555	ACN54555 Cotton an
C 343	45.8	3.0	648	6	ABQ60739	ABQ60739 Human col
C 344	45.8	3.0	706	6	ABQ42146	ABQ42146 Oligonucle
C 345	45.8	3.0	706	6	ABQ42147	ABQ42147 Oligonucle
C 346	45.8	3.0	847	14	ADZ71063	ADZ71063 Human chr
C 347	45.8	3.0	1194	14	ADZ71076	ADZ71076 Human chr
C 348	45.8	3.0	1508	14	ADZ70993	ADZ70993 Human chr
C 349	45.8	3.0	4041	3	AAA70170	AAA70170 Plasmodi
C 350	45.8	3.0	5107	6	ABL33066	ABL33066 Human imm
C 351	45.8	3.0	5364	6	ABK40005	ABK40005 Human che
C 352	45.8	3.0	5454	3	AAA70189	AAA70189 Plasmodi
C 353	45.8	3.0	6754	6	ABL70346	ABL70346 Chemical
C 354	45.8	3.0	6754	6	AA613305	AA613305 Human gen
C 355	45.8	3.0	8067	6	ABN80224	ABN80224 Human che
C 356	45.8	3.0	8759	8	ABZ10238	ABZ10238 Haematopo
C 357	45.8	3.0	8759	8	ABZ10110	ABZ10110 Haematopo
C 358	45.8	3.0	8759	10	ADB54214	ADB54214 Pretreat
C 359	45.8	3.0	8759	10	ADE84148	ADE84148 Human lym
C 360	45.8	3.0	8759	13	ADS89514	ADS89514 Oligonucle
C 361	45.8	3.0	12405	4	AA645330	AA645330 Chemical
C 362	45.8	3.0	12405	6	ABK28169	ABK28169 DNA trans
C 363	45.8	3.0	12405	6	AA661143	AA661143 Human gen
C 364	45.8	3.0	17534	6	ABK40026	ABK40026 Human che
C 365	45.8	3.0	17848	4	AA645323	AA645323 Chemical
C 366	45.8	3.0	17848	6	ABK39976	ABK39976 Human che
C 367	45.8	3.0	17848	6	ABK28164	ABK28164 DNA trans
C 368	45.8	3.0	110000	2	AAV21209_15	Continuation (16 o
C 369	45.8	3.0	110000	5	AA161373_4	Continuation (5 of
C 370	45.6	3.0	310	4	AAH71505	AAH71505 Human cer
C 371	45.6	3.0	303	5	ABV44911	ABV44911 Human pro
C 372	45.6	3.0	603	8	ACA39423	ACA39423 Prokaryot
C 373	45.6	3.0	752	14	ADZ70933	ADZ70933 Human chr
C 374	45.6	3.0	3582	3	AAA70241	AAA70241 Plasmodi
C 375	45.6	3.0	6794	6	ABK31264	ABK31264 Signal tr
C 376	45.6	3.0	6794	6	ABL70219	ABL70219 Chemical
C 377	45.6	3.0	6794	6	AA661174	AA661174 Human gen
C 378	45.6	3.0	8900	13	AD89686	AD89686 Oligonucle
C 379	45.6	3.0	8985	14	ABZ22175	ABZ22175 Plasmodi
C 380	45.6	3.0	19459	6	ABK31212	ABK31212 Signal tr
C 381	45.6	3.0	19459	6	ABL70527	ABL70527 Chemical
C 382	45.6	3.0	23272	10	AA663508	AA663508 Mycoplasma
C 383	45.6	3.0	23272	12	ACC69138	ACC69138 M. genita
C 384	45.6	3.0	23272	12	ADN48943	ADN48943 Mycoplasma

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FT /transl_except= (pos:1529..1531, aa:Xaa)
FT /note= "Xaa = unknown"
XX WO9955859-A2.
XX
XX
XX PD 04-NOV-1999.
XX
XX PF 28-APR-1999; 99WO-BP003025.
XX
XX PR 29-APR-1998; 98EP-00201392.
XX
XX PA (VLA-) VLAMS INTERUNIVERSITAIR INST BIOTECHNOL.
XX
XX PY Pype SMC, Remacle JBFJG, Huybroeck DFE;
XX
XX WPI: 2000-062029/05.
XX P-PSDB; AAY56021.
XX
XX Novel proteins used to treat inflammatory diseases, NF-kappaB related
XX diseases and for improvement of anti-tumor treatments.
XX
XX Claim 11; Page 45-46; 48pp; English.
XX
XX This sequence represents the gene encoding human CD40 receptor
XX interacting protein 4C4. The protein is a functional protein capable of
XX interacting with the cytoplasmic domain of CD40 and/or other receptors of
XX the tumour necrosis factor (TNF) receptor superfamily such as CD30 and
XX TNF receptor 1, where the protein has no homology to TNF receptor
XX associated factor (TRAF)-proteins. The CD40 binding proteins can be used
XX as modulators of the CD40 signalling pathway, especially to diagnose and
XX treat TRAF-related, CD40-related, NF-kappaB related and/or Jun (kinase)-
XX related diseases, and for the improvement of anti-tumour diseases.
XX Diseases which may be treated include atherosclerosis, arthritis,
XX multiple sclerosis, systemic lupus erythematosus, graft rejection, graft
XX versus host disease, allergy, and autoimmune disease. The proteins can be
XX used to sensitize tumour cells to anti-tumour treatments and to screen
XX for compounds which interfere with the interaction of the proteins with
XX other protein components of the TRAF, CD40 or NF-kappaB related pathway
XX
SQ Sequence 1536 BP; 530 A; 248 C; 342 G; 413 T; 0 U; 3 Other;

Query Match 99.8%; Score 1533; DB 3; Length 1536;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAAGAGGCTCCGGGAGATAGCGGACAGTAGGGCTGCCCTCTTTTGAAGCGGT 60
DB 1 AGAAGAGGCTCCGGGAGATAGCGGACAGTAGGGCTGCCCTCTTTTGAAGCGGT 60

QY 61 TTTCGTCTCTTCCGCGAGTGGCTCCAGCTCACGAGGGCGGTCCCGGTAGCGGA 120
DB 61 TTTCGTCTCTTCCGCGAGTGGCTCCAGCTCACGAGGGCGGTCCCGGTAGCGGA 120

QY 121 GCGGTGTCAGGGCGGGAAGGGAGTGGTGGCGCTGCGGCGTAGGAGCAGCAGGAGCAG 180
DB 121 GCGGTGTCAGGGCGGGAAGGGAGTGGTGGCGCTGCGGCGTAGGAGCAGCAGGAGCAG 180

QY 181 TGTGTCTGTTCAGCGCGGCGTGGAGACATGGGAGACCCGGGGTCGGAATATAGAAATC 240
DB 181 TGTGTCTGTTCAGCGCGGCGTGGAGACATGGGAGACCCGGGGTCGGAATATAGAAATC 240

QY 241 TGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACACGAGTGAATGAAGACACAT 300
DB 241 TGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACACGAGTGAATGAAGACACAT 300

QY 301 TCAGTTTGTTCAGTGAAGGACCATCGAGACCTGTTTGAATACATCGATCTGCTGTGG 360
DB 301 TCAGTTTGTTCAGTGAAGGACCATCGAGACCTGTTTGAATACATCGATCTGCTGTGG 360

QY 361 TGATGATGAAACCCCTAGCGCTATTATATAGTGAATTTCTGTTTCTTAAATGCCAAACG 420

DB 361 TGATGATGAAACCCCTAGCGCTATTATAGTGAATTTCTGTTTCTTAAATGCCAAACG 420
QY 421 ACAGGGTGATTTTGGCATTTTAAATATGAAGAGTGAAGAACAGACACAGAAATAA 480
DB 421 ACAGGGTGATTTTGGCATTTTAAATATGAAGAGTGAAGAACAGACACAGAAATAA 480
QY 481 TGAAGTGAGCAAAATCACTGCAGATTCTCTAAGCAAGGAAACACATTTTCGAGTATAT 540
DB 481 TGAAGTGAGCAAAATCACTGCAGATTCTCTAAGCAAGGAAACACATTTTCGAGTATAT 540
QY 541 AGAACACCAATCATTTGAAGAAAGCCCATCTTTTCATCAAGAAAGAAATAGATAATCT 600
DB 541 AGAACACCAATCATTTGAAGAAAGCCCATCTTTTCATCAAGAAAGAAATAGATAATCT 600
QY 601 TGTGCTTCCAGATTGTTGGAATGAAGAAACAGCATTTATGTTTACAGAACATACAAATG 660
DB 601 TGTGCTTCCAGATTGTTGGAATGAAGAAACAGCATTTATGTTTACAGAACATACAAATG 660
QY 661 GCTTGAATGAAGAGGTAATTTAGGATGTAAGGATTGTTTCAGCAGTTTCGGCATTTGGG 720
DB 661 GCTTGAATGAAGAGGTAATTTAGGATGTAAGGATTGTTTCAGCAGTTTCGGCATTTGGG 720
QY 721 ATCGAAAGCAGAAAGCATGTCCATGTCTCAAGGAATGGATTGCATATTTAGTAACCCC 780
DB 721 ATCGAAAGCAGAAAGCATGTCCATGTCTCAAGGAATGGATTGCATATTTAGTAACCCC 780
QY 781 TAATGGCAGTAAATAACTACTAGCAAGCTTCTACGAAAGAAATTTAGGAAACATGA 840
DB 781 TAATGGCAGTAAATAACTACTAGCAAGCTTCTACGAAAGAAATTTAGGAAACATGA 840
QY 841 TGTTTCTAAAGCCCATGTAATTTCAAGATTGTTTAAAGGAATCAACTAATGATTCAT 900
DB 841 TGTTTCTAAAGCCCATGTAATTTCAAGATTGTTTAAAGGAATCAACTAATGATTCAT 900
QY 901 TTGTAATTTAGTGAATTAACAAATAATAAATAATTTGATGCTACTGTAAAGATTTTCAA 960
DB 901 TTGTAATTTAGTGAATTAACAAATAATAAATAATTTGATGCTACTGTAAAGATTTTCAA 960
QY 961 TACTGTTTACAGTTTGTAGTAAACATACAGACCTTTTATCTGATATGAGGGGGCAGAGA 1020
DB 961 TACTGTTTACAGTTTGTAGTAAACATACAGACCTTTTATCTGATATGAGGGGGCAGAGA 1020
QY 1021 ATTACAGAAAGAAATGAGAGGTAATTTGTTTAAATACAGTTTACAGTGCACCAAGAT 1080
DB 1021 ATTACAGAAAGAAATGAGAGGTAATTTGTTTAAATACAGTGCACCAAGAT 1080
QY 1081 AGCAGACATATTGCAAGAAAGAAATGAAGATGAAGATATTTAAGATATTTAGAGAGAA 1140
DB 1081 AGCAGACATATTGCAAGAAAGAAATGAAGATGAAGATATTTAAGATATTTAGAGAGAA 1140
QY 1141 TGCCAAATCTGTATCATATAATTTGATGAGGCACTTACAGTTTCAAGAAAGAAACCCCTAGT 1200
DB 1141 TGCCAAATCTGTATCATATAATTTGATGAGGCACTTACAGTTTCAAGAAAGAAACCCCTAGT 1200
QY 1201 GATTTATCTCCAGTGCACAAATTCAGTGCCTCTGCTGATTTGTTTGTGGCTTTT 1260
DB 1201 GATTTATCTCCAGTGCACAAATTCAGTGCCTCTGCTGATTTGTTTGTGGCTTTT 1260
QY 1261 AAAAGAAATGTTGTCACATATAGCAGAGTGTATTTGTCATATTTGACTACTTTTAA 1320
DB 1261 AAAAGAAATGTTGTCACATATAGCAGAGTGTATTTGTCATATTTGACTACTTTTAA 1320
QY 1321 TGATTTGTGTTTTACAAATGAATTTTGAAGCAAAATTTAATTTGCTTCTGATGG 1380
DB 1321 TGATTTGTGTTTTACAAATGAATTTTGAAGCAAAATTTAATTTGCTTCTGATGG 1380
QY 1381 TGCTAATACAACTCGGGAAGAAAGTCTGGAGTAGCTACAAATTTGTTAGAAATTTTCC 1440
DB 1381 TGCTAATACAACTCGGGAAGAAAGTCTGGAGTAGCTACAAATTTGTTAGAAATTTTCC 1440
QY 1441 TGAAATCATCATTTTGGAACTGTTTAAATCATCGATTGCTCAATTTGCTGATTTCTAT 1500


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QY 864 TTCAGGATTGTTTAAAGGAATCAACTAATGATTCAATTTGTAATTTAGTGCAATAACAAA 923
Db 873 TTCAGGATTGTTTAAAGGAATCAACTAATGATTCAATTTGTAATTTAGTGCAATAACAAA 932
QY 924 ATAATAAAAAATATTGATGCTACTCTGTAATAAGTTTCAATACTGTTTACAGTTTGTAGTAAAC 983
Db 933 ATAATAAAAAATATTGATGCTACTCTGTAATAAGTTTCAATACTGTTTACAGTTTGTAGTAAAC 992
QY 984 ATAACAGACTTATCTGATATATTAGGGGGCAAGAGAAATTACAGGAAAAAATGAGAGG 1043
Db 993 ATAACAGACTTATCTGATATATTAGGGGGCAAGAGAAATTACAGGAAAAAATGAGAGG 1052
QY 1044 TAAATTTGTTTAAATACACGTTTACAGTGCAACAGAAATAGCAACATATTGCAAAAGAAA 1103
Db 1053 TAAATTTGTTTAAATACACGTTTACAGTGCAACAGAAATAGCAACATATTGCAAAAGAAA 1112
QY 1104 TGAAGTAGAAGATATTAAAGAAATATTATAGAGAGAAATGCCAAAATCTGTATCATATTTG 1163
Db 1113 TGAAGTAGAAGATATTAAAGAAATATTATAGAGAGAAATGCCAAAATCTGTATCATATTTG 1172
QY 1164 ATGAGGCATCTACAGTTTCAAGAGAAAACCAACCTAGTGTATTTATCTCCAGTGCACAATTC 1223
Db 1173 ATGAGGCATCTACAGTTTCAAGAGAAAACCAACCTAGTGTATTTATCTCCAGTGCACAATTC 1232
QY 1224 AGTCAGCTCCTGCACCTGTTATGTTTATTTGTCGCTTAAAGAAATTTGGTGTCAACTATAG 1283
Db 1233 AGTCAGCTCCTGCACCTGTTATGTTTATTTGTCGCTTAAAGAAATTTGGTGTCAACTATAG 1292
QY 1284 CAGAGTGATTTGTCATACATATTATGACTACTTTAAATGATTTGTGTTTTACAAATGAAT 1343
Db 1293 CAGAGTGATTTGTCATACATATTATGACTACTTTAAATGATTTGTGTTTTACAAATGAAT 1352
QY 1344 ATTTGAAGCAATTTAAATGATTTGTTTCTGATGGTGCTAATACAAACCTGGGAAGAA 1403
Db 1353 ATTTGAAGCAATTTAAATGATTTGTTTCTGATGGTGCTAATACAAACCTGGGAAGAA 1412
QY 1404 AGTCGAGTAGCTACAAATTTGTTAGAAAATTTTCTGAAATCATCATTTGGAACGTTT 1463
Db 1413 AGTCGAGTAGCTACAAATTTGTTAGAAAATTTTCTGAAATCATCATTTGGAACGTTT 1472
QY 1464 TAAATCATCGATTACAAATTTGTCACCTTGATGATTTCTATATCCGAAATATAAACTAATTC 1523
Db 1473 TAAATCATCGATTACAAATTTGTCACCTTGATGATTTCTATATCCGAAATATAAACTAATTC 1532
QY 1524 ATTTAA 1529
Db 1533 ATTTAA 1538
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RESULT 3

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ADP76786
ID ADF76786 standard; cDNA; 4061 BP.
XX
AC ADF76786;
XX
XX
XX 26-FEB-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein cDNA seqID 461.
XX
XX human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neurotrophic factor; hormone; cell receptor;
KW receptor-ligand interaction; cytoskeletal; chondrocyte; tumour; ss; gene.
XX
OS Homo sapiens.
XX
XX WO2003072035-A2.
XX
XX 04-SEP-2003.
XX
XX 21-FEB-2003; 2003WO-US005241.
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XX
PR 22-FEB-2002; 2002US-0359461P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
PI Williams PM, Wood WI, Wu TD;
XX
PI WPI; 2003-721702/68.
DR P-P8DB; ADF76787.
XX
PT New PRO polypeptides, useful for diagnosing and treating an immune
PT related disorder, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
PT diabetes mellitus.
XX
PS Claim 2; SEQ ID NO 461; 918pp; English.
XX
CC This invention relates to novel nucleic acids encoding human PRO secreted
CC and transmembrane proteins. Extracellular proteins play important roles
CC in the formation, differentiation and maintenance of multicellular
CC organisms. The fate of many individual cells (for example proliferation,
CC migration or differentiation) is typically governed by information
CC received from other cells and the immediate environment. The information
CC is often transmitted by secreted polypeptides (for example mitogenic
CC factors, survival factors, cytotoxic factors, differentiation factors,
CC neurotrophic factors and hormones) which are received and interpreted by diverse
CC cell receptors or membrane bound proteins. These membrane bound proteins
CC and receptors may be of use as pharmaceutical and diagnostic agents, such
CC as in the blocking of receptor-ligand interactions. The current invention
CC provides the amino acid sequences of novel human membrane bound receptors
CC and proteins, along with the cDNA sequences encoding them. The novel
CC proteins of the invention may have cytostatic activities through the
CC stimulation of chondrocytes. The nucleic acids of the invention may be
CC useful for the manufacture of a medicament for diagnosing or treating a
CC tumour in a mammal. In addition, they may be useful for measuring or
CC detecting the expression of a tumour associated gene. The present
CC sequence is a cDNA sequence which encodes a human PRO protein of the
CC invention.
XX
SQ Sequence 4061 BP; 1470 A; 597 C; 720 G; 1274 T; 0 U; 0 Other;
Query Match 73.7%; Score 1131.6; DB 10; Length 4061;
Best Local Similarity 99.6%; Pred. No. 9.5e-250;
Matches 1134; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 391 TCATATCTCTGTTCTCTAAATGCCAAAACGACAGGGTGAATTTTTCGATTTTAAATAT 450
Db 1519 TCAGATTCGTGTTTCTTAAATGCCAAAACGACAGGGTGAATTTTTCGATTTTAAATAT 1578
QY 451 GAAGAGGTGAAACACAGACAGAAATTAATGAAGTGAGCAAAATCACTCCAGATTTGTC 510
Db 1579 GAAGAGGTGAAACACAGACAGAAATTAATGAAGTGAGCAAAATCACTCCAGATTTGTC 1638
QY 511 TAAGCAAGGAACCAACATTTTCGAGTATATAGAACCAACCAATCATTTGAAGAAAAGCCATC 570
Db 1639 TAAGCAAGGAACCAACATTTTCGAGTATATAGAACCAACCAATCATTTGAAGAAAAGCCATC 1698
QY 571 ACTTTCATCAAGAAAGAAATAGATAATCTTGTGCTTCAGATTTTGGAAATGGAATGAAAACA 630
Db 1699 ACTTTCATCAAGAAAGAAATAGATAATCTTGTGCTTCAGATTTTGGAAATGGAATGAAAACA 1758
QY 631 AGCATTTATGTTTACAGAACCAATCAAAATGCTTGAATTAAGAGAGTAAATAGGATG 690
Db 1759 AGCATTTATGTTTACAGAACCAATCAAAATGCTTGAATTAAGAGAGTAAATAGGATG 1818
QY 691 TAAGGATTTGTTTCAGCAGTTTCGGCATTTGGGATCGAAAGCAGAAAAGCATGTCATGTGTC 750
Db 1819 TAAGGATTTGTTTCAGCAGTTTCGGCATTTGGGATCGAAAGCAGAAAAGCATGTCATGTGTC 1878
QY 751 CAAGGAATGGATGTCATATTTAGTAAACCCCTTAATGGCAGTAAATAAACTACTAGGCAAGC 810
Db 1879 CAAGGAATGGATGTCATATTTAGTAAACCCCTTAATGGCAGTAAATAAACTACTAGGCAAGC 1938
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Qy 811 TTCTCTACGAAAAAATTTAGGGAACATGATGTTCTAAAGCCCATGGTAAATTCAGGA 870
Db 1939 TTCTCTACGAAAAAATTTAGGGAACATGATGTTCTAAAGCCCATGGTAAATTCAGGA 1998
Qy 871 TTTGTTAAAGGAATCAACTAATGATTCAAATTTGTAATTTAGTCATAAACAATAATAA 930
Db 1999 TTTGTTAAAGGAATCAACTAATGATTCAAATTTGTAATTTAGTCATAAACAATAATAA 2058
Qy 931 AAATATTGATCTACTGTAAAAAGTTTCAATFACCTGTTTACAGTTTAGTAAACAATACAG 990
Db 2059 AAATATTGATCTACTGTAAAAAGTTTCAATFACCTGTTTACAGTTTAGTAAACAATACAG 2118
Qy 991 ACCTTTATCTGATATTTAGGGGGCAAGAGAATACAGAAAAAATGAGAGGTAAATTG 1050
Db 2119 ACCTTTATCTGATATTTAGGGGGCAAGAGAATACAGAAAAAATGAGAGGTAAATTG 2178
Qy 1051 TTTAAATACAGTTTACAGTCAACAAGAATAGCAGACATATTGCAAAAGAAATGAAGAT 1110
Db 2179 TTTAAATACAGTTTACAGTCAACAAGAATAGCAGACATATTGCAAAAGAAATGAAGAT 2238
Qy 1111 GAAGATATTTAAGAAATATTATAGAGAGAAATGCCAAATCTGTATCATATAATTGATGAGGC 1170
Db 2239 GAAGATATTTAAGAAATATTATAGAGAGAAATGCCAAATCTGTATCATATAATTGATGAGGC 2298
Qy 1171 ATCTACAGTTTCAAGAAAAACCACTAGTGAATTTATCTCCAGTGCACAAATTCAGTCAGC 1230
Db 2299 ATCTACAGTTTCAAGAAAAACCACTAGTGAATTTATCTCCAGTGCACAAATTCAGTCAGC 2358
Qy 1231 TCCTGCACCTGTTATGTTATTTGTTGGCTTTTAAAGAAATTTGGTCAACTATAGCAGAGTG 1290
Db 2359 TCCTGCACCTGTTATGTTATTTGTTGGCTTTTAAAGAAATTTGGTCAACTATAGCAGAGTG 2418
Qy 1291 TATTGTCAATACATTAATGACTACTTTAAATGATTTGGTTTACAAATGAATATTTCGAA 1350
Db 2419 TATTGTCAATACATTAATGACTACTTTAAATGATTTGGTTTACAAATGAATATTTCGAA 2478
Qy 1351 AGCAAAATTAATTCGATTTGTTCTGATGGTGTGCTAATAACANCTCGGGAAGAAAGTCTGG 1410
Db 2479 AGCAAAATTAATTCGATTTGTTCTGATGGTGTGCTAATAACANCTCGGGAAGAAAGTCTGG 2538
Qy 1411 AGTAGCTCAAAATTTAGAAATTTTCCGAAATCATCATTTTGGAACTGTTTAAATCA 1470
Db 2539 AGTAGCTCAAAATTTAGAAATTTTCCGAAATCATCATTTTGGAACTGTTTAAATCA 2598
Qy 1471 TCGATTACAAATTTGTCACCTTGATGATTCATATCCGAAATAAACAATTAATCAATTTAA 1529
Db 2599 TCGATTACAAATTTGTCACCTTGATGATTCATATCCGAAATAAACAATTAATCAATTTAA 2657

RESULT 4
ID AA192516 standard; cdna; 632 BP.
XX AC AA192516;
XX DT 06-NOV-2001 (first entry)
XX DE Human polynucleotide SEQ ID NO 12576.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX OS Homo sapiens.
XX PN WO200164835-A2.
XX PD 07-SEP-2001.
XX PF 26-FEB-2001; 2001WO-US004927.

PR 28-FEB-2000; 2000US-00515126.
XX 18-MAY-2000; 2000US-00577409.
PA (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-514838/56.
DR P-PSDB; AAO12585.
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX Claim 1; SEQ ID NO 12576; 1399pp + Sequence Listing; English.
XX The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA00010-AA013910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, hematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 632 BP; 172 A; 132 C; 177 G; 151 T; 0 U; 0 Other;

Query Match 37.8%; Score 580.2; DB 4; Length 632;
Best Local Similarity 97.8%; Pred. No. 3.1e-123;
Matches 588; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Qy 25 GCGGACAGTAGGGCTGCCCTCTTTTGAAGCGGTTTTTCTCTTTCCGCCAGTGGCC 84
Db 32 GCGGACAGTAGGGCTGCCCTCTTTTGAAGCGGTTTTTCTCTTTCCGCCAGTGGCC 91
Qy 85 TCCAGCTCACGAGGGGGGGTCCCGGTAGCGGAGGGGGTGCAGGGCGGGAAGGGAG 144
Db 92 TCCAGCTCACGAGGGGGGGTCCCGGTAGCGGAGGGGGTGCAGGGCGGGAAGGGAG 151
Qy 145 TGGTGGGGCTGGCGAGTAGGACAGGAGGAGGAGTGGTGTCTCAGCGCGCCGCTCGG 204
Db 152 TGGTGGGGCTTCGGCAGTAGGACAGGAGGAGGAGTGGTGTCTCAGCGCGCCGCTCGG 211
Qy 205 AGACATGGGAGACCCGGGGTCGGAAATAATAGAAATCTGTCCCTCCAGCTGGCCCTGAGGC 264
Db 212 AGACATGGGAGACCCGGGGTCGGNAATAATAGAAATCTGTCCCTCCAGCTGGCCCTGAGGC 271
Qy 265 ATCTGAGTCAACACCGGATGAAATGAAGACGACATTCAGTTGTCTGAGTGAAGACCATC 324
Db 272 ATCTGAGTCAACACCGGATGAAATGAAGACGACATTCAGTTGTCTGAGTGAAGACCATC 331
Qy 325 GAGACCTGTTCTTGAATACATCGATCTGCTGTGGTGATGATGAACCCCTAGCGCCTA 384
Db 332 GAGACCTGTTCTTGAATACATCGATCTGCTGTGGTGATGATGAACCCCTAGCGCCTA 391
Qy 385 TTATAGTGATATTTCTGTTTCTTAAATGCCAAACGACAGGGGTGATTTTTTGCATTTTTT 444
Db 392 TTATAGTGATATTTCTGTTTCTTAAATGCCAAACGACAGGGGTGATTTTTTGCATTTTTT 451
Qy 445 AAATATGAAGAAGGTGAAAAACAGACACAGAAAAATAATGAAGTGAAGCAAAAATCTGAG 504
Db 452 AAATGTGAAGAAGGTGAAAAACAGACACAGAAAAATAATGAAGTGAAGCAAAAATCTGAG 511
Qy 505 ATTGTCTAAGCAAGGAACCAATTTTCGAGTATATAGAACCAACCAATCATTTGAAGAAA 564
Db 512 ATTGTCTAAGCAAGGAACCAATTTTCGAGTATATTTGAACCAACCAATCATTTGAAGAAA 571
Qy 565 GCCATCACTTTTCATCAAGAAAAAATAATAGTAATCTTTGTGCTTCCAGATTTGTTGGAATGA 624

CC male or female contraception, menopausal and post-menopausal disorders in
CC women, heart diseases and for the treatment of aging due to reduced
CC hormonal activity. The present sequence encodes human COASTER protein
CC sequence #2
XX

PS Sequence 4999 BP; 1614 A; 858 C; 1037 G; 1490 T; 0 U; 0 Other;
XX
Query Match 20.7%; Score 317.6; DB 6; Length 4999;
Best Local Similarity 90.9%; Pred. No. 1.8e-62;
Matches 360; Conservative 0; Mismatches 34; Indels 2; Gaps 2;
QY 1 AGAGAAAGAGGCTCCGGGGAGATAGCGGACAGTGAAGGCTGCCCTCTTTTGAAGCGGT 60
DB 16 AGAGAAAGCGGCTCCGGGGGATAGCGGGCCAGTAAAGGGCCGCTCTCTCTTTGAAGAGGT 75
QY 61 TTT-CGTCTCTTTCCCGCAGTGGCTCCAGCTACGAGGGGCGGGTCCCGGTAGCGCG 119
DB 76 TTTGGGTCTCTTTCCCGCGTGGCGCTCAGCGAGGGCGGGTCCCGGTAGCGCC 135
QY 120 AGGCGGTCCAGGGCGGGAAGGGAGTGTGGCGGTGCGGAG-TAGGGACAGCAGGAGC 178
DB 136 AGGCGGTCCAGGGCGGGAAGGGAGTTCGTGGCGAGCGGCGGCAAGGGACAGCAGGAGC 195
QY 179 AGTGTGTCTGTCCAGCGGCGCTCCGAGACATGGGAGACCGGGGTCCGAAATATAGAA 238
DB 196 AGTGTGTCTGTCCAGCGGCGCTCCGAGACATGGGAGACCGGGGTCCGAGATATAGAA 255
QY 239 TCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAACGGATGAAATGAAGACGAC 298
DB 256 TCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAACGGATGAAATGAAGACGAC 315
QY 299 ATTCAAGTTGTGAGGAGGACCATCGAGACCTGTTCTTGAATACATCGATCTGCTGT 358
DB 316 ATTCAAGTTGTGAGGAGGACCATTACGACCTGTTCTTGAATACATCGATCTGCTGT 375
QY 359 GGTGATGATGAAACCCCTAGCGCCCTATTATAGTAT 394
DB 376 AGTGAATGAGAGCCTTAGCACCTCTTATCTATCTGAT 411

RESULT 8
ADX07795
ID ADX07795 standard; DNA; 4999 BP.
XX
AC ADX07795;
XX
DT 21-APR-2005 (first entry)
XX
DE Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 2360.
XX
KW cytosstatic; cyclin-dependent kinase; cdk; biomarker; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2005012875-A2.
XX
PD 10-FEB-2005.
XX
PF 29-JUL-2004; 2004WO-US024424.
XX
PR 29-JUL-2003; 2003US-0490890P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Li M, Rupnow BA, Webster KR, Jackson DG, Wong TW;
XX
DR WPI; 2005-163068/17.
DR P-PSDB; ADX07796.
XX
PT Biomarkers useful for predicting or determining the response of a mammal
PT to a cancer treatment comprising administration of a modulator of cyclin-
PT dependent kinase activity.
XX

PS Claim 5; SEQ ID NO 2360; 141pp; English.
XX
CC This invention describes a novel method of predicting or determining
CC whether a mammal will respond or is responding to an anti-cancer agent
CC that modulates cyclin-dependent kinase (cdk) activity. The method
CC comprises measuring the level of one or more biomarkers selected from
CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID
CC NO.1246 (Genbank EST W28729) is especially preferred). The method of the
CC invention is utilized in a kit for determining or predicting whether
CC patient would be susceptible or resistant to treatment by an agent
CC modulating cdk activity. The invention also describes a method for
CC utilizing individualized genetic profiles for treating diseases and
CC disorders based on patient's response and molecular level, specialized
CC microarrays comprising the biomarkers described, antibodies directed
CC against the biomarkers and a cell culture model to identify biomarkers.
CC The cdk modulator is preferably N-5-[(5-(1,1-Dimethylethyl)-2-
CC oxazolyl)methylthio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-
CC tartaric acid salt. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This
CC sequence encodes a biomarker used in the method of the invention.
XX

SEQ Sequence 4999 BP; 1614 A; 858 C; 1037 G; 1490 T; 0 U; 0 Other;
XX
Query Match 20.7%; Score 317.6; DB 14; Length 4999;
Best Local Similarity 90.9%; Pred. No. 1.8e-62;
Matches 360; Conservative 0; Mismatches 34; Indels 2; Gaps 2;
QY 1 AGAGAAAGAGGCTCCGGGGAGATAGCGGACAGTGAAGGCTGCCCTCTTTGAAGCGGT 60
DB 16 AGAGAAAGCGGCTCCGGGGGATAGCGGGCCAGTAAAGGGCCGCTCTCTCTTTGAAGAGGT 75

QY 61 TTT-CGTCTCTTTCCCGCAGTGGCTCCAGCTACGAGGGGCGGGTCCCGGTAGCGCG 119
DB 76 TTTGGGTCTCTTTCCCGCGTGGCGCTCAGCGAGGGCGGGTCCCGGTAGCGCC 135
QY 120 AGGCGGTCCAGGGCGGGAAGGGAGTGTGGCGGTGCGGAG-TAGGGACAGCAGGAGC 178
DB 136 AGGCGGTCCAGGGCGGGAAGGGAGTTCGTGGCGAGCGGCGGCAAGGGACAGCAGGAGC 195
QY 179 AGTGTGTCTGTCCAGCGGCGCTCCGAGACATGGGAGACCGGGGTCCGAAATATAGAA 238
DB 196 AGTGTGTCTGTCCAGCGGCGCTCCGAGACATGGGAGACCGGGGTCCGAGATATAGAA 255
QY 239 TCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAACGGATGAAATGAAGACGAC 298
DB 256 TCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAACGGATGAAATGAAGACGAC 315
QY 299 ATTCAAGTTGTGAGGAGGACCATCGAGACCTGTTCTTGAATACATCGATCTGCTGT 358
DB 316 ATTCAAGTTGTGAGGAGGACCATTACGACCTGTTCTTGAATACATCGATCTGCTGT 375
QY 359 GGTGATGATGAAACCCCTAGCGCCCTATTATAGTAT 394
DB 376 AGTGAATGAGAGCCTTAGCACCTCTTATCTATCTGAT 411

RESULT 9
ABK12407
ID ABK12407 standard; cDNA; 5143 BP.
XX
AC ABK12407;
XX
DT 05-JUN-2002 (first entry)
XX
DE cDNA #2 encoding human COASTER protein sequence #4.
XX
KW Human; COASTER; modulation of transcriptional activity; nuclear receptor;
KW steroid receptor; coactivator; coactivation process; contraception;
KW hormone-stimulated tumour growth; post-menopausal disorder; aging;
KW heart disease; contraceptive; cytostatic; cardiant; gene; ss.
XX
OS Homo sapiens.

```
XX FH Key Location/Qualifiers
XX FT CDS 226..3411
XX FT /*tag= a
XX FT /product= "COASTER protein #4"
XX PN WO200216426-A2.
XX XX 28-FEB-2002.
XX XX 16-AUG-2001; 2001WO-EP009499.
XX XX 21-AUG-2000; 2000EP-00202905.
XX XX 14-MAY-2001; 2001EP-00201771.
XX XX (ALKU ) AKZO NOBEL NV.
XX XX Dechering KJ, Mosselman S;
XX XX WPI; 2002-280916/32.
XX XX P-PSDB; AAU77901.
XX XX Novel COASTER protein useful for producing anti-COASTER antibodies which
XX XX are useful in diagnosis of disorders involving changes in the
XX XX coactivation process.
XX XX Example; Fig 1; 78pp; English.
XX XX The present invention relates to the isolation of a human COASTER protein
XX XX with several different amino acid sequences, and the polynucleotide
XX XX sequences encoding them. The sequences of the invention can be used in a
XX XX method of modulation of transcriptional activity promoted by a responsive
XX XX nuclear receptor (e.g. a steroid receptor), and a coactivator (e.g. a
XX XX COASTER protein). The COASTER protein is useful in the diagnosis of
XX XX disorders involving changes in the coactivation process. The method of
XX XX the invention is useful for determining the action of hormones and
XX XX mechanisms for control of transcription of genes in general. The method
XX XX is also useful for developing new medicines to specifically influence
XX XX physiological processes related to the functioning of a nuclear receptor
XX XX for therapeutic, diagnostic, cosmetic and contraceptive purposes. The
XX XX method can be used for the treatment of hormone-stimulated tumour growth,
XX XX male or female contraception, menopausal and post-menopausal disorders in
XX XX women, heart diseases and for the treatment of aging due to reduced
XX XX hormonal activity. The present sequence encodes human COASTER protein
XX XX sequence #4
XX XX Sequence 5143 BP; 1655 A; 883 C; 1067 G; 1538 T; 0 U; 0 Other;
XX XX
XX XX Query Match 20.7%; Score 317.6; DB 6; Length 5143;
XX XX Best Local Similarity 90.9%; Pred. No. 1.8e-62;
XX XX Matches 360; Conservative 0; Mismatches 34; Indels 2; Gaps 2;
XX XX
XX QY 1 AGAGAAAGAGGCTCCGGGGAGATAGCGGACAGTGAGGGCTGCCCTCTTTTGAAGCGGT 60
XX DB 16 AGAGAAAGCGGCTCCGGGGGATAGCGGGCGAGTAAGGGCGCTCTCTTTGAAGAGGT 75
XX QY 61 TTTT-CGTCTCTTTCCGCGAGTGGCTCCAGCTCACGCGAGGGGGGGTCCCGGTAGCGCG 119
XX DB 76 TTTTGGTCTCTTTCCGCGGGTGGCTCGGGCTCACGCGAGGGGGTCCCGGTAGCGCC 135
XX QY 120 AGGCGGTGCAGGGCGGGAAGGGAGTGGTGGCGCTCGGCGAG-TAGGACAGCAGAGC 178
XX DB 136 AGGCGGTGCAGGGCGGGAAGGGAGTTCGTGGCGACGGCGGGCAAGGGACAGCAGGAGC 195
XX QY 179 AGTGGTGTCTGCAGCGCGCGTCCGAGACATGGAGACCGGGGTCCGAATATAGAA 238
XX DB 196 AGTGGTGTCTGCAGCGCGCGCTCGAGACATGGAGACCGGGGTCCGAGATATAGAA 255
XX QY 239 TCTGTCCCTCCAGCTGGCGCTTAGGCGATCTCGAGTCAACACCGATGAAATGAAGACGAC 298
XX DB 256 TCTGTCCCTCCAGCTGGCGCTTAGGCGATCTCGAGTCAACACCGATGAAATGAAGACGAC 315
XX QY 299 ATTCAAGTTTGTTCAGTGAAGGACCATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGT 358
XX DB 316 ATTCAAGTTTGTTCAGTGAAGGACCATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGT 375
XX QY 359 GGTGATGATGAAAAACCTAGCGCTTATTATAGTAT 394
XX DB 376 AGTGAATGATGAGAGGCTAGCACCTCTTATCTATGAT 411
XX
XX RESULT 10
XX ABK12394
XX ID ABK12394 standard; cDNA; 5144 BP.
XX XX
XX AC ABK12394;
XX XX
XX DT 05-JUN-2002 (first entry)
XX XX
XX DE cDNA #1 encoding human COASTER protein sequence #4.
XX XX
XX KW Human; COASTER; modulation of transcriptional activity; nuclear receptor;
XX KW steroid receptor; coactivator; coactivation process; contraception;
XX KW hormone-stimulated tumour growth; post-menopausal disorder; aging;
XX KW heart disease; contraceptive; cytostatic; cardiant; gene; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT CDS 226..3412
XX FT /*tag= a
XX FT /product= "COASTER protein #4"
XX FT /transl_except= (pos:2974..2977, aa:Gln)
XX FT /note= "This codon has an apparent 1 nucleotide insertion
XX FT which alters the reading frame"
XX PN WO200216426-A2.
XX XX
XX PD 28-FEB-2002.
XX XX
XX PF 16-AUG-2001; 2001WO-EP009499.
XX XX
XX PR 21-AUG-2000; 2000EP-00202905.
XX PR 14-MAY-2001; 2001EP-00201771.
XX XX
XX XX (ALKU ) AKZO NOBEL NV.
XX XX
XX XX Dechering KJ, Mosselman S;
XX XX WPI; 2002-280916/32.
XX XX P-PSDB; AAU77901.
XX XX Novel COASTER protein useful for producing anti-COASTER antibodies which
XX XX are useful in diagnosis of disorders involving changes in the
XX XX coactivation process.
XX XX Example; Fig 1; 78pp; English.
XX XX The present invention relates to the isolation of a human COASTER protein
XX XX with several different amino acid sequences, and the polynucleotide
XX XX sequences encoding them. The sequences of the invention can be used in a
XX XX method of modulation of transcriptional activity promoted by a responsive
XX XX nuclear receptor (e.g. a steroid receptor), and a coactivator (e.g. a
XX XX COASTER protein). The COASTER protein is useful in the diagnosis of
XX XX disorders involving changes in the coactivation process. The method of
XX XX the invention is useful for determining the action of hormones and
XX XX mechanisms for control of transcription of genes in general. The method
XX XX is also useful for developing new medicines to specifically influence
XX XX physiological processes related to the functioning of a nuclear receptor
XX XX for therapeutic, diagnostic, cosmetic and contraceptive purposes. The
XX XX method can be used for the treatment of hormone-stimulated tumour growth,
XX XX male or female contraception, menopausal and post-menopausal disorders in
XX XX women, heart diseases and for the treatment of aging due to reduced
XX XX hormonal activity. The present sequence encodes human COASTER protein
XX XX sequence #4
XX XX Sequence 5143 BP; 1655 A; 883 C; 1067 G; 1538 T; 0 U; 0 Other;
XX XX
XX XX Query Match 20.7%; Score 317.6; DB 6; Length 5143;
XX XX Best Local Similarity 90.9%; Pred. No. 1.8e-62;
XX XX Matches 360; Conservative 0; Mismatches 34; Indels 2; Gaps 2;
XX XX
XX QY 1 AGAGAAAGAGGCTCCGGGGAGATAGCGGACAGTGAGGGCTGCCCTCTTTTGAAGCGGT 60
XX DB 16 AGAGAAAGCGGCTCCGGGGGATAGCGGGCGAGTAAGGGCGCTCTCTTTGAAGAGGT 75
XX QY 61 TTTT-CGTCTCTTTCCGCGAGTGGCTCCAGCTCACGCGAGGGGGGGTCCCGGTAGCGCG 119
XX DB 76 TTTTGGTCTCTTTCCGCGGGTGGCTCGGGCTCACGCGAGGGGGTCCCGGTAGCGCC 135
XX QY 120 AGGCGGTGCAGGGCGGGAAGGGAGTGGTGGCGCTCGGCGAG-TAGGACAGCAGAGC 178
XX DB 136 AGGCGGTGCAGGGCGGGAAGGGAGTTCGTGGCGACGGCGGGCAAGGGACAGCAGGAGC 195
XX QY 179 AGTGGTGTCTGCAGCGCGCGTCCGAGACATGGAGACCGGGGTCCGAATATAGAA 238
XX DB 196 AGTGGTGTCTGCAGCGCGCGCTCGAGACATGGAGACCGGGGTCCGAGATATAGAA 255
XX QY 239 TCTGTCCCTCCAGCTGGCGCTTAGGCGATCTCGAGTCAACACCGATGAAATGAAGACGAC 298
XX DB 256 TCTGTCCCTCCAGCTGGCGCTTAGGCGATCTCGAGTCAACACCGATGAAATGAAGACGAC 315
XX QY 299 ATTCAAGTTTGTTCAGTGAAGGACCATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGT 358
```



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KW genome mapping; biodiversity; genetic disorder.
XX Homo sapiens.
XX US2003073623-A1.
XX 17-APR-2003.
XX 30-JUL-2001; 2001US-00918995.
XX 30-JUL-2001; 2001US-00918995.
XX (DRMA/) DRMANAC R T.
XX (LABA/) LABAT I.
XX (STAC/) STACHE-CRAIN B.
XX (DICK/) DICKSON M C.
XX (JONE/) JONES L W.
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX WPI; 2003-615964/58.
XX New polynucleotide sequences obtained from various cDNA libraries, useful
XX as hybridization probes, as oligomers for PCR, for chromosome and gene
XX mapping, in the recombinant production of protein, or in generating
XX antisense DNA or RNA.
XX Claim 1; SEQ ID NO 28032; 44pp; English.
XX The invention relates to an isolated polynucleotide comprising any one of
XX 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
XX determined by the technique of SBH (sequencing by hybridisation). Also
XX included is a purified polypeptide comprising a sequence corresponding to
XX a reading frame of the novel polynucleotide. The nucleic acid sequences
XX are useful in diagnostics as expressed sequence tags (EST) for
XX identifying expressed genes or for physical mapping of the human genome,
XX in forensics, in assessing biodiversity, or in identifying mutations
XX responsible for genetic disorders and other traits. The nucleotide
XX sequences are also useful as hybridisation probes, as oligomers for PCR,
XX for chromosome and gene mapping, in the recombinant production of
XX protein, or in generating antisense DNA or RNA. The purified polypeptide
XX is useful for generating antibodies specific for it. The present sequence
XX is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
XX for this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?docID=20030073623
XX SQ Sequence 448 BP; 142 A; 82 C; 119 G; 91 T; 0 U; 14 Other;
Query Match 20.1%; Score 308; DB 9; Length 448;
Best Local Similarity 81.4%; Pred. No. 1.1e-60;
Matches 402; Conservative 0; Mismatches 11; Indels 81; Gaps 1;
Qy 128 CAGGCGGGAAGGAGTGTTGGCGCTGCGGCGAGTAGGACACGACGAGCAGTGGTGCT 187
Db 35 CGGGGCAANNNGAGNGGCGGCTGCGGCGAGTAGGACACGACGAGCAGTGGTGCT 94
Qy 188 GTACGCGCGCGCTCGGAGACATGGGAGACCGCGGTCGGAATAAATAGATCTGTCCCT 247
Db 95 GTCAGCGCGCGCTCGGAGACATGGGAGACCGCGGTCGGAATAAATAGATCTGTCCCT 154
Qy 248 CCAGCTGGCCCTGAGGCATCTGAGTCAACACGGATGAATAAGACGACATTCAGTTT 307
Db 155 CCAGCTGGCCCTGAGGCATCTGAGTCAACACGGATGAATAAGACGACATTCAGTTT 214
Qy 308 GTCAGTGAAGACCATCGAGACCTGTTCTTGAATACATCGATCTGTGGTGATGAT 367
Db 215 GTCAG----- 219
Qy 368 GAAACCTAGCGCTATTATAGTGATATCTGTTCTCTAAATGCCAAACGACAGGTT 427
Db 220 -----TATCTGTTTCTCTAAATGCCAAACGACAGGTT 253
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Qy 428 GATTTTTCGATTTTAAATATGAAGAAGGTGAAACACAGACACAGAAATATGAAGTG 487
Db 254 GATTTTTCGATTTTAAATATGAAGAAGGTGAAACACAGACACAGAAATATGAAGTG 313
Qy 488 AGCAAAATCACTGCAGATTGCTTAAGGCAAGGAAACCACTTCGAGTATATAGAACA 547
Db 314 AGCAAAATCACTGCAGATTGCTTAAGGCAAGGAAACCACTTCGAGTATATAGAACA 373
Qy 548 CCAATCATTGAAGAAAGCCATCATTTCATCAAGAAAGAAATAGATATCTTGTGCTT 607
Db 374 CCAATCATTGAAGAAAGCCATCATTTCATCAAGAAAGAAATAGATATCTTGTGCTT 433
Qy 608 CCAGATTGTTGAA 621
Db 434 CCAGATTGTTGAA 447
RESULT 13
ADC32216
ID ADC32216 standard; cDNA; 5245 BP.
XX
AC ADC32216;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human novel cDNA contig sequence, SEQ ID NO:2298.
XX
KW Human; diagnostic; drug screening; forensics; gene mapping;
KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW ulcers; osteoporosis; autoimmune disease; cancer;
KW molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW neuroprotective; antianemic; anticoagulant; thrombolytic; vulnerary;
KW antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW gene therapy; chromosome 6; ss.
XX
OS Homo sapiens.
XX WO2003029271-A2.
XX
PD 10-APR-2003.
XX
PF 24-SEP-2002; 2002WO-US030474.
XX
PR 24-SEP-2001; 2001US-0324631P.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
XX Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
XX Halley-Vicente D, Drmanac RT;
XX WPI; 2003-371981/35.
XX P-PSDB; ADC32983.
XX
XX New polynucleotide and polypeptide useful for diagnosing, preventing or
XX treating conditions such as neurodegenerative diseases, anemias, platelet
XX disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
XX cancer.
XX Example 2; SEQ ID NO 2298; 1185pp; English.
XX
XX The invention relates to 971 novel human cDNA sequences (ADC29919-
XX ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
XX invention also relates to nucleic acid sequences over 99% identical with
XX the novel human cDNAs. The invention additionally encompasses expression
XX vectors and host cells comprising a nucleic acid of the invention; the
XX recombinant production of a polypeptide of the invention; an antibody
XX against a polypeptide of the invention; a method of detecting
XX polynucleotides or polypeptides of the invention; and methods of
XX identifying a compound which binds to a polypeptide of the invention. The
XX invention further discloses methods of preventing, treating or
XX ameliorating a medical condition; kits comprising polynucleotide probes
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CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC contig sequences corresponding to the cDNA sequences of the invention
CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC -ADC33394). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anaemia, platelet
CC disorders, wounds, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a human contig
CC sequence used in an example of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 5245 BP; 1697 A; 900 C; 1069 G; 1579 T; 0 U; 0 Other;

Query Match 19.6%; Score 301.6; DB 10; Length 5245;

Best Local Similarity 90.5%; Pred. No. 8.9e-59;

Matches 333; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 28 GACGAGTGGAGGCTGCCCTCTTTTGAAGCGGTTTT-CGTCTCTTTTCGCGCAGTGGCCTC 86
DB |||||
DB 14 GAGGATTTCGTCGCGCTCCTCTTTTGAAGAGGTTTTGGGTCTCTTTTCGCGCGTGGCGTC 73
QY 87 CCACTCAGCAGGCGCGGTCGCGGTAGCCGAGCGGTGACGGCGGGAAGGGAGTG 146
DB |||||
DB 74 GCGGCTCAGCAGGCGGCGGTCGCGGTAGCGCAGCGGTGACGGCGGGAAGGGGATTC 133
QY 147 GTGGCGGCTGCGGAGTGGGACAGCAGGAGCGTGGTCTCTCAGCGGCGGCGTGGAG 206
DB |||||
DB 134 GTGGCGACGCGCGGCGGAGCAGCAGGAGCGTGGTCTCTCAGCGGCGGCGTGGAG 193
QY 207 ACATGGGAGACCGGGGTCGGAATAATAGAAATCTGTCCCTCCAGTGGCCCTGAGGCAT 266
DB |||||
DB 194 ACATGGGAGACCGGGTTCGAGATATAGATCTGTCCCTCCAGTGGCCCTGAGGCAT 253
QY 267 CTGAGTCAACACCGATGAATGAAGACGACATTCAGTTTGTCTAGTGAAGACCATCGA 326
DB |||||
DB 254 CTGAGTCAACACCGATGAATGAAGACGACATTCAGTTTGTCTAGTGAAGACCATTCAC 313
QY 327 GACCTGTTCTTGAATACATCGATCTGCTGTGTGTGATGATGAACCCCTAGCGCTATT 386
DB |||||
DB 314 GACCTGTTCTTGAATACATTCATGCTGGTCAGCAGTATGATGAAGAGCCCTAGCCTCTT 373
QY 387 ATAGTGAT 394
DB |||||
DB 374 ATACTGAT 381

RESULT 14

AA81317

ID AA81317 standard; cDNA; 3363 BP.

XX

AC AA81317;

DT

XX 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #17121.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

FN

XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US008631.
PF
XX 31-MAR-2000; 2000US-00540217.
PR
XX 23-AUG-2000; 2000US-00649167.
PR
XX (HYSE-) HYSEQ INC.
PA
XX Drmanac RT, Liu C, Tang YT;
PI
XX WPI; 2001-639362/73.
DR
XX P-PSDB; ABG17130.
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 17121; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have application in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3363 BP; 1073 A; 640 C; 755 G; 895 T; 0 U; 0 Other;

Query Match 19.6%; Score 301.4; DB 5; Length 3363;
Best Local Similarity 91.2%; Pred. No. 8.3e-59;
Matches 331; Conservative 0; Mismatches 31; Indels 1; Gaps 1;

QY 33 GTGAGGGTGGCCCTCTTTTGAAGCGGTTTT-CGTCTCTTTTCGCGCAGTGGCCTCCCAGC 91
DB |||||
DB 1 GTAAGGGCGCTCTCTCTTTGAAGAGGTTTTGCGTCTCTTTCCGCGGTGGCGC 60
QY 92 TCACGACGGGCGGTCGCCGTAGCGCGGTGACGGCGGTGAGGCGGGAAGGGAGTGTGGC 151
DB |||||
DB 61 TCACGACGGGCGGTCGCCGTAGCGCGGTGAGCGCGGTGAGGCGGGAAGGGAGTGTGGC 120
QY 152 GCGTCGCGCAGTAGGACAGCAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 211
DB |||||
DB 121 GACGCGCGGCGGACAGCAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
QY 212 GGAGACCGGGTGGAAATATAGAAATCTGTCTCCAGTGGCCCTGAGGCATCTGAG 271
DB |||||
DB 181 GGAGACCGGGTGGAGATATAGAAATCTGTCTCCAGTGGCCCTGAGGCATTTGAG 240
QY 272 TCAACACCGATGAATAATGAACGACATTCAGTTTGTGTGTGTGTGTGTGTGTGTGTGT 331
DB |||||
DB 241 TCAACACCGATGAATAATGAACGACATTCAGTTTGTGTGTGTGTGTGTGTGTGTGTGT 300
QY 332 GTTCTTGAATACATCGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 391
DB |||||
DB 301 GTTCTTGAATACATCTGT 360

Qy 392 GAT 394
Db 361 GAT 363

RESULT 15
ADC30333 standard; cDNA; 5089 BP.

AC AC30333;
AC AC30333;
DT 18-DEC-2003 (first entry)
XX Human novel cDNA sequence, SEQ ID NO:415.
XX Human; diagnostic; drug screening; forensics; gene mapping;
KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW ulcers; osteoporosis; autoimmune disease; cancer;
KW molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
KW antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW gene therapy; chromosome 6; gene; ss.
XX Homo sapiens.
OS
XX
XX WO2003029271-A2.
XX
XX 10-APR-2003.
XX
XX 24-SEP-2002; 2002WO-US030474.
XX
XX 24-SEP-2001; 2001US-0324631P.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
XX Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
XX Haley-Vicente D, Drmanac RT;
XX
XX WPI; 2003-371981/35.
XX
XX P-PSDB; ADC31304.
XX
XX New polynucleotide and polypeptide useful for diagnosing, preventing or
XX treating conditions such as neurodegenerative diseases, anemias, platelet
XX disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
XX cancer.
XX
XX Claim 1; SEQ ID NO 415; 1185pp; English.
XX
XX The invention relates to 971 novel human cDNA sequences (ADC29919-
XX ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
XX invention also relates to nucleic acid sequences over 99% identical with
XX the novel human cDNAs. The invention additionally encompasses expression
XX vectors and host cells comprising a nucleic acid of the invention; the
XX recombinant production of a polypeptide of the invention; an antibody
XX against a polypeptide of the invention; a method of detecting
XX polynucleotides or polypeptides of the invention; and methods of
XX identifying a compound which binds to a polypeptide of the invention. The
XX invention further discloses methods of preventing, treating or
XX ameliorating a medical condition; kits comprising polynucleotide probes
XX and/or monoclonal antibodies for carrying out the methods of the
XX invention; methods for the identification of compounds that modulate the
XX expression or activity of the polynucleotide and/or polypeptide; and 767
XX contig sequences corresponding to the cDNA sequences of the invention
XX (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
XX -ADC33394). The nucleic acids and polypeptides of the invention are
XX useful in diagnostics, drug screening, forensics, gene mapping, in the
XX identification of mutations responsible for genetic disorders or other
XX traits, for assessing biodiversity, and in producing many other types of
XX data and products dependent on DNA and amino acid sequences. They are
XX also used for treating diseases such as Parkinson's disease, Alzheimer's

CC disease and other neurodegenerative diseases, anaemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a specifically
CC claimed human cDNA sequence of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 5089 BP; 1640 A; 872 C; 1042 G; 1535 T; 0 U; 0 Other;
Query Match 19.2%; Score 295.4; DB 10; Length 5089;
Best Local Similarity 91.0%; Pred. No. 2.3e-57;
Matches 325; Conservative 0; Mismatches 31; Indels 1; Gaps 1;
Qy 39 GCTGCCCTCTTTTGAAGCGGTTTT-CGTCTCTTTCCGCCAGTGGCTCCACGCTCACGC 97
Db 1 GCGCTCTCTCTTTGAAGAGGTTTTCGGTCTCTTCCGCCGCTGGCGCTCACGC 60
Qy 98 AGGGCGGGTCCCGGTAGCGCGAGCGGTGTCAGGGCGGGAAGGGGAGTGGTGGCGGTGC 157
Db 61 AGGGCGGGTCCCGGTAGCGCGAGCGGTGTCAGGGCGGGAAGGGGAGTTCGTGGCGACGC 120
Qy 158 GGCAGTAGGACAGCAGGAGCAGTGGTGTCTCAGCGCGCGCGTCCGAGACATGGGAGAC 217
Db 121 GCGCGCAGGACAGCAGGAGCAGTGGTGTCTCAGCGCGCGCGTCCGAGACATGGGAGAC 180
Qy 218 CCGGGGTCCGAAATAATAGAACTCTGCTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACA 277
Db 181 CCGGGGTCCGAGATATAGAACTCTGCTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACA 240
Qy 278 ACCGATGAAATGAAGACGACATTCAGTTTGTCTCAGTGAAGGACCATCGAGACCTGTTCTT 337
Db 241 ACCGATGAAATGAAGACGACATTCAGTTTGTCTCAGTGAAGGACCATTCAGACCTGTTCTT 300
Qy 338 GAATACATCATCTGCTCTGTGTGATGATGAACCCCTAGCGCTATTATAGTGAT 394
Db 301 GAATACATGATCTGCTGCTGATGATGAAGAGCCCTAGCACCTCTTATATCTGAT 357

RESULT 16
AAC01653
ID AAC01653 standard; cDNA; 274 BP.
XX
XX AAC01653;
XX
XX 06-OCT-2000 (first entry)
XX
XX Human secreted protein 5' EST, SEQ ID NO: 1651.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
XX
XX Homo sapiens.
XX
XX EP1033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-00200610.
XX
XX 26-FEB-1999; 99US-0122487P.
XX
XX (GBST) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX WPI; 2000-500381/45.
XX P-PSDB; AAG01647.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for

PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 1; SEQ ID NO 1651; 71pp + Sequence Listing; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. An ORF has been identified within the
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC derived from 30 different tissues. EST sequences usually correspond
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC well suited for isolating cDNA sequences derived from the 5' ends of
CC mRNAs and even in those cases where longer cDNA sequences have been
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC mRNAs with intact 5' ends and can therefore be used to obtain full length
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC gene therapy and chromosome mapping procedures. They are used to obtain
CC upstream regulatory sequences and to design expression and secretion
CC vectors
XX
SQ Sequence 274 BP; 62 A; 50 C; 96 G; 48 T; 0 U; 8 Other;

Query Match 17.6%; Score 270.8; DB 3; Length 274;
Best Local Similarity 97.1%; Pred. No. 3.3e-52;
Matches 266; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 102 GCGGTCCTCCGTTAGCGGAGCGGTGCAGGCGGCGGAGGAGTGTGGCGCTCGGCA 161
DB 1 GCGGTCCTCCGTTAGCGGAGCGGTGCAGGCGGCGGAGGAGTGTGGCGCTCGGCA 60

QY 162 GTAGGACAGCAGGAGCAGTGTGTCTCAGCGCGGCGCTCGGACATGGGAGACCCGG 221
DB 61 GTAGGACAGCAGGAGCAGTGTGTCTCAGCGCGGCGCTCGGACATGGGAGACCCGG 120

QY 222 GGTCCGGAATATAGAACTGTGCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAACGG 281
DB 121 GGTCCGGAATATAGAACTGTGCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAACGG 180

QY 282 ATGAATGAAGACACCATTCAGTTTGTTCAGTGAAGGACCATCGAGACCTGTTCTTGAAT 341
DB 181 ATGAATGAAGACACCATTCAGTTTGTTCAGTGAAGGACCATCGAGACCTGTTCTTGAAT 240

QY 342 ACATCGATCTGCTGTGTGTGTATGATGAAACCC 375
DB 241 ACATCGATCTGCTGTGTGTGTATGATGAAACCC 274

RESULT 17
ADR52788
ID ADR52788 standard; DNA; 4961 BP.
XX
AC ADR52788;
XX
DT 18-NOV-2004 (first entry)
XX
DE Drug therapy altered expressed gene #139.
XX
KW drug activity monitoring; expression profile; gene expression;
KW peripheral blood sample; peripheral blood mononuclear cell; drug therapy;
KW CCI-779; immunosuppressant; rapamycin; mammalian target of rapamycin;
KW mTOR; ds.
XX
OS Homo sapiens.
XX
PN WO2004072265-A2.
XX
PD 26-AUG-2004.
XX
PF 11-FEB-2004; 2004WO-US004118.
XX
PR 11-FEB-2003; 2003US-0446133P.
PR 03-APR-2003; 2003US-0459782P.
PR 23-JAN-2004; 2004US-0538246P.

XX (AMHP) WYETH.
PA (BURC/) BURCZYNSKI M.
PA (TWIN/) TWINE N.
PA (DORN/) DORNER A. J.
PA (TREP/) TREPICCHIO W. L.
XX Burczynski M, Twine N, Dorner AJ, Trepicchio WL;
XX WPT; 2004-642301/62.
XX
XX Monitoring drug activities in vivo comprises comparing an expression
XX profile of a gene in a peripheral blood sample of a patient before and
XX after drug therapy.
XX
XX Disclosure; SEQ ID NO 139; 136pp; English.
XX
CC The invention relates to a method of monitoring drug activities in vivo
CC by comparing an expression profile of at least one gene in a peripheral
CC blood sample of a patient to a reference expression profile of the at
CC least one gene, where the at least one gene is differentially expressed
CC in peripheral blood mononuclear cells (PBMCs) of patients who have a non-
CC blood disease and are subjected to a drug therapy as compared to PBMCs
CC isolated from the patient before the drug therapy, and where the patient
CC has the non-blood disease and is being treated by the drug therapy. The
CC method, kit, and nucleic acid array are useful for monitoring drug
CC activities in vivo. The drug is especially CCI-779, an ester analogue of
CC the immunosuppressant rapamycin which is a potent inhibitor of the
CC mammalian target of rapamycin (mTOR). This sequence represents a gene
CC expressed in BMC altered by the drug therapy. (Note: this sequence does
CC not form part of the printed specification but was obtained in electronic
CC format from WIPO at ftp.wipo.int/pub/published_pct_sequences/).
XX
SQ Sequence 4961 BP; 1628 A; 834 C; 987 G; 1512 T; 0 U; 0 Other;

Query Match 13.6%; Score 208.2; DB 13; Length 4961;
Best Local Similarity 94.3%; Pred. No. 2.7e-37;
Matches 216; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 166 GGACGACGAGGAGCAGTGTGTCTCAGCGCGGCGCTCGGACATGGGAGACCCGGGTC 225
DB 1 GGACGACGAGGAGCAGTGTGTCTCAGCGCGGCGCTCGGACATGGGAGACCCGGGTC 60

QY 226 GGAAATATAGAACTGTGCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAACGATGA 285
DB 61 GGAGTATATAGAACTGTGCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAACGATGA 120

QY 286 AAATGAAGACGACATTCAGTTTGTTCAGTGAAGGACCATCGAGACCTGTTCTTGAATACAT 345
DB 121 AAATGAAGACGACATTCAGTTTGTTCAGTGAAGGACCATTCAGACCTGTTCTTGAATACAT 180

QY 346 CGATCTGCTGTGTGTGTATGATGAAACCCCTAGCGCCTATTATAGTGTAT 394
DB 181 TGATCTGTCAGCAGTGTGTATGATGAAAGCCCTAGACACCTCTTTATAGTGTAT 229

RESULT 18
AAS81318
ID AAS81318 standard; cDNA; 2039 BP.
XX
AC AAS81318;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #17122.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX

PD 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US008631.
PF 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
PI WPI; 2001-639362/73.
XX P-FSDB; ABG17131.
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX Claim 1; SEQ ID NO 17122; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
PS sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 2039 BP; 620 A; 472 C; 454 G; 491 T; 0 U; 2 Other;
Query Match 11.1%; Score 170; DB 5; Length 2039;
Best Local Similarity 98.8%; Pred. No. 1.1e-28;
Matches 170; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 142 GAGTGTGGCGGCTGCGGCAGTAGGACAGCAGGAGCAGTGGTCTGTCTGACGCGGCGGT 201
Db 1 GAGNGGCGGCTGCGGCAGTAGGACAGCAGGAGCAGTGGTCTGTCTGACGCGGCGGT 60
Qy 202 CGGAGACATGGGAGACCCGGGTGCGAAATTAATGAGATCTGTCTCAGTGGCCCTGA 261
Db 61 CGGAGACATGGGAGACCCGGGTGCGAAATTAATGAGATCTGTCTCAGTGGCCCTGA 120
Qy 262 GGCATCTGAGTCAACACGGATGAATGAAGACGACATTCAGTTTGTGAGT 313
Db 121 GGCATCTGAGTCAACACGGATGAATGAAGACGACATTCAGTTTGTGAGT 172
RESULT 19
ADV43036
ID ADV43036 standard; cDNA; 3042 BP.
XX AC
XX ADV43036;
XX
XX 10-MAR-2005 (first entry)
DT
XX Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 664.
XX
XX microarray; psychoneuroendocrinimmune; chronic fatigue;
KW

KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW cancer; neoplasm; infection; expressed sequence tag; ss.
XX Homo sapiens.
XX WO2004108899-A2.
XX 16-DEC-2004.
XX 04-JUN-2004; 2004WO-US017686.
XX 04-JUN-2003; 2003US-0475915P.
PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Nicholson A, Vernon SD;
PI WPI; 2005-031682/03.
XX New microarray comprising probes for genes involved in
PT psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT condition associated with PNI activity, e.g., inflammatory or infectious
PT diseases.
XX Claim 1; SEQ ID NO 664; 254pp; English.
XX The invention relates to a new microarray which comprises probes for
CC genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC microarray is useful in diagnosing a condition associated with PNI
CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC cancer and infection. The present sequence represents a
CC psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC SEQ ID NO 1829 are provided.
XX
XX Sequence 3042 BP; 1009 A; 569 C; 648 G; 816 T; 0 U; 0 Other;
Query Match 10.8%; Score 165.2; DB 14; Length 3042;
Best Local Similarity 93.0%; Pred. No. 1.7e-27;
Matches 173; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Qy 209 ATGGGAGACCCGGGTGCGAAATTAATGAGATCTGTCTCAGTGGCCCTGAGGCACT 268
Db 1 ATGGGAGACCCGGGTGCGAGATAATGAGATCTGTCTCAGTGGCCCTGAGGCACT 60
Qy 269 GAGTCAACACCGGATGAAATGAAGACGACATTCAGTTTGTCTGAGGACCATCGAGA 328
Db 61 GAGTCAACACCGGATGAAATGAAGACGACATTCAGTTTGTCTGAGGACCATCGAGA 120
Qy 329 CCTGTTCTTGAATACATCGATCTGGTCTGTGGTGTGATGATGAAACCCCTAGCGCTATTAT 388
Db 121 CCTGTTCTTGAATACATCGATCTGGTCTGTGGTGTGATGATGAAAGCGCTTAGCCTCTTAT 180
Qy 389 ACTGAT 394
Db 181 ACTGAT 186
RESULT 20
ABK12397
ID ABK12397 standard; cDNA; 3183 BP.
XX AC
XX ABK12397;
XX
XX 05-JUN-2002 (first entry)
DT
XX cDNA #2 encoding human COASTER protein sequence #3.
XX Human; COASTER; modulation of transcriptional activity; nuclear receptor;
KW steroid receptor; coactivator; coactivation process; contraception;
KW hormone-stimulated tumour growth; post-menopausal disorder; aging;
KW heart disease; contraceptive; cytostatic; cardiant; gene; ss.
XX


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OS Homo sapiens.
XX Key Location/Qualifiers
FH CDS 1..3183
FT /*tag= a
FT /partial
FT /product= "COASTER protein #3"
FT /note= "This sequence lacks a stop codon"
XX
XX WO200216426-A2.
XX
XX 28-FEB-2002.
XX
XX 16-AUG-2001; 2001WO-EP009499.
XX
XX 21-AUG-2000; 2000EP-00202905.
XX
XX 14-MAY-2001; 2001EP-00201771.
XX
XX (ALKU ) AKZO NOBEL NV.
XX
XX Dechering KJ, Mosselman S;
XX
XX WPI; 2002-280916/32.
XX
XX P-PSDB; AAU77900.
XX
XX Novel COASTER protein useful for producing anti-COASTER antibodies which
XX are useful in diagnosis of disorders involving changes in the
XX coactivation process.
XX
XX Claim 11; Page 66-67; 78pp; English.
XX
XX The present invention relates to the isolation of a human COASTER protein
XX with several different amino acid sequences, and the polynucleotide
XX sequences encoding them. The sequences of the invention can be used in a
XX method of modulation of transcriptional activity promoted by a response
XX nuclear receptor (e.g. a steroid receptor), and a coactivator (e.g. a
XX COASTER protein). The COASTER protein is useful in the diagnosis of
XX disorders involving changes in the coactivation process. The method of
XX the invention is useful for determining the action of hormones and
XX mechanisms for control of transcription of genes in general. The method
XX is also useful for developing new medicines to specifically influence
XX physiological processes related to the functioning of a nuclear receptor
XX for therapeutic, diagnostic, cosmetic and contraceptive purposes. The
XX method can be used for the treatment of hormone-stimulated tumour growth,
XX male or female contraception, menopausal and post-menopausal disorders in
XX women, heart diseases and for the treatment of aging due to reduced
XX hormonal activity. The present sequence encodes human COASTER protein
XX sequence #3
XX
XX Sequence 3183 BP; 1048 A; 593 C; 678 G; 864 T; 0 U; 0 Other;
SQ
Query Match 10.8%; Score 165.2; DB 6; Length 3183;
Best Local Similarity 93.0%; Pred. No. 1.7e-27;
Matches 173; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 209 ATGGGAGACCGGGTCGGAATAATAGAACTCTGCTCCAGCTGGCCCTGAGGCATCT 268
Db 1 ATGGGAGACCGGGTCGGAATAATAGAACTCTGCTCCAGCTGGCCCTGAGGCATCT 60
QY 269 GAGTCAACACCGATGAATAATGAAGACGACATTCAGTTTGTGTCAGTGAAGGACCATCGAGA 328
Db 61 GAGTCAACACCGATGAATAATGAAGACGACATTCAGTTTGTGTCAGTGAAGGACCATCGAGA 120
QY 329 CCTGTTCTTTGAATACATCGATCTGGTCTGTGGTGATGATGAACCCCTAGCCGCTATTAT 388
Db 121 CCTGTTCTTTGAATACATCGATCTGGTCTGTGGTGATGATGAAGAGCCTAGCACCTCTTAT 180
QY 389 AGTGAT 394
Db 181 ACTGAT 186
RESULT 21
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AAS81316
ID AAS81316 standard; cDNA; 394 BP.
XX
AC AAS81316;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #17120.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR P-PSDB; ABG17129.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 1; SEQ ID NO 17120; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping.
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
XX coding sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 394 BP; 110 A; 103 C; 111 G; 70 T; 0 U; 0 Other;
SQ
Query Match 10.7%; Score 164.8; DB 5; Length 394;
Best Local Similarity 98.8%; Pred. No. 9.2e-28;
Matches 166; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 147 GTGGCGGCTGGCGCAGTAGGACACAGCAGGAGCAGTGGTCTGTACGCGCGCGTCGGAG 206
Db 17 GTGGCGGCTGGCGCAGTAGGACACAGCAGTGGTCTGTACGCGCGCGTCGGAG 76
QY 207 ACATGGGAGACCCGGGGTCGGAAATAGTAATCTGTCCCTCAGCTGGCCCTTGAGCAT 266
Db 77 ACATGGGAGACCCGGGGTCGGAGATAATAGTAATCTGTCCCTCAGCTGGCCCTTGAGCAT 136
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QY 267 CTGAGTCAACACGATGAAATGAAGACGACATTCAGTTTGTCAAGT 314
Db 137 CTGAGTCAACACGATGAAATGAAGACGACATTCAGTTTGTCAAGT 184

RESULT 22
AAS79405
ID AAS79405 standard; cDNA; 394 BP.
XX AC AAS79405;
XX AC
XX 13-FEB-2002 (first entry)
XX DE DNA encoding novel human diagnostic protein #15209.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX P-PSDB; ABG15218.
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX Claim 1; SEQ ID NO 15209; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 394 BP; 110 A; 103 C; 111 G; 70 T; 0 U; 0 Other;
XX Query Match 10.7%; Score 164.8; DB 5; Length 394;
XX Best Local Similarity 98.8%; Pred. NO. 9.2e-28;
XX Matches 166; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 147 GTGGCGGTGGGATGAGGACGACGATGCTGTGCTGTCAGCGCGGCTCGGAG 206
Db 137 CTGAGTCAACACGATGAAATGAAGACGACATTCAGTTTGTCAAGT 184

RESULT 23
AAI1954/C
ID AAI1954 standard; cDNA; 121 BP.
XX AC AAI1954;
XX AC
XX 06-NOV-2001 (first entry)
XX DE Human polynucleotide SEQ ID NO 12014.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX KW tissue growth factor; immunomodulatory; cancer; leukaemia;
XX KW nervous system disorders; arthritis; inflammation; ss.
XX OS Homo sapiens.
XX PN WO200164835-A2.
XX PD 07-SEP-2001.
XX PF 26-FEB-2001; 2001WO-US004927.
XX PR 28-FEB-2000; 2000US-00515126.
XX PR 18-MAY-2000; 2000US-00577409.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-514838/56.
XX P-PSDB; AAO12023.
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.
XX Claim 1; SEQ ID NO 12014; 1399pp + Sequence Listing; English.
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO3910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 121 BP; 26 A; 38 C; 33 G; 24 T; 0 U; 0 Other;
XX Query Match 5.5%; Score 83.8; DB 4; Length 121;
XX Best Local Similarity 92.6%; Pred. No. 2.4e-05;
XX Matches 86; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 175 GAGCAGTGGTGTCTCAGCGCGGCTCGGAGACATCGGAGACCCCGGGTTCGGAATAAT 234
Db 101 GAACAGTGGTGTCTCAGCGCGGCTCGGAGACATCGGAGACCCCGGGTTCGGAATAAT 42
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QY	235	AGAATCTGTCCTCCAGCTGGCCCTGAGGCATCTG	269
Db	41	AGAACTGTCCTCCAGCTGGCCCTGTTTCATCG	7
RESULT 24			
ID	ABL34358/c		
XX	ABL34358 standard; DNA; 12237 BP.		
AC	ABL34358;		
DT	26-MAR-2002 (first entry)		
DE	Human immune system associated gene SEQ ID NO: 2331.		
XX	Human; immune system disease; cytosine methylation; antiasthmatic;		
KW	antiarteriosclerotic; antianemic; cytostatic; nootropic;		
KW	neuroprotective; anti-HIV; anticonvulsant; ophthalmological;		
KW	anti-rheumatic; antiarthritis; antidiabetic; antipsoriatic;		
KW	antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;		
KW	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;		
KW	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;		
db.			
OS	Homo sapiens.		
XX	WO200200928-A2.		
PN	03-JAN-2002.		
PD	02-JUL-2001; 2001WO-EP007537.		
PP	30-JUN-2000; 2000DE-01032529.		
XX	01-SEP-2000; 2000DE-01043826.		
PR	(EPIG-) EPIGENOMICS AG.		
PA	Olek A, Piepenbrock C, Berlin K;		
PI	WPI; 2002-130909/17.		
XX			
PT	Nucleic acid comprising fragment of chemically modified gene, useful for		
PT	diagnosis and treatment of diseases associated with abnormal cytosine		
PT	methylation.		
XX			
PS	Claim 1; SEQ ID NO 2331; 32pp + Sequence Listing; German.		
XX			
CC	The present invention provides a number of human immune system associated		
CC	genes which are modified by the methylation of cytosines. The sequences		
CC	can be used in the diagnosis and treatment of immune system disorders,		
CC	including eye diseases such as retinopathy, neovascular glaucoma and		
CC	macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid		
CC	leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,		
CC	rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel		
CC	diseases. The present sequence is a gene of the invention		
XX			
SQ	Sequence 12237 BP; 3050 A; 207 C; 3024 G; 5956 T; 0 U; 0 Other;		
Query Match			
Best Local Similarity 4.4%; Score 67.8; DB 6; Length 12237;			
Matches 343; Conservative 0; Mismatches 422; Indels 2; Gaps 2;			
QY	445	AAATATGAAGAGGTGAAACACAGACAGAAATATGAAGTGAGCAAAAATCACTGCAG	504
Db	6924	AAAAAATAAATAATCAACAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	6865
QY	505	ATTGCTAGGCAAGGACCACTTTCCAGTATATAGAACCAATCATTTGAAGAAA	564
Db	6864	AAAAAATAAATAATCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	6805
QY	565	GCATCACTTTTCATCAAGAAAGAAATAGATATCTTGTGCTTCAGATTGTTGGAATGA	624
Db	6804	AACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	6746

QY	625	AAAAACAAGCATTTTATGTTTACAGAACCAATACAAATGGCTTGAATATAAAGAGGTAAATT	684
Db	6745	TAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	6686
QY	685	AGGATGTAAGGATTTTCAGCAGTTCCGGATTTTCGGATTCGAAAGCAGAAAAGCATGTCCA	744
Db	6685	TAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	6626
QY	745	TGTCGCCAGGAATGGATTTGCATATTTAGTAACCCCTAATGGCAGTATATAAACTACTAG	804
Db	6625	AAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	6566
QY	805	GCAAGCTTCTCAGCAAAAAAATAAATAGGGAACATGATGTTTCTAAAGCCCATGTTAAAT	864
Db	6565	ATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	6506
QY	865	TCAGGATTTGTTAAAGGAATCACTAATGATTCATTTGTAATTTAGTGCATATAACAAAA	924
Db	6505	AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	6446
QY	925	TAAATAAATAAATTCATGCTACTGCTGTAAGAGTTTTTCAATACTGTTTACAGTTTAGTAAACA	984
Db	6445	AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	6386
QY	985	TACAGACCTTTTATCTGATATTGAGGGGCAAGAGATTACAGGAAAAAATAATGGAGAGGT	1044
Db	6385	AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	6326
QY	1045	AAATTTGTTTAAATACACGTTTACAGTGCACCAAGAAATAGCAGAACATATTGCAAAAAGAAAT	1104
Db	6325	AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	6266
QY	1105	GAAGATGAAGATATTTAAGATATTTATAGAGAGAGATGCCAAATCTGTATC-ATAATTG	1163
Db	6265	AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	6206
QY	1164	ATGAGGCATCTACAGTTTCAAGAAACACCCCTAGTGTATTTATCTC	1210
Db	6205	ATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	6159
RESULT 25			
ID	AAS46735/c		
XX	AAS46735 standard; DNA; 6292 BP.		
AC	AAS46735;		
DT	18-DEC-2001 (first entry)		
DE	Tumour suppressor gene derived chemically modified sequence #459.		
XX	Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;		
KW	tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;		
KW	cytosine methylation; ds.		
OS	Homo sapiens.		
XX	WO200168912-A2.		
PD	20-SEP-2001.		
XX	15-MAR-2001; 2001WO-EP002955.		
PR	15-MAR-2000; 2000DE-01013847.		
PR	06-APR-2000; 2000DE-01019058.		
PR	07-APR-2000; 2000DE-01019173.		
PR	30-JUN-2000; 2000DE-01032529.		
PR	01-SEP-2000; 2000DE-01043826.		
XX	(EPIG-) EPIGENOMICS AG.		
PA	Olek A, Piepenbrock C, Berlin K;		
PI			

AC ADA71938;
 XX 20-NOV-2003 (first entry)
 DT Rice gene, SEQ ID 5263.
 DE Plant; bacterial infection; fungal infection; viral infection; rice;
 XX gene; ds.
 KW Oryza sativa.
 XX WO200300898-A1.
 PN 03-JAN-2003.
 PD 22-JUN-2001; 2001WO-IB001105.
 XX 22-JUN-2001; 2001WO-IB001105.
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y,
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX WPI; 2003-175290/17.
 DR Identifying at least one gene involved in plant resistance or response to
 XX pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.
 XX Claim 27; SEQ ID NO 5263; 899pp; English.
 PS The present invention relates to a method (M1) for identifying genes
 XX involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC the expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.
 XX Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
 SQ

Query Match 4.0%; Score 60.8; DB 8; Length 2000;
 Best Local Similarity 10.1%; Pred. No. 0.0015;
 Matches 100; Conservative 458; Mismatches 415; Indels 15; Gaps 5;

QY 71 TTCGCCAGTGGCCTCCAGCTCAGCAGGCGGGGTCCTCGGTAGCGGAGCGGTGCGAG 130
 DB 8 WKSRCSSWRRRRMYMAGMWSCARMGSSRMSRMSKSKYKSCGCKMTTRRSKWY 67
 QY 131 GCGCGGAAGGAGTGGTGGCGGCTCGGAGTGGAGCAGGAGGAGTGGTCTGTC 190
 DB 68 SASSASGRTGKSSWSGSGYSGKMKYKRSKRWGRGRGRMRMRMRMRRCARSOR 127
 QY 191 AGCGCGGCGTGGAGACATGGAGACCGCGGTCGGAATAATAGAA---TCTGTCCC 246
 DB 128 MAGSGRMMGGKRSMSYMWVCYARGCGSKRKSKGSGWGTCTRRGARGSGMSGAKYK 187
 QY 247 TCCAGTGGCCTCGGAGCATCTGAGTCAACACGAGATGAATGAAGACGACATTCAGTT 306
 DB 188 SGMSKRMWSSCGRSGRRSAYSRYYGTSRKYGTYKWTYYSASRCMRYMTTYSWA 247
 QY 307 TGTCAGTGAAGACCATCAGA---CCTGTTCTTGAATACGATCTGCTGTGCTGA 363
 DB 248 CSYTWCRSKRSMWMMKMRKMRWSRSYGSWSYKMMCTAYKYSYRWCTMYRGGW 307
 QY 364 TGATGAAACCCCTAGCGCCTATTATAGTATATCTGTTTCTCTTAAATGCCAAACGACA 423
 DB 308 RGATRWGRYSRMMWYKMYWYRGYKMGKRWAGRMMSRCRWSKACYMYRWRW 367

QY 424 GGGTGATTTTTCATTTTAAATATGAAGAGGTGAAACACAGACACAGAAATAATGA 483
 DB 368 RMTERRWAKSSRTSRKKKWKCKRKYKBMGYSRMRSCKPARKWKRCSRGRWKG 427
 QY 484 AGTCAGCAAAATACATGCGAGATTGTCTAAGGCAAAAGAACCAATTTTCGATATAGA 543
 DB 428 CRGCMTCRMKSYGNMRWKSWMKSKYKMSRMRYRKKKCSRTTMMGTRGGMMGTGR 487
 QY 544 ACAACCATCATTTGAAGAAAGCCATCATTCTTCAATCAAGAAAGAAATAGATACTTGT 603
 DB 488 CRYKRGSKMKKCRRRRWRMYRWRKYYSARITMYRCARKEYSYSAARAKARCWYRGK 547
 QY 604 GCTTCCAGATTGTTGGAATGAAAAACAAGCAATTTATGTTTACAGAAACATACAAATGGCT 663
 DB 548 GYYW--AGWMMKRYKRYMYWYKMMWYKYSKCSWYKMSYKMSKARKAGAKMKRS 605
 QY 664 TGAATAAAAGAGGTAAATTAGGATGAAGATTGTTTTCAGCAGTTCGGCATTTGGGATC 723
 DB 606 KMSAWSKMSRSCRKCRKCSAKRSYAMMGMTSGSRMSRWKSYTCYWRKWSGMSKSTC 665
 QY 724 GAAAGCAGAAAGCATGTCATGTGTCCAAGAAATGGATTGCATATTTAGTAA---CCCC 780
 DB 666 TWTYMSKYTYAKYGSYRMYRMYRMYRMYRMYRMYRMYRMYRMYRMYRMYRMYRMYR 725
 QY 781 TAATGGCAGTAATAAACTACTAGGCAAGCTTCTCTACGAAAAAATAATAGGGAACATGA 840
 DB 726 SGRIWTSWYKCKSKWYRMYWYWSWAKTWKRYATRMWMMWYRYSKWTWCTM 785
 QY 841 TGTCTTAAAGCCCATGTTAAATTCAGGATTTGTTAAAGGAATCAACTAATGATCAAT 900
 DB 786 WGYWYWRMYRMYRMYRMYRMYRMYRMYRMYRMYRMYRMYRMYRMYRMYRMYRMYR 845
 QY 901 TTGTAATTTAGTGCATAAAACAAATAATAAAATATTCATGCTA---CTGTAAAAGTTT 957
 DB 846 RKARYWKKWATWCATTKRMTKGAKEWATWAKAWRYKYSWMMRAWYKYKTRTRYKT 905
 QY 958 CAATCTCTTTTACAGTTTGTAGTAAACATACACAGACCTTTATCTGATATTGAGGGGCAAG 1017
 DB 906 CWWKARWGSWAYWMMWWSKAKMMWMMWKGGRWGTKYWYCTTWKMACGRATKYMCCAG 965
 QY 1018 AGAATTACAGGAAAAAATGGAGAGGTA 1045
 DB 966 WMYYSYSWTRTYWRTWRWMMWASSRTA 993

RESULT 30
 AAX33181
 ID AAX33181 standard; DNA; 6644 BP.
 XX AAX33181;
 AC AAX33181;
 XX 25-JUN-1999 (first entry)
 DT Base sequence of the plasmid pRx-i-res-bar.
 XX
 DE
 XX
 KW Compo virus; bar; viral vector; expression; apoptosis; resistance; crmA;
 KW bcl-2; bcl-x1; FLIP; survivin; IAP; IAP; adenovirus; cancer;
 KW autoimmune disease; graft rejection reaction; inflammation;
 KW inflammatory disease; ss.
 XX
 OS Synthetic.
 OS Compo virus.
 XX
 XX WO9913073-A2.
 PN
 PD 18-MAR-1999.
 XX
 XX 07-SEP-1998; 98WO-JP004010.
 PF
 XX 08-SEP-1997; 97JP-00259235.
 XX
 XX (RPRG-) RPR GENCELL ASIA PACIFIC INC.

XX Hamada H;
 PI
 XX
 DR WPI; 1999-243728/20.
 XX
 PT New apoptosis-resistant virus-sensitive cell.
 XX
 PS Example 1; Page 38-41; 5lpp; English.
 XX

CC The present invention describes an apoptosis-resistant virus-sensitive cell line into which an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis-associated genes. These can then be used in a variety of diseases for which the induction of apoptosis by gene transfer, or where the inhibition of harmful apoptosis, is therapeutic. The recombinant viruses are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an adenovirus vector capable of expressing an apoptosis-associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the base sequence of the plasmid pX-ires-bsr, which contains the cowpox virus bsr gene, and is used in an example from the present invention

XX Sequence 6644 BP; 2166 A; 1573 C; 1424 G; 1481 T; 0 U; 0 Other;
 SQ Query Match 4.0%; Score 60.8; DB 2; Length 6644;
 Best Local Similarity 42.9%; Pred. No. 0.0024;
 Matches 302; Conservative 0; Mismatches 402; Indels 0; Gaps 0;

Qy	432	TTTTGCATTTTAAATATGAAGAGGTGAAACAGACAGACAGAAAATAATGAAGTGAACA	491
Db	3727	TCITGCGAGTTGCAAAAAA	3786
Qy	492	AAATATCTGCGAGATTGTCTAAGGCAAGGACACACATTTTCGAGTATATAGAACACAA	551
Db	3787	AAAAA	3846
Qy	552	TCATTGAAGAAAGCCATCTTTTCATCAAGAAAGAAATAGATAATCTTTGTGCTCCAG	611
Db	3847	AAAAA	3906
Qy	612	ATTGTTGGAATGAAACAGCATTTATGTTTACAGAACATACAAATGGCTTGAAATAA	671
Db	3907	AAAAA	3966
Qy	672	AAGAGGTAAATTAAGGATGTAAGGATTGTTTCAGCAGTTCGGCATTTGGGATCGAAAGCAG	731
Db	3967	AAAAA	4026
Qy	732	AAAAAGCATGTCCATGTGTGCAAGGAATGGATTGCAATATTTAGTAAACCCCTTAATGGCAGTA	791
Db	4027	AAAAA	4086
Qy	792	ATAAACTACTAGCAGAGCTTCTCTACGAAAAAAATTTAGGGAAACATGATGTTTCTAAAG	851
Db	4087	AAAAA	4146
Qy	852	CCCATGGTAAATTCAGGNTTTGTTAAAGGAATCAACTAATGATTCAATTTGTAATTAG	911
Db	4147	AAAAA	4206
Qy	912	TGCATAACAAATAATAAATAATATTGATGCTACTGTAAAGTTTTCATACTGTTTACA	971
Db	4207	AAAAA	4266

Search completed: December 3, 2005, 11:01:21
 Job time : 964.215 secs

Qy	972	GTTTGTAAACATACAGACCTTTTATCTGATATTGAGGGGCAAGAGATTATACAGAAA	1031
Db	4267	AAAAA	4326
Qy	1032	AAAAATGGAGAGGTAAATTTGTTTAAATACACGTTTACAGTGCACCAAGAATAGCAGAACATA	1091
Db	4327	AAAAA	4386
Qy	1092	TTGCAAAAGAAATGAAGATGAAGATATTTTAAGAAATATTATAGAA	1135
Db	4387	AAAAA	4430

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 09:15:11 ; Search time 7825.93 Seconds
(without alignments)
11156.694 Million cell updates/sec

Title: US-10-757-745-5
Perfect score: 1536
Sequence: 1 agagaagaggctcgaggga.....attaatcatttaantataa 1536

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : GenEmbl.*

1: gb.ba.*
2: gb.in.*
3: gb.env.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pr.*
9: gb.ro.*
10: gb.sts.*
11: gb.sy.*
12: gb.un.*
13: gb.vi.*
14: gb.htg.*
15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1533	99.8	1336	6	BD205492 CD40-Inte
2	1533	99.8	1336	6	ARS94296 Sequence
3	1533	99.8	1536	6	AX011603 Sequence
4	1486.8	96.8	2878	8	BC041125 Homo sapi
5	1359	88.5	1377	8	BC012011 Homo sapi
6	1348.4	87.8	1383	8	BC029372 Homo sapi
7	1131.6	73.7	4061	8	AB046806 Homo sapi
8	1131.6	73.7	101666	8	AL450489 Human DNA
9	968.6	63.1	2022	6	CQ730647 Sequence
10	762.2	49.6	246801	14	AC163142 Bos tauru
11	758.6	49.4	788	10	BV658452 S215P6503
12	730.2	47.5	183375	14	AC150471 Macropus
13	329	21.4	352	6	CQ707746 Sequence
14	317.6	20.7	4999	6	AX419136 Sequence
15	317.6	20.7	4999	8	AX419137 Sequence
16	317.6	20.7	4999	8	AY055204 Homo sapi
17	317.6	20.7	5144	6	AX419138 Sequence
18	317.6	20.7	5144	6	AX419139 Sequence

19	287	18.7	3420	8	BC021712
20	270.8	17.6	274	6	BD025398
21	270.8	17.6	274	6	AX885788 Sequence
22	222.4	14.5	5100	8	HSM808227
23	221.2	14.4	3247	8	BC098382
24	208.2	13.6	4961	6	CQ861506 Sequence
25	208.2	13.6	4961	8	AB011148 Homo sapi
26	190.8	12.4	249308	14	AC157307 Bos tauru
27	165.2	10.8	3042	6	AX419140 Sequence
28	165.2	10.8	3042	6	AX419141 Sequence
29	165.2	10.8	3183	6	AX419144 Sequence
30	165.2	10.8	3183	6	AX419145 Sequence
31	153.6	10.0	1928	9	BC019546 Mus muscu
32	149.8	9.8	5165	9	AX122541 Mus muscu
33	147.8	9.6	3597	9	BC062154 Mus muscu
34	139.8	9.1	248967	14	AC156472 Bos tauru
35	131.2	8.5	115345	8	AC008147 Homo sapi
36	125.2	8.2	30355	14	AL358948 Homo sapi
37	125.2	8.2	94734	8	HS232P20 Human DNA
38	122.2	8.0	174508	14	AC009436 Homo sapi
39	83	5.4	184302	8	AL162393 Human DNA
40	74.4	4.8	164571	5	CR847897 Zebrafish
41	73.6	4.8	93791	14	AC138073 Homo sapi
42	73.2	4.8	238881	14	AC084103 Mus muscu
43	73.2	4.8	247243	14	AC163668 Mus muscu
44	72	4.7	170627	14	AC125567 Rattus no
45	70.8	4.6	1142	15	AJ840525 Arabidops
46	70.8	4.6	23697	14	AC151103 Bos tauru
47	70.4	4.6	66993	14	AC152762 Bos tauru
48	70.2	4.6	235278	14	AC138074 Homo sapi
49	70.2	4.6	267870	14	AC097601 Rattus no
50	69.8	4.5	282289	14	AC152242 Bos tauru
51	68.4	4.5	199551	14	AC006281 Plasmodi
52	68.2	4.4	1328	15	AJ840631 Arabidops
53	67.8	4.4	824	5	AX932270 Gallus ga
54	67.6	4.4	12337	6	AX347260 Sequence
55	67.2	4.4	154625	14	CR936360 Homo sapi
56	67.2	4.4	199183	14	CR848789 Danio rer
57	66.8	4.3	99923	8	AX932889 Gallus ga
58	66.8	4.3	158431	14	AC079409 Homo sapi
59	66.6	4.3	110000	14	AC025316 Homo sapi
60	66.6	4.3	180784	14	CR753903 Danio rer
61	66.2	4.3	840	15	CR391963 Danio rer
62	66.2	4.3	840	15	CNS0180X Botrytis
63	65.6	4.3	286208	14	AC117140 Rattus no
64	65.6	4.2	60807	5	CR352225 Zebrafish
65	65	4.2	163312	8	AL138995 Human chr
66	65	4.2	175577	14	AC022462 Homo sapi
67	64.4	4.2	302156	2	AC116977 Dictyoste
68	64.4	4.2	121560	5	CR383667 Zebrafish
69	63.8	4.2	257757	2	AE014837 Plasmodi
70	63.4	4.1	39352	15	AC149394 Phakopsor
71	63.4	4.1	250029	2	AE014820 Plasmodi
72	63.2	4.1	110000	2	AC116305.3 Continuation (4 of
73	63.2	4.1	2627	8	BC042450 Homo sapi
74	63	4.1	2627	8	BC058853 Homo sapi
75	63	4.1	65433	5	AL935315 Zebrafish
76	63	4.1	136176	5	AL929119 Zebrafish
77	63	4.1	175544	14	AC117342 Rattus no
78	62.8	4.1	6292	6	AX251493 Sequence
79	62.8	4.1	7442	5	AX251441 Zebrafish
80	62.8	4.1	173690	5	AX465211 Sequence
81	62.8	4.1	226290	14	CR936408 Danio rer
82	62.8	4.1	3683	6	AX598999 Sequence
83	62.6	4.1	620	10	BV240263 S234P6219
84	62.4	4.1	1141	6	AR579680 Sequence
85	62.4	4.1	1141	6	AX083744 Sequence
86	62.4	4.1	6668	6	AX346599 Sequence
87	62.4	4.1	64707	2	AC115607 Dictyoste
88	62.4	4.1	110000	14	TANN2.16 Continuation (17 o
89	62.4	4.1	198714	14	CR388037 Danio rer
90	62.4	4.1	200960	14	CR848802 Danio rer
91	62.2	4.0	200960	14	CR848802 Danio rer

92	62	4.0	271546	2	AE014843	AE014843 Plasmodium	165	58.4	3.8	225236	14	BX936371	BX936371 Danio rer
93	61.8	4.0	40291	15	AY654900	AY654900 Kluyverom	c 166	58.4	3.8	340552	2	PFA929354	AL929354 Plasmodium
94	61.6	4.0	208886	14	CR392341	CR392341 Danio rer	c 167	58.2	3.8	653	8	HS329294	HS329294 Homo sapi
95	61.6	4.0	281723	2	PFA929359	AL929359 Plasmodium	c 168	58.2	3.8	3683	6	AX598853	AX598853 Sequence
96	61.6	4.0	289973	14	AC1135678	AC1135678 Rattus no	c 169	58.2	3.8	93475	5	AL1672088	AL1672088 Zebrafish
97	61.4	4.0	125623	2	AC115599	AC115599 Dictyoste	c 170	58.2	3.8	144604	14	BX899179	BX899179 Danio rer
98	61.4	4.0	158740	2	AC159452	AC159452 Trypanoso	c 171	58.2	3.8	14553	5	AL935272	AL935272 Zebrafish
99	61.4	4.0	347050	2	PFA929351	AL929351 Plasmodium	c 172	58.2	3.8	157210	5	BX928756	BX928756 Zebrafish
100	61.2	4.0	220339	14	CR855206	CR855206 Danio rer	c 173	58.2	3.8	213582	14	CR847926	CR847926 Danio rer
101	61	4.0	158613	14	CR854915	CR854915 Danio rer	c 174	58	3.8	461	6	CQ410653	CQ410653 Sequence
102	61	4.0	179286	5	BX897685	BX897685 Zebrafish	c 175	58	3.8	34548	6	AX349035	AX349035 Sequence
103	61	4.0	181119	5	BX247869	BX247869 Zebrafish	c 176	58	3.8	88037	14	PFMAL13P8	AL056782 Plasmodiu
104	61	4.0	250195	2	AE014831	AE014831 Plasmodium	c 177	58	3.8	110000	14	CT009752_4	Continuation (5 of
105	60.8	4.0	200195	2	AX655393	AX655393 Sequence	c 178	58	3.8	110000	14	CT009752_5	Continuation (6 of
106	60.8	4.0	6644	6	E23356	E23356 Virus vecto	c 179	58	3.8	110000	14	PFMAL13_18	Continuation (19 o
107	60.8	4.0	7372	6	E23357	E23357 Virus vecto	c 180	58	3.8	110000	14	PFMAL13P1_12	Continuation (13 o
108	60.8	4.0	7797	6	E23355	E23355 Virus vecto	c 181	58	3.8	154143	5	BX927207	BX927207 Zebrafish
109	60.8	4.0	7996	6	E23359	E23359 Virus vecto	c 182	58	3.8	163936	14	AC149960	AC149960 Strongylo
110	60.8	4.0	178914	14	CR753874	CR753874 Danio rer	c 183	57.8	3.8	17605	1	AE002145	AE002145 Ureaplasma
111	60.8	4.0	200582	5	AL923016	AL923016 Zebrafish	c 184	57.8	3.8	105320	2	AC116920	AC116920 Dictyoste
112	60.8	4.0	206479	14	CR854941	CR854941 Danio rer	c 185	57.8	3.8	125958	2	AC115592	AC115592 Dictyoste
113	60.8	4.0	217543	14	AC163195	AC163195 Bos tauru	c 186	57.8	3.8	140484	5	CR854834	CR854834 Zebrafish
114	60.6	3.9	131682	8	AL672277	AL672277 Human DNA	c 187	57.8	3.8	167590	5	AC093689	AC093689 Homo sapi
115	60.6	3.9	134784	5	BX890608	BX890608 Zebrafish	c 188	57.8	3.8	167954	1	BX842645	BX842645 Mycoplasma
116	60.6	3.9	197142	14	CR388410	CR388410 Danio rer	c 189	57.8	3.8	174235	5	BX236546	BX236546 Zebrafish
117	60.6	3.9	207516	8	AC097108	AC097108 Homo sapi	c 190	57.8	3.8	185135	5	BX005248	BX005248 Zebrafish
118	60.4	3.9	202872	14	AC016160	AC016160 Homo sapi	c 191	57.8	3.8	215607	5	BX569798	BX569798 Zebrafish
119	60.2	3.9	2330	8	AB168794	AB168794 Macaca fa	c 192	57.8	3.8	229052	14	CR855306	CR855306 Danio rer
120	60.2	3.9	9588	15	MIKLCOX1	X57546 K.lactis mi	c 193	57.8	3.8	231912	14	AC087566	AC087566 Mus muscu
121	60.2	3.9	182923	5	AL954767	AL954767 Zebrafish	c 194	57.8	3.8	302156	2	AC116977	AC116977 Dictyoste
122	60.2	3.9	202208	14	CR759891	CR759891 Danio rer	c 195	57.6	3.8	6109	6	AX251772	AX251772 Sequence
123	60.2	3.9	349751	2	PFMAL4P3	AL035476 Plasmodium	c 196	57.6	3.8	6109	6	AX345228	AX345228 Sequence
124	60	3.9	294258	14	AC156066	AC156066 Bos tauru	c 197	57.6	3.8	6286	6	AX251345	AX251345 Sequence
125	59.8	3.9	1141	6	AS793680	AS793680 Sequence	c 198	57.6	3.8	17674	6	AX346246	AX346246 Sequence
126	59.8	3.9	1141	6	AC083744	AC083744 Sequence	c 199	57.6	3.8	34340	14	BX957360	BX957360 Danio rer
127	59.8	3.9	171105	2	AC007532	AC007532 Drosophil	c 200	57.6	3.8	102019	5	BX510307	BX510307 Zebrafish
128	59.8	3.9	190801	2	AC009212	AC009212 Drosophil	c 201	57.6	3.8	110000	2	AC116957_2	Continuation (3 of
129	59.8	3.9	295289	2	AE003603	AE003603 Drosophil	c 202	57.6	3.8	110000	14	PFMAL13_14	Continuation (15 o
130	59.6	3.9	12142	6	AX346575	AX346575 Sequence	c 203	57.6	3.8	115990	5	BX890614	BX890614 Zebrafish
131	59.6	3.9	151374	5	BX004972	BX004972 Zebrafish	c 204	57.6	3.8	176239	5	BX248246	BX248246 Zebrafish
132	59.6	3.9	153184	5	BX005005	BX005005 Zebrafish	c 205	57.6	3.8	254050	2	PFA929358	AL929358 Plasmodium
133	59.6	3.9	250029	2	AE014839	AE014839 Plasmodium	c 206	57.6	3.8	258658	2	AE014832	AE014832 Plasmodium
134	59.4	3.9	162859	14	AC021369	AC021369 Homo sapi	c 207	57.6	3.8	348034	2	CR382400	CR382400 Plasmodium
135	59.4	3.9	165420	8	AC093771	AC093771 Homo sapi	c 208	57.4	3.7	6048	6	AX458486	AX458486 Sequence
136	59.4	3.9	210246	5	BX511081	BX511081 Zebrafish	c 209	57.4	3.7	146768	14	BX927333	BX927333 Danio rer
137	59.2	3.9	7218	6	I66494	I66494 Sequence 14	c 210	57.4	3.7	154561	5	CR391989	CR391989 Zebrafish
138	59.2	3.9	8056	6	AX598046	AX598046 Sequence	c 211	57.4	3.7	157544	5	CR762435	CR762435 Zebrafish
139	59.2	3.9	139489	14	CR376794	CR376794 Danio rer	c 212	57.4	3.7	178247	5	BX248504	BX248504 Zebrafish
140	59.2	3.9	181272	5	BX548256	BX548256 Zebrafish	c 213	57.4	3.7	212505	14	CR759831	CR759831 Danio rer
141	59.2	3.9	184438	14	CR847497	CR847497 Danio rer	c 214	57.4	3.7	216817	5	BX957274	BX957274 Zebrafish
142	59.2	3.9	189080	14	BX649407	BX649407 Danio rer	c 215	57.2	3.7	67970	2	PFMAL1P3	AL031746 Plasmodium
143	59.2	3.9	250053	2	AE014825	AE014825 plasmodium	c 216	57.2	3.7	90373	2	AC115680	AC115680 Dictyoste
144	59	3.8	6419	6	AX345169	AX345169 Sequence	c 217	57.2	3.7	104992	14	AC005504	AC005504 Plasmodium
145	59	3.8	7597	6	AX345915	AX345915 Sequence	c 218	57.2	3.7	114226	14	AC004710	AC004710 Plasmodium
146	59	3.8	155885	14	CR848672	CR848672 Danio rer	c 219	57.2	3.7	116496	5	CR753832	CR753832 Zebrafish
147	58.8	3.8	7814	6	AX251284	AX251284 Sequence	c 220	57.2	3.7	136490	14	AC005507	AC005507 Plasmodium
148	58.8	3.8	142168	14	CR388191	CR388191 Danio rer	c 221	57.2	3.7	250237	14	AC160076	AC160076 Bos tauru
149	58.8	3.8	148385	14	CR749764	CR749764 Danio rer	c 222	57.2	3.7	250421	2	AE014849	AE014849 Plasmodium
150	58.8	3.8	168212	5	CR352223	CR352223 Zebrafish	c 223	57.2	3.7	254436	2	AE014827	AE014827 Plasmodium
151	58.8	3.8	187264	14	CR847945	CR847945 Danio rer	c 224	57	3.7	105682	2	AC116957_3	Continuation (4 of
152	58.8	3.8	303091	14	AC084799	AC084799 Mus muscu	c 225	57	3.7	172747	8	AL1359835	AL1359835 Human DNA
153	58.6	3.8	43537	5	CR457458	CR457458 Zebrafish	c 226	56.8	3.7	3856	1	AP250390	AP250390 Caronell
154	58.6	3.8	110000	1	BA000021_0	BA000021 wigglewo	c 227	56.8	3.7	111882	2	AC115612	AC115612 Dictyoste
155	58.6	3.8	143903	5	BX247887	BX247887 Zebrafish	c 228	56.8	3.7	151298	5	BX537274	BX537274 Zebrafish
156	58.6	3.8	180422	5	BX548162	BX548162 Zebrafish	c 229	56.8	3.7	165202	14	CR848683	CR848683 Danio rer
157	58.6	3.8	196490	14	AC005507	AC005507 Plasmodium	c 230	56.8	3.7	171996	5	CR005176	CR005176 Zebrafish
158	58.6	3.8	196859	8	AC087277	AC087277 Homo sapi	c 231	56.8	3.7	222530	14	CR931764	CR931764 Danio rer
159	58.6	3.8	250421	2	AE014849	AE014849 Plasmodium	c 232	56.6	3.7	4430	2	AY160097	AY160097 Dictyoste
160	58.4	3.8	105682	2	AC116957_3	Continuation (4 of	c 233	56.6	3.7	8043	2	AY183918	AY183918 Drosophil
161	58.4	3.8	130540	14	AC079417	AC079417 Mus muscu	c 234	56.6	3.7	40611	2	AC116987	AC116987 Dictyoste
162	58.4	3.8	165215	14	BX470120	BX470120 Danio rer	c 235	56.6	3.7	50000	6	AX392735	AX392735 Sequence
163	58.4	3.8	180950	5	BX255894	BX255894 Zebrafish	c 236	56.6	3.7	101956	5	BX255963	BX255963 Zebrafish
164	58.4	3.8	197499	5	BX950214	BX950214 Zebrafish	c 237	56.6	3.7	162546	5	BX548051	BX548051 Zebrafish

238	56.6	3.7	169760	5	BX511310	BX511310 Zebrafish	C 311	55.6	3.6	348034	2	CR382400	CR382400 Plasmodium
239	56.6	3.7	174359	14	CR855123	CR855123 Danio rer	C 312	55.4	3.6	8222	6	AX705374	AX705374 Sequence
240	56.6	3.7	225581	14	BX537105	BX537105 Danio rer	C 313	55.4	3.6	8222	6	AX705396	AX705396 Sequence
241	56.6	3.7	235392	13	AF250284	AF250284 Amsacta m	C 314	55.4	3.6	11222	6	AX822354	AX822354 Sequence
242	56.6	3.7	249867	14	AC127704	AC127704 Plasmodium	C 315	55.4	3.6	11222	6	AX822482	AX822482 Sequence
243	56.4	3.7	6968	2	AF170073	AF170073 Plasmodium	C 316	55.4	3.6	11222	6	AX825994	AX825994 Sequence
244	56.4	3.7	77835	14	PFMAL13p2_3	Continuation (4 of	C 317	55.4	3.6	11222	6	AX826122	AX826122 Sequence
245	56.4	3.7	110000	14	PFMAL13_04	Continuation (5 of	C 318	55.4	3.6	13784	6	AX348449	AX348449 Sequence
246	56.4	3.7	110000	14	PFMAL13_23	Continuation (24 of	C 319	55.4	3.6	20422	2	AE001421	AE001421 Plasmodium
247	56.4	3.7	110000	14	PFMAL13_05	Continuation (6 of	C 320	55.4	3.6	29143	2	AC115594	AC115594 Dictyostoe
248	56.4	3.7	110000	14	TANN2_02	Continuation (3 of	C 321	55.4	3.6	141721	14	AC149953	AC149953 Strongylo
249	56.4	3.7	155885	14	CR848672	CR848672 Danio rer	C 322	55.4	3.6	141721	14	CR354586	CR354586 Danio rer
250	56.4	3.7	249943	2	AE014823	AE014823 Plasmodium	C 323	55.4	3.6	153787	5	AX936336	AX936336 Zebrafish
251	56.2	3.7	396	6	AR391230	AR391230 Sequence	C 324	55.4	3.6	153787	5	AX936336	AX936336 Zebrafish
252	56.2	3.7	396	6	AR392935	AR392935 Sequence	C 325	55.4	3.6	153787	5	AX936336	AX936336 Zebrafish
253	56.2	3.7	396	6	AR489665	AR489665 Sequence	C 326	55.4	3.6	153787	5	AX936336	AX936336 Zebrafish
254	56.2	3.7	396	6	AR493906	AR493906 Sequence	C 327	55.4	3.6	153787	5	AX936336	AX936336 Zebrafish
255	56.2	3.7	396	6	AX093235	AX093235 Sequence	C 328	55.4	3.6	153787	5	AX936336	AX936336 Zebrafish
256	56.2	3.7	49306	2	AC115606	AC115606 Dictyostoe	C 329	55.4	3.6	153787	5	AX936336	AX936336 Zebrafish
257	56.2	3.7	69572	14	AC120376	Continuation (3 of	C 330	55.4	3.6	218351	14	CR848819	CR848819 Danio rer
258	56.2	3.7	110000	14	AL954295_2	Continuation (3 of	C 331	55.4	3.6	218351	14	CR848819	CR848819 Danio rer
259	56.2	3.7	121960	14	CR931809	CR931809 Medicago	C 332	55.4	3.6	218351	14	CR848819	CR848819 Danio rer
260	56.2	3.7	125031	5	BX248494	BX248494 Zebrafish	C 333	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
261	56.2	3.7	158481	5	BX001012	BX001012 Zebrafish	C 334	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
262	56.2	3.7	184067	14	CR855257	CR855257 Danio rer	C 335	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
263	56.2	3.7	184535	14	CNS05TCU	AL35100 Homo sapi	C 336	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
264	56.2	3.7	217883	14	CR847977	CR847977 Danio rer	C 337	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
265	56.2	3.7	347582	2	PFMAL4P1	AL034557 Plasmodium	C 338	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
266	56.2	3.7	348657	14	BX548252	AL929250 Zebrafish	C 339	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
267	56	3.6	94534	5	CR735141	CR735141 Zebrafish	C 340	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
268	56	3.6	108767	5	BX248503	BX248503 Zebrafish	C 341	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
269	56	3.6	138314	14	CR812466	CR812466 Danio rer	C 342	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
270	56	3.6	139980	14	CR855330	CR855330 Danio rer	C 343	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
271	56	3.6	140181	14	CR848026	CR848026 Danio rer	C 344	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
272	56	3.6	143585	14	AC013349	AC013349 Homo sapi	C 345	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
273	56	3.6	145117	14	CR855388	CR855388 Danio rer	C 346	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
274	56	3.6	150495	14	CR847510	CR847510 Danio rer	C 347	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
275	56	3.6	162948	5	CR352217	CR352217 Zebrafish	C 348	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
276	56	3.6	169865	5	BX085194	BX085194 Zebrafish	C 349	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
277	56	3.6	183141	14	CR407564	CR407564 Danio rer	C 350	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
278	56	3.6	225010	14	BX511028	BX511028 Zebrafish	C 351	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
279	56	3.6	333221	2	AC116986	AC116986 Dictyostoe	C 352	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
280	56	3.6	347050	2	PFAL29351	AL929351 Plasmodium	C 353	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
281	56	3.6	349418	2	CR382398	CR382398 Plasmodium	C 354	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
282	56	3.6	1722	15	MISC38	X00846 Yeast mitoc	C 355	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
283	55.8	3.6	1722	15	MISC38	X04566 Yeast mitoc	C 356	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
284	55.8	3.6	1722	15	YMTWTGE	K03309 Saccharomyc	C 357	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
285	55.8	3.6	10347	2	PFALVAR	L42244 Plasmodium	C 358	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
286	55.8	3.6	84911	5	BX927196	BX927196 Zebrafish	C 359	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
287	55.8	3.6	101595	5	BX248241	BX248241 Zebrafish	C 360	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
288	55.8	3.6	119721	8	AC093655	AC093655 Homo sapi	C 361	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
289	55.8	3.6	155204	5	AC007926	AC007926 Trypanoso	C 362	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
290	55.8	3.6	159375	5	BX005001	BX005001 Zebrafish	C 363	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
291	55.8	3.6	171342	14	AX571679	AX571679 Danio rer	C 364	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
292	55.8	3.6	177575	5	AL953867	AL953867 Zebrafish	C 365	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
293	55.8	3.6	181168	5	AX293540	AX293540 Zebrafish	C 366	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
294	55.8	3.6	194184	5	BX510306	BX510306 Zebrafish	C 367	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
295	55.8	3.6	212999	14	AC151201	AC151201 Bos tauru	C 368	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
296	55.8	3.6	267042	14	CR382382	CR382382 Danio rer	C 369	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
297	55.8	3.6	4096	2	AF362374	AF362374 Dictyostoe	C 370	55.2	3.6	218351	14	CR848819	CR848819 Danio rer
298	55.6	3.6	110000	1	BA000026_01	Continuation (2 of	C 371	55.6	3.6	218351	14	CR848819	CR848819 Danio rer
299	55.6	3.6	110000	1	BA000026_02	Continuation (3 of	C 372	55.6	3.6	218351	14	CR848819	CR848819 Danio rer
300	55.6	3.6	110000	14	BX901880_2	Continuation (6 of	C 373	55.6	3.6	218351	14	CR848819	CR848819 Danio rer
301	55.6	3.6	120875	5	CR450800	Continuation (6 of	C 374	55.6	3.6	218351	14	CR848819	CR848819 Danio rer
302	55.6	3.6	120875	5	CR450800	Continuation (6 of	C 375	55.6	3.6	218351	14	CR848819	CR848819 Danio rer
303	55.6	3.6	174384	14	AC009524	AC009524 Homo sapi	C 376	55.6	3.6	218351	14	CR848819	CR848819 Danio rer
304	55.6	3.6	192187	2	AC117072	AC117072 Dictyostoe	C 377	55.6	3.6	218351	14	CR848819	CR848819 Danio rer
305	55.6	3.6	198181	14	CR855385	CR855385 Danio rer	C 378	55.6	3.6	218351	14	CR848819	CR848819 Danio rer
306	55.6	3.6	236406	14	AC079489	AC079489 Mus muscu	C 379	55.6	3.6	218351	14	CR848819	CR848819 Danio rer
307	55.6	3.6	257757	2	AE014837	AE014837 Plasmodium	C 380	55.6	3.6	218351	14	CR848819	CR848819 Danio rer
308	55.6	3.6	288969	14	CR854836	CR854836 Danio rer	C 381	55.6	3.6	218351	14	CR848819	CR848819 Danio rer
309	55.6	3.6	330050	2	PFAL29355	AL929355 Plasmodium	C 382	55.6	3.6	218351	14	CR848819	CR848819 Danio rer
310	55.6	3.6	330050	2	PFAL29355	AL929355 Plasmodium	C 383	55.6	3.6	218351	14	CR848819	CR848819 Danio rer

384	54.4	3.5	76568	2	MBREV	AF538053 Monosiga	C 457	53.6	3.5	164219	5	BX005205	BX005205 Zebrafish
385	54.4	3.5	93569	14	AC136806	AC136806 Rattus no	458	53.6	3.5	164288	14	AC128949	AC128949 Rattus no
386	54.4	3.5	146570	2	AC117076	AC117076 Dictyoste	459	53.6	3.5	164741	5	BX005455	BX005455 Zebrafish
387	54.4	3.5	148833	14	CR753884	CR753884 Danio rer	460	53.6	3.5	164987	14	CR848720	CR848720 Danio rer
388	54.4	3.5	148854	5	AL954171	AL954171 Zebrafish	461	53.6	3.5	169418	8	AC104163	AC104163 Homo sapi
389	54.4	3.5	171571	5	AL929078	AL929078 Zebrafish	462	53.6	3.5	178193	14	AC068949	AC068949 Homo sapi
390	54.4	3.5	152919	9	AL732464	AL732464 Mouse DNA	463	53.6	3.5	178273	14	AC005308	AC005308 Plasmodiu
391	54.4	3.5	203472	5	CR376844	CR376844 Zebrafish	464	53.6	3.5	182871	2	AC117176	AC117176 Dictyoste
392	54.4	3.5	215287	14	AC079432	AC079432 Mus muscu	465	53.6	3.5	190981	5	AF063866	AF063866 Melanoplu
393	54.4	3.5	237176	14	CR392026	CR392026 Danio rer	466	53.6	3.5	236120	13	AF063866	AF063866 Zebrafish
394	54.4	3.5	250029	2	AE014816	AE014816 Plasmodiu	467	53.6	3.5	250531	2	AE014845	AE014845 Plasmodiu
395	54.4	3.5	252650	2	AE014847	AE014847 Plasmodiu	468	53.4	3.5	584	2	AF201315	AF201315 Dugesia p
396	54.2	3.5	1197	15	AJ840663	AJ840663 Arabidops	469	53.4	3.5	612	6	AR619959	AR619959 Sequence
397	54.2	3.5	3488	2	AF447563	AF447563 Plasmodiu	470	53.4	3.5	728	10	BV594815	BV594815 S215P6256
398	54.2	3.5	3489	2	AF447568	AF447568 Plasmodiu	471	53.4	3.5	939	2	AY356401	AY356401 Aedes aeg
399	54.2	3.5	9539	6	AX277889	AX277889 Sequence	472	53.4	3.5	2009	6	AX457067	AX457067 Sequence
400	54.2	3.5	9539	6	AX323366	AX323366 Sequence	473	53.4	3.5	3365	1	MEFTGSRNA	M32222 M. fervidus
401	54.2	3.5	55372	14	CR759965	CR759965 Danio rer	474	53.4	3.5	6457	2	AC115613	AC115613 Dictyoste
402	54.2	3.5	68421	5	BX005423	BX005423 Zebrafish	475	53.4	3.5	41879	15	AC149385	AC149385 Phakopsor
403	54.2	3.5	79882	14	BX908758	Continuation (6 of	476	53.4	3.5	109612	8	AL512503	AL512503 Human DNA
404	54.2	3.5	83435	5	BX640469	BX640469 Zebrafish	477	53.4	3.5	167918	5	BX936450	BX936450 Zebrafish
405	54.2	3.5	110000	14	AE017245	Continuation (7 of	478	53.4	3.5	172522	14	CR388051	CR388051 Danio rer
406	54.2	3.5	110000	14	CT009752	Continuation (4 of	479	53.4	3.5	179458	5	AL929284	AL929284 Zebrafish
407	54.2	3.5	141118	14	CR391998	CR391998 Danio rer	480	53.4	3.5	180836	14	AC025241	AC025241 Homo sapi
408	54.2	3.5	148833	14	CR753884	CR753884 Danio rer	481	53.4	3.5	181284	14	CR855260	CR855260 Homo sapi
409	54.2	3.5	149165	5	BX005354	BX005354 Zebrafish	482	53.4	3.5	182212	5	AL928952	AL928952 Zebrafish
410	54.2	3.5	174383	5	AL929216	AL929216 Zebrafish	483	53.4	3.5	184290	5	BX323446	BX323446 Zebrafish
411	54.2	3.5	179510	14	AC013820	AC013820 Homo sapi	484	53.4	3.5	217621	14	BX901924	BX901924 Danio rer
412	54.2	3.5	191146	5	BX530070	BX530070 Zebrafish	485	53.4	3.5	250029	2	AE014830	AE014830 Plasmodiu
413	54.2	3.5	225164	14	CR855270	CR855270 Danio rer	486	53.4	3.5	254449	2	AE014817	AE014817 Plasmodiu
414	54.2	3.5	234081	2	PFMAL4P2	AL035475 Plasmodiu	487	53.4	3.5	258658	2	AE014832	AE014832 Plasmodiu
415	54.2	3.5	250053	2	AE014825	AE014825 Plasmodiu	488	53.4	3.5	333321	2	AC116986	AC116986 Dictyoste
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417	54.2	3.5	313050	2	PF929352	AL929352 Plasmodiu	490	53.2	3.5	3149	2	AF019981	AF019981 Dictyoste
418	54	3.5	3499	2	AF447555	AF447555 Plasmodiu	491	53.2	3.5	3617	15	MTWVCYTB	X66594 W.makrlii ml
419	54	3.5	33651	2	AC114261	AC114261 Dictyoste	492	53.2	3.5	15548	6	AX347057	AX347057 Sequence
420	54	3.5	82139	2	AC115684	AC115684 Dictyoste	493	53.2	3.5	19124	2	PF929353	AX40608 Plasmodiu
421	54	3.5	110000	14	PFMAL13_09	Continuation (10 o	494	53.2	3.5	19124	6	AR089157	AR089157 Sequence
422	54	3.5	110000	14	PFMAL13_19	Continuation (20 o	495	53.2	3.5	61052	14	AC123513	AC123513 Dictyoste
423	54	3.5	110000	14	PFMAL8P1_02	Continuation (3 of	496	53.2	3.5	110000	14	PFMAL13_22	Continuation (23 o
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425	54	3.5	162294	14	CR855307	CR855307 Danio rer	498	53.2	3.5	110000	14	PFMAL7P1_00	AL844506 Plasmodiu
426	54	3.5	170260	5	BX890570	BX890570 Zebrafish	499	53.2	3.5	110000	14	PFMAL7P1_07	Continuation (8 of
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428	54	3.5	199866	14	CR854926	CR854926 Danio rer							
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430	54	3.5	251551	2	AE014844	AE014844 Plasmodiu							
431	54	3.5	254242	14	CR678435	CR678435 Danio rer							
432	54	3.5	265985	14	AC087226	AC087226 Mus muscu							
433	53.8	3.5	6254	6	AX346522	AX346522 Sequence							
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ALIGNMENTS

RESULT 1	BD205492	LOCUS	BD205492	CD40-Interacting and TRAF-interacting protein.	1536 bp	DNA	linear	PAT 17-JUL-2003
DEFINITION	BD205492	LOCUS	BD205492	CD40-Interacting and TRAF-interacting protein.	1536 bp	DNA	linear	PAT 17-JUL-2003
ACCESSION	BD205492	LOCUS	BD205492	CD40-Interacting and TRAF-interacting protein.	1536 bp	DNA	linear	PAT 17-JUL-2003
VERSION	BD205492.1	LOCUS	BD205492.1	CD40-Interacting and TRAF-interacting protein.	1536 bp	DNA	linear	PAT 17-JUL-2003
KEYWORDS	UP 2002512796-A/3.	LOCUS	UP 2002512796-A/3.	CD40-Interacting and TRAF-interacting protein.	1536 bp	DNA	linear	PAT 17-JUL-2003
SOURCE	Homo sapiens (human)	LOCUS	Homo sapiens (human)	CD40-Interacting and TRAF-interacting protein.	1536 bp	DNA	linear	PAT 17-JUL-2003
ORGANISM	Homo sapiens	LOCUS	Homo sapiens	CD40-Interacting and TRAF-interacting protein.	1536 bp	DNA	linear	PAT 17-JUL-2003
REFERENCE	1 (bases 1 to 1536)	LOCUS	1 (bases 1 to 1536)	CD40-Interacting and TRAF-interacting protein.	1536 bp	DNA	linear	PAT 17-JUL-2003
AUTHORS	Pyke,S.M.C., Ghislain,J.E.F.J., Remacle and Huylebroeck,D.F.E.	LOCUS	Pyke,S.M.C., Ghislain,J.E.F.J., Remacle and Huylebroeck,D.F.E.	CD40-Interacting and TRAF-interacting protein.	1536 bp	DNA	linear	PAT 17-JUL-2003
TITLE	CD40-Interacting and TRAF-interacting protein	LOCUS	CD40-Interacting and TRAF-interacting protein	CD40-Interacting and TRAF-interacting protein.	1536 bp	DNA	linear	PAT 17-JUL-2003
JOURNAL	Patent: JP 2002512796-A 3 08-MAY-2002;	LOCUS	Patent: JP 2002512796-A 3 08-MAY-2002;	CD40-Interacting and TRAF-interacting protein.	1536 bp	DNA	linear	PAT 17-JUL-2003
COMMENT	VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE VZW	LOCUS	VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE VZW	CD40-Interacting and TRAF-interacting protein.	1536 bp	DNA	linear	PAT 17-JUL-2003
	OS Homo sapiens (human)	LOCUS	OS Homo sapiens (human)	CD40-Interacting and TRAF-interacting protein.	1536 bp	DNA	linear	PAT 17-JUL-2003
	PN JP 2002512796-A/3	LOCUS	PN JP 2002512796-A/3	CD40-Interacting and TRAF-interacting protein.	1536 bp	DNA	linear	PAT 17-JUL-2003
	PD 08-MAY-2002	LOCUS	PD 08-MAY-2002	CD40-Interacting and TRAF-interacting protein.	1536 bp	DNA	linear	PAT 17-JUL-2003
	PF 28-APR-1999 JP 2000546003	LOCUS	PF 28-APR-1999 JP 2000546003	CD40-Interacting and TRAF-interacting protein.	1536 bp	DNA	linear	PAT 17-JUL-2003
	PR 29-APR-1998 EP 98201392.2	LOCUS	PR 29-APR-1998 EP 98201392.2	CD40-Interacting and TRAF-interacting protein.	1536 bp	DNA	linear	PAT 17-JUL-2003
	PI STEFAN MARIA CHRISTIAAN PYPE,	LOCUS	PI STEFAN MARIA CHRISTIAAN PYPE,	CD40-Interacting and TRAF-interacting protein.	1536 bp	DNA	linear	PAT 17-JUL-2003
	PI JACQUES EMILE FERNAND JOSIANE GHISLAIN REMACLE, PI DANNY	LOCUS	PI JACQUES EMILE FERNAND JOSIANE GHISLAIN REMACLE, PI DANNY	CD40-Interacting and TRAF-interacting protein.	1536 bp	DNA	linear	PAT 17-JUL-2003

FRANCOIS EVELINE HUYLEBROECK
PC C12N15/09,A61K38/00,A61P9/10,A61P19/02,A61P25/00,A61P35/00, PC
A61P37/02,
PC A61P37/06,A61P43/00,C07K14/47,C07K16/18,G01N33/15,G01N33/50,
PC G01N33/566,
PC C12N15/00,A61K37/02
CC CD40-Interacting and TRAF-Interacting protein. FH Key
Location/Qualifiers
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Location/Qualifiers
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FEATURES

source
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.9e-249;
Matches 1536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 841 TGTTCCTAAAGCCCATGTTAAATTCAGGATTTGTTAAAGGAATCACTAATGATTCAT 900
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RESULT 2

AR594296
LOCUS AR594296 1536 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 5 from patent US 6812203.
ACCESSION AR594296
VERSION AR594296.1 GI:56643902
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1536)
AUTHORS Pye,S.M.C., Remacle,J.B.F. and Huylebroeck,D.F.E.
TITLE CD40-Interacting and TRAF-Interacting proteins
JOURNAL Patent: US 6812203-A 5 02-NOV-2004;
Vlaams Interuniversitair Instituut voor Biotechnologie VZW;
Wijngaarde;
WOX;
Location/Qualifiers
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ORIGIN

Query Match 99.8%; Score 1533; DB 6; Length 1536;
Best Local Similarity 100.0%; Pred. No. 4.9e-249;
Matches 1536: Conservative 0; Mismatches 0; Indels 0

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Qy	121	GGCGGTGCAGGGCGGGAGGGGAGTGGTGGCGCTGCGGCAGTAGGGACAGCAGGAGCAG	180
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Qy	181	TGTTGCTGTCAGCGCGCCCTCGGAGACATGGGAGACCCGGGGTCGGAAATATAGAAATC	240
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Qy	301	TCAGTTTGTTCAGTGAAGGACATCGAGACCTGTTCTTTGAAATACATGATCTCGTCTGTGG	360
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Qy	361	TGATGATGAAAAACCTAGCGCCTATTATAGTAGATATCTGTTCTTAAATGCCAAAAACG	420
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Qy	481	TGAAGTGAGCAAAAATCACTGCGATTTGCTTAGGGCAAGGAAACCAATTTTCAGTATAT	540
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Qy	541	AGAACACCAATCAATTCAGAAAAAGCCATCACTTTTCATCAAGAGAAAGAAATAGATATCT	600
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PUBMED REFERENCE AUTHORS TITLE JOURNAL	12477932 2. (bases 1 to 2878) Director MGC Project. Direct Submission Submitted (13-DEC-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbe@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc_mgc@nhgri.nih.gov Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
REMARK COMMENT	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 82 Row: m Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein. Location/Qualifiers 1. .2878 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clones="MGC:47798 IMAGE:5785266" /tissue_type="Uterus, leiomyosarcoma" /clone_lib="NIH_MGC_71" /lab_host="DH10B" /note="Vector: pCMV-SPORT6" 1. .2878 /gene="KIAA1586" /db_xref="GeneID:57691" 171..2534 /gene="KIAA1586" /codon_start=1 /product="KIAA1586" /protein_id="AAH41125.1" /db_xref="GI:2699563" /db_xref="GeneID:57691" /translation="MGDPGSEIIIESVPPAGPEASESTTDENNEDIQVSGSPRPVLE YIDLVCGDENPSAYSDILFPKPKRGDFLPLFNKKVKTFTENNEVSKNHCRLSK AKEPHFYEQIPIIEEPKPSLSKKEIDNLVLPDCWKEKQAFMEQYKWEIKEGKLG CKDCSAVRHLGSAKEKHVHSKEWIAVLTVPNGSKTTRQASLRKIKIREDHVSKAHGK IODLKSTSDSICNLVHKQNNKNDATVKVNTVYSLVKNRPLSDIEGARELOEKQ GEVNCILNTRVSATRIAEHAKEMQKIFKNIIEENAKICILIDEASTVSKTTIVYL CCTIQSPAPVPLVAKELVSTIAECINLTLLNDCGFTNSELKANLIAPFCSDGA NTILGRKSGVKKLENFPEIWIWNLNHRILQLSDDSISEIKOINHLKIFIDKIYSI YHOPNQTKLLGTVAKELETEIIKIGVMGPRWACSLQAAATVAHWAYPILYMHFSH SYGLAKRLANFLQDIALMIDILEEFSVLSTALQSRSTNIKAOKLIRKTRALRN LKICGTQVESIQEDLIKSDPKDIPFNKNKNFNALPRSILLDNIIOHMLRLISDRNH EDIENYDLPPESTWPEEITSPWAGEKTLFHLCKILKYVDLNDREFEVNNIKSN NVSIPITTYIKRAKIVSTIANSBAERGFNLMIICTRVNSLTIHVSDLMINLLG KELADWDATPPVKWSNCHRLATDTVRQKSTKVFHENQAIWNLK"
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DEFINITION BC029372
VERSION BC029372.1 GI:20809463
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo (1 to 1383)
REFERENCE 1 (bases 1 to 1383)
AUTHORS Strausberg, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1383)
Strausberg, R.
Direct Submission
Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-x@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 41 Row: p Column: 2
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
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RESULT 7
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DEFINITION
ACCESSION AB046806
VERSION AB046806.1 GI:10047246
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SOURCE
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Hominidae; Homo.
REFERENCE
1 (sites) Nagase, T., Kikuno, R., Nakayama, M., Hirose, M. and Ohara, O.
AUTHORS Prediction of the coding sequences of unidentified human genes.
TITLE XVIII. The complete sequences of 100 new cDNA clones from brain
which code for large proteins in vitro
JOURNAL DNA Res. 7 (4), 273-281 (2000)
PUBMED 10997877
REFERENCE
2 (bases 1 to 4061)
AUTHORS Ohara, O., Nagase, T. and Kikuno, R.
DIRECT SUBMISSION
TITLE Submitted (03-AUG-2000) Osamu Ohara, Kazusa DNA Research Institute,
JOURNAL Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba
292-0812, Japan (E-mail: cdna@info.kazusa.or.jp,
URL: http://www.kazusa.or.jp/huge, Tel: 81-438-52-3913,
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Qy	1411	AGTAGCTACAAAATTTGTAGAAAATTTCTCGAAATCATCATTTGGAACCTGTTTAAATCA	1470
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RESULT 8			
AL450489	101666 bp	DNA	linear PRI 18-MAY-2005
LOCUS			
DEFINITION	Human DNA sequence from clone RP11-203B9 on chromosome 6 Contains the 3' end of gene FLJ30162, a novel gene, the 5' end of gene KIAA0576, the 3' end of a novel gene and a CpG island, complete sequence.		
ACCESSION	AL450489		
VERSION	AL450489.12	GI:15022239	
KEYWORDS	HTG; FLJ30162; KIAA0576.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 101666)		
AUTHORS	Leongamornlert,D.		
TITLE	Direct Submission		
JOURNAL	Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk		
COMMENT	<p>Clone requests: clonerequest@sanger.ac.uk</p> <p>On Jul 26, 2001 this sequence version replaced gi:14715364.</p> <p>The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:</p> <p>En., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at</p> <p>http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at</p> <p>http://www.sanger.ac.uk/HGP/Chr6</p> <p>RP11-203B9 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see</p> <p>http://www.chori.org/bacpac/home.htm</p> <p>VECTOR: pBACE3.6</p> <p>----- Genome Center</p> <p>Center: Wellcome Trust Sanger Institute</p> <p>Center code: SC</p> <p>Web site: http://www.sanger.ac.uk</p> <p>Contact: vegas@sanger.ac.uk</p> <p>-----</p> <p>This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.</p>		
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RESULT 9
CQ730647
LOCUS
DEFINITION
CQ730647
ACCESSION
CQ730647
VERSION
CQ730647.1
KEYWORDS
SOURCE
ORGANISM
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Homo sapiens
Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1
Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
Patent: WO 02068579-A.16581 06-SEP-2002;
PE Corporation (NY) (US)
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Best Local Similarity 99.6%; Pred. No. 1e-153;
Matches 971; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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RESULT 10
AC163142/c
LOCUS   246801 bp      DNA      linear      HTG 01-JUL-2005
DEFINITION Bos taurus clone CH240-79H13, *** SEQUENCING IN PROGRESS ***, 25
unordered pieces.
ACCESSION AC163142
VERSION   AC163142.2 GI:68300456
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE   Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiattheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 246801)
AUTHORS Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
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Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
Weinstock, G. and Gibbs, R. A.
Direct Submission
Unpublished
2 (bases 1 to 246801)
Worley, K. C.
Direct Submission
Submitted (05-JUN-2005) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 246801)
Cow Genome Sequencing Consortium.
Direct Submission
Submitted (01-JUL-2005) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jun 29, 2005 this sequence version replaced gi:66955947.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with 'Ns' to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: FBZ
Center clone name: CH240-79H13
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 236819 bases at least Q40
Consensus quality: 239101 bases at least Q30
Consensus quality: 241053 bases at least Q20
Estimated insert size: 239811; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 25 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 10509 10558: gap of 50 bp
* 10559 77693: contig of 67135 bp in length

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* 173001 191200: contig of 18200 bp in length
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* 227762 227811: gap of 50 bp
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Qy 564 AGCCATCACTTTTCATCAAGAAAGAAATAGATAATCTTGTGCTTCCAGATTTGGGAATG 623
Db 148388 AGCGTCTATCTTCATCAAGGAAAAATGGATAATCTTGTGCTTCCAGATTTGGGAATG 148329

Qy 624 AAAACAAGCATTTATCTTTTACAGAAACAATACAATGCTTGAATATAAGAAAGTAAAT 683
Db 148328 AAAACAAGTGGTATGTTTACAGAACAGTACAATGCTTGAATATAAGAAAGTAAAT 148269

Qy 684 TAGGATGTAAGGATTTGTTTCAGCAGTTCCGCATTTGGGATTCGAAAGCAAGAAAGCATGTCC 743
Db 148268 TAGGATGTAAGGATTTACTCAACAGTTCCAGATTTGGGATTAAGAGCAAGATCATGTTC 148209

Qy 744 ATGTGTCAGAGGAATGATTTGCATATTTAGTAACCCCTAATGCGCAGTAATAAACTACTA 803
Db 148208 ACATGTCCAGGAGTGGATTCATATTTGGTAA-CCCTAATGGCAATTTATAAACTATTA 148150

Qy 804 GGCAGCTTCTCTACGAAAAAATTAGGGAACATGATTTTCTAAAGCCCATGTAATA 863
Db 148149 GACAGGCTTCTCTCGAAAAAATTAAGGAGCATGATTTCTAAAGCCCATGTAATA 148090

Qy 864 TTCAGGATTTGTTAAAGGAATCAACTAATGATTCAAATTTGTAATTTAGTGATCAAAACAAA 923
Db 148089 TTCAGGA-TTGTAAAGGAATCAATTAATGACTCAGTTCTTAATTTAGTGCAATAAAT 148031

Qy 924 ATAATAAAATATTTAGTGTCTACTCTATAAAGTTTTCAATCTGTTTACAGTTTAGTAAAC 983
Db 148030 GTAATAAAATGTTGATGCTACTCTATAAAGTTTTCAAGACAGTTTATAGTTTAGTAAAC 147971

Qy 984 ATACAGACCTTTTATCTGATATTCAGGGGCAAGGAATTTACAGGAAAAAATCGAGAGG 1043
Db 147970 ATAATAGACCTTAGTCTGATCTCAGAGGCAATAGAAATTAAGAGAAAAATGGGGT-- 147913

Qy 1044 TAAATTTGTTTAAATACACGTTTACAGTGCAACAGAAATAGCAGAAATATTCAAAAAGAAA 1103
Db 147912 -----AGAAATAGCAGTGCATGCCGCAAAAGAAA 147885

Qy 1104 TGAAGATGAAGATATTTAAGAAATATTTAGAAAGAAATGCCAAATCTGTATCATATTTG 1163
Db 147884 TGAAGATGACAAATCTTTAAGGATATTTAGAAAGAAAGGCCCAAAATCTGTCTTATAGTTG 147825

Qy 1164 ATGAGGATCTACAGTTTCAAGAAACCCACCTAGTGTATTTATCTCCAGTGCAAAATTC 1223
Db 147824 ATGAGGATCTCCAGTTTGAAGAAAGAGGACCCCTCGTATTTATGTCGATACACAGTAT 147765

Qy 1224 AGTCAGCTCTCTGCACCTGTTTATGTTATTTTGGGCTTTAAAAAGAAATGGTGTCAACTATAG 1283
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Db 147764 AGTCAGCTCCTGCCAGGTTATGTTGTTTGTACTTTAAAGAACTGGTGCAGCTACAG 147705
QY 1284 CAGAGGTATTTCTCAATCATTTAGCTACTTTAAATGATTTGCTGTTTACAAATGAAT 1343
Db 147704 TGAATGATCTTTCAGTACGTTTTCGAGTACTTTAAATGATTTGCTGTTTACAAATGAAT 147645
QY 1344 ATTTGAAAGCAAATTTAAATGCAATTTTGTCTGATGGTCTAATACAAACCTGGGAAGAA 1403
Db 147644 ATTTGAAAGCAAATTTAAATGCAATTTTATCCTGATGGTCTAATACAAATGCTGGTAGAA 147585
QY 1404 AGCTGGAGTAGCTACAAATTTGTAGAAAATTTTCCGTAATCATCATTTGGAACTGTT 1463
Db 147584 AGCTGGAGTAGCCAGAGTGGTTAGAAAATTTTCCGTAATTTATTTGGAACTGTT 147525
QY 1464 TAAATCATCGATTACAAATTTGTCACTTGATGTTCTATATCCGAAATATAAAACAAATTAATC 1523
Db 147524 TAAACATCAATTTGATTTGTCACTTGATGACTCAATATCTGAAATATAAAACAAATGTAATC 147465
QY 1524 ATTTAA 1529
Db 147464 ATTTAA 147459

RESULT 11
BV658452
LOCUS S21SP6503RD4.T0 Clara Pan troglodytes troglodytes STS 16-APR-2005
DEFINITION BV658452 788 bp DNA linear STS genomic,
sequence tagged site.
ACCESSION BV658452
VERSION BV658452.1 GI:62686423
KEYWORDS STS.
SOURCE Pan troglodytes troglodytes
ORGANISM Pan troglodytes troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
REFERENCE 1 (bases 1 to 788)
AUTHORS Mikkelson,T.S., Hillier,W.L., Bichler,E.E., Zody,M.C. and
Jaffe,D.B.
TITLE Initial Sequence of the Chimpanzee Genome and Comparison with the
Human Genome
JOURNAL Unpublished (2005)
COMMENT Contact: Michael C. Zody
Broad Institute of MIT and Harvard
320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172580933
Fax: 6172580933
Email: mczody@broad.mit.edu
Primer A: No sequence submitted
Primer B: No sequence submitted
STS size: 788
Protocol:
23,021,928 chimpanzee whole genome shotgun reads were aligned to
the Human genome NCBI
Build 34 (hg16, July 2003). Chimp WGS reads were from 9 donors,
including Clint (Pan
troglodytes verus), 3 other Pan troglodytes verus chimps
(Donald, Karlén, Yvonne), 3 Pan
troglodytes troglodytes chimps (Noemie, Masuku, Clara) and 2 chimps
of unknown origin
(Gon, Unknown Chimp). Common names: Pan troglodytes verus is the
western chimp and Pan
troglodytes troglodytes is the central chimp. To be included in
chimpanzee SNP discovery, a
read must be at least 500bp in length, at least 50% of its base
calls must have Phred
score >= 20, at least 30% of its base calls must satisfy
SNQS(30,25) (single strand NQS, the
base in question has Phred score >= 30, the surrounding 10 bases in
the read have Phred
score >= 25), and the read must have at least 200 bp SNQS(30,25)
bases. Reads not uniquely

placed in the genome and read pairs whose two ends were not
consistently placed were
discarded. After above filtering, NQS(30,25) standard was applied
to all pairs of
overlapping reads to call NQS bases and SNPs. Alignments (between
two reads) with less
than 100 NQS bases or with SNP rate > 0.01 were discarded. To
exclude alignment between two
copies of a single read, comparisons between two reads that share
95% of their genome
alignments (>95% bases of read A and >95% bases of read B were
placed at the same locus
of human genome) were discarded.
Location/Qualifiers
FEATURES
source
1..788
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/mol_type="genomic DNA"
/sub_species="troglodytes"
/db_xref="taxon:37011"
/clone_lib="Clara"
<1..>788

Query Match 49.4%; Score 758.6; DB 10; Length 788;
Best Local Similarity 98.7%; Pred. No. 3.5e-118;
Matches 775; Conservative 0; Mismatches 9; Indels 1; Gaps 1;
QY 529 TTTCAGGTATATAGAACCAACCAATCATTTGAGAGAAAGCCATCCTTTTCATCAAGAAAGA 588
Db 5 TTTCAGGTATATATGAAAC--ACCAATCATTTGAGAGAAAGCCATCCTTTTCATCAAGAAAGA 63
QY 589 AATAGATATCTTTGTCTTCCAGATTTGTTGAAATGAAACAAAGCAATTTATGTTTACAGA 648
Db 64 AATAGATATCTTTGTCTTCCAGATTTGTTGAAATGAAACAAAGCAATTTATGTTTACGGA 123
QY 649 ACAATACAAATGGCTTGAAATATAAGAGAGGTAAATATAGGATTAAGGATTTGTTACAGCAGT 708
Db 124 ACAATACAAATGGCTTGAAATATAAGAGAGGTAAATATAGGATTAAGGATTTGTTACAGCAGT 183
QY 709 TCGGCATTTGGATCGAAGCAGAAAGCAATGTCCTCATGTGTCCTCAAGGAATGATTTGCATA 768
Db 184 TCGGCATTTGGATCGAAGCAGAAAGCAATGTCCTCATGTGTCCTCAAGGAATGATTTGCATA 243
QY 769 TTTAGTAACCCCTAATGGCAGTAAATAAATACTAGGCAAGCTTCTCTACGAAAAAATAAT 828
Db 244 TTTAGTAACCCCTAATGGCAGTAAATAAATACTAGGCAAGCTTCTCTACGAAAAAATAAT 303
QY 829 TAGGGAACATGATGTTTCTAAAGCCCATGGTAAATTCAGGATTTGTTAAAGGAATCAAC 888
Db 304 TAGGGAACATGATGTTTCTAAAGCCCATGGTAAATTCAGGATTTGTTAAAGGAATCAAC 363
QY 889 TAATGATTCATTTGTTAATTTAGTGCTATACAAACAAATATAAATAATTTATGATGCTACTGT 948
Db 364 TAATGATTCATTTGTTAATTTAGTGCTATACAAACAAATATAAATAATTTATGATGCTACTGT 423
QY 949 AAAAGTTTTCAATCTGTTTACAGTTTATAGTAAACATAACAGACCTTTATCTGATATTGA 1008
Db 424 AAAAGTTTTCAATCTGTTTACAGTTTATAGTAAACATAACAGACCTTTATCTGATATTGA 483
QY 1009 GGGGGCAAGAGAAATTAACAGGAAAAAATTCGAGAGGTAAATTTGTTTAAATATACAGTTACAG 1068
Db 484 GGGGGCAAGAGAAATTAACAGGAAAAAATTCGAGAGGTAAATTTGTTTAAATATACAGTTACAG 543
QY 1069 TGCAACAGAAATAGCAGAACATATTTGCAAAAGAAATGAGATGAGATATTTTAAAGAAATAT 1128
Db 544 TGCAACAGAAATAGCAGAACATATTTGCAAAAGAAATGAGATGAGATATTTTAAAGAAATAT 603
QY 1129 TATAGAAGAGAAATGCAAAATCTGTATCATATTTGATGAGGATCTTACAGTTTCAAGAA 1188
Db 604 TATAGAAGAGAAATGCAAAATCTGTATCATATTTGATGAGGATCTTACAGTTTCAAGAA 663
QY 1189 AACCAACCTTAGTATTTATCTCCAGTGCAAAATTCAGTCAGCTCTCGACCTGTTATGTT 1248

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Db      664 AACACCTAGTATTTATCTCCAGTGCACAAATTCAGTCAGCTCCTCGACCTGTTATTGT 723
Qy      1249 ATTGTGGCTTTAAAGAAATGGTGTCAACTATATAGCAGAGTGTTATTCATCAATATT 1308
Db      724 ATTGTGGCTCTAAAGAAATGGTGTGCGATATAGCAGAGTGTTATTCATCAATATTATT 783
Qy      1309 GACTA 1313
Db      784 GACTA 788

RESULT 12
AC150471/c
LOCUS   AC150471      183375 bp      DNA      linear      HTG 21-JUL-2004
DEFINITION Macropus eugenii clone ME_KBa-623119, WORKING DRAFT SEQUENCE, 8
unordered pieces.
ACCESSION AC150471
VERSION   AC150471.1 GI:50428613
KEYWORDS  HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE    Macropus eugenii (tammar wallaby)
ORGANISM  Macropus eugenii
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
REFERENCE 1 (bases 1 to 183375)
AUTHORS   Antonellis,A., Ayete,K., Benjamin,B., Blakesley,R.W.,
          Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,B.,
          Coleman,H., Daki,N., Engle,J., Guan,X., Gupta,J., Haghighi,P.,
          Han,J., Hansen,N., Ho,S.-L., Hu,P., Hurle,B., Idol,J.R., Jones,C.,
          Karlins,E., Kim,H., Kwong,P., Laric,P., Larson,S., Lee-Lin,S.-Q.,
          Legaspi,R., Madden,M., Maduro,Q.L., Maduro,V.B., Margulies,E.H.,
          Masello,C., Maskeri,B., McDowell,J., Mullikin,J.C., Peguifran,C.,
          Park,M., Portnoy,M.B., Prasad,A., Puri,O., Reddix-Dugue,N.,
          Schandler,K., Schueler,M.G., Shah,K., Sison,C., Stantripop,S.,
          Thomas,J.W., Thomas,P.J., Tsipouri,V., Vogt,J.L., Wetherby,K.D.,
          Young A. and Green,E.D.
TITLE     NISC Comparative Sequencing Initiative
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 183375)
AUTHORS   Green,E.D.
TITLE     Direct Submission
JOURNAL   Submitted (21-JUL-2004) NIH Intramural Sequencing Center, 8717
          Grovemont Circle, Gaithersburg, MD 20877, USA
COMMENT   ----- Genome Center
          Center: NIH Intramural Sequencing Center
          Center code: NISC
          Web site: http://www.nisc.nih.gov
          Contact: nisc.zoo@hri.nih.gov
          ----- Project Information
          Center project name: fmz
          Center clone name: 623119
          ----- Summary Statistics
          Sequencing vector: plasmid; n/a; 100% of reads
          Chemistry: Dye-terminator Big Dye; 100% of reads
          Assembly program: Phrap; version 0.990319
          Consensus quality: 177593 bases at least Q40
          Consensus quality: 178172 bases at least Q30
          Consensus quality: 178629 bases at least Q20
          Insert size: 154000; agarose-fp
          Insert size: 182675; sum-of-contigs
          Quality coverage: 9.99x in Q20 bases; agarose-fp
          Quality coverage: 8.42x in Q20 bases; sum-of-contigs
          -----
          * NOTE: This is a 'working draft' sequence. It currently
          * consists of 8 contigs. The true order of the pieces
          * is not known and their order in this sequence record is
          * arbitrary. Gaps between the contigs are represented as
          * runs of N, but the exact sizes of the gaps are unknown.
          * This record will be updated with the finished sequence
          * as soon as it is available and the accession number will
          * be preserved.
          *
          * 1 2752: contig of 2752 bp in length
          * 2753 2852: gap of unknown length
          * 2853 6856: contig of 4004 bp in length

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* 6857 6956: gap of unknown length
* 12448: contig of 5492 bp in length
* 12549: gap of unknown length
* 25491: contig of 12942 bp in length
* 25591: gap of unknown length
* 25591: contig of 20777 bp in length
* 46368: gap of unknown length
* 46468: contig of 16280 bp in length
* 62748: gap of unknown length
* 62848: contig of 49719 bp in length
* 112567 112666: gap of unknown length
* 112667 183375: contig of 70709 bp in length.

FEATURES
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         source          1..183375
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                        /mol_type="genomic DNA"
                        /db_xref="taxon:9315"
                        /clone="ME_KBa-623119"
                        /clone_lib="ME_KBa"
         misc_feature    1..2752
                        /note="assembly_fragment"
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                        /estimated_length=unknown
         misc_feature    2853..6856
                        /note="assembly_fragment"
         gap             6857..6956
                        /estimated_length=unknown
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                        /note="assembly_fragment"
                        clone_end:SP6
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         misc_feature    46468..62747
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         gap             62748..62847
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                        /note="assembly_fragment"

ORIGIN
Query Match      47.5%; Score 730.2; DB 14; Length 183375;
Best Local Similarity 80.7%; Pred. No. 1.2e-113;
Matches 917; Conservative 0; Mismatches 204; Indels 15; Gaps 5;

Qy      403 TCCTAAAATGCCAAAACGACAGGGTGATTTTTCGATTTTAAATATGAAGAAGGTCAA 462
Db      110175 TCCTAAAATGCCAAAACGCGAGAGTGATCTATTTCAGTTTTTTAAATGTGAAGAAGGTCAA 110116
Qy      463 AACACACACAGAAATATGAAGTGAGCAAAAATCCTGCAGATGTCTAAGGCAAGGA 522
Db      110115 AACACACACAGAA---AACGAGATGACTGAAAATCCTGTGGAGTGTGGAAGTCCAAGGA 110059
Qy      523 ACCACATTTCAGTATATAGAACCAACCAATCATTTGAGAAAAGCCATCTTTCATCAA 582
Db      110058 ACCCACTTTTGAATCTGTGTGAACACAGACTCTTCCTGGAAGAAAAGCCATCATCTTTCATCAA 109999
Qy      583 GAAAGAAATAGATAATCTTGTGCTTCCAGATTGTTGGAATGAAAACCAAGCATTTATGTT 642

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Db 109998 GGNAGAAATGTATACTTTGTGCTCCAGATTGCTGGAAACAAAAGCAAGCCTTTCTCTT 109999
Qy 643 TACAGCAATACAAATCGCTTGAATAAAGAGGTAATAGATGTAAGGATGTTTC 702
Db 109998 CACAGAAATGATAAATGGCTTGAGATAAGGAAGGTAGATTAGGAAGTATGCTC 109879
Qy 703 AGCAGTTCGGCATTTGGGATCGAAAGCAGAAAGCATGTCATGTGTCACAGGAATGAT 762
Db 109878 CATAGTTCAGCACTTAGGATCAGAGCAGAAAGCATGTCATGTTTCCAAAGAGTGGAT 109819
Qy 763 TGCATATTTAGTAACCCCTTAATGCGAGTAATAAACTAGGCAAGCTTCTCTACGAAA 822
Db 109818 TGCCCAATTTGGTAACCCCAATGGAAGTAATAAAATTAAGCAAGCTTCTTTATGAAA 109759
Qy 823 AAAAATTTAGGACATGATGTTCTTAAGCCCATGTAATAATCAGGATTTGTTAAAGGA 882
Db 109758 AAAAATGAGAGAACATGATGTTCTTAAGCCCATTAACAAAATTCAGGATTTGTTAAAGA 109699
Qy 883 AT---CAACTAATGATTCAAATTTGTAATTTTAGTGCAATAAACAATAAATAAATAATTGA 939
Db 109698 ATCTCTTCTAGTGAATCAGTTCCAATTTTATCTTAACCAATACAAAACATTTGA 109639
Qy 940 TGCTACTGTAAAGTTTTCATATCTGTTTACAGTTTGTAAAGCAATACAGACCTTTATC 999
Db 109638 TGCTACTGTAAAGTTTTCATATCTGTTTACAGTTTGTAAAGCAATACAGACCTTTATC 109579
Qy 1000 TGATATTTGAGGGGCAAGAGATTTACAGGAATAAATGGA-----GAGGTAAATGTTT 1053
Db 109578 TGACATTTGAGGGGGTGAGAGAGATTAAGAGAGAGAGGTCGATGTCGGCAGTGTGTT 109519
Qy 1054 AAATACACGTTACAGTGCAACAAGAAATAGCAGAAATATGCAAAAGAAATGAAGATGAA 1113
Db 109518 ACATACAGATACAGTGCAACAAGAAATAGCAGAAATATGCAAAAGAAATGAAGAGAA 109459
Qy 1114 GATATTTAAGAAATATATAGAGAGAAATGCCAAAATCTGTATCATATGATGAGGCATC 1173
Db 109458 GGTATTTAAGAAATATCATAGAGAGAAATGCCAAAATC-GTGTCTCTGATGGATGAGATGTC 109400
Qy 1174 TACAGTTTCAAGAAACACCCCTAGTGAATTTATCTCCAGTGCAAAATCAGTCAGCTCC 1233
Db 109399 TGCAGTTTCCAAAGAAATAGCCCTAGTGAATTTATCTCCAGTGCAACCGTTTGGTCCCTCC 109340
Qy 1234 TSCACCTGTATGTTATTTGTCGCTTTAAAGAAATGGTGCTCAACTATAGCAGAGTGAT 1293
Db 109339 GTCACTGTAAATGTTATTTGTCGCTTTAAAGAAATGATGTCACAGCTGCCAA--GCAT 109282
Qy 1294 TGTCAATACATTAATGACTACTTTAAATGATTTGTTTAAAGAAATGATTTTCAAAAGC 1353
Db 109281 TGTCAATACATTTGGTGTCTGCTTTAAATGACTGTGCTTTCAATATGACTATTTCAAGC 109222
Qy 1354 AAATTTAATGCAATTTGTTCTGATGGTGCTAATAACAACTGGGAAGAGTCTGGAGT 1413
Db 109221 CACCCTAATTTGCAATTTGTTCCGATGGTGCTCAATCAATGTTGGGAAGAGTCTAGAGT 109162
Qy 1414 AGCTACAAATTTGTAGAAAATTTTCTGCAATCATCATTTGGAATCTGTTTAAATCATCG 1473
Db 109161 AGCTGTGAAGTTATTTGGAATAATTTTCCCAAGATCATTAATTTGGCACTGTATCAATCATCG 109102
Qy 1474 ATTACAAATTTGCTATGATGATTTATATCCGAAATATAAACAATAATTAATCATTTAA 1529
Db 109101 ACTGCAGTTGTCACTTTGATGATTCATATCCGAAATAGAACGATTAATCATTTTA 109046

RESULT 13
LOCUS CQ707746 352 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 52672 from Patent WO02070737.
ACCESSION CQ707746
VERSION CQ707746.1 GI:42268515
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 52672 12-SEP-2002;
Chondrogene Inc. (CA)
FEATURES
source 1. 352
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 21.4%; Score 329; DB 6; Length 352;
Best Local Similarity 99.2%; Pred. No. 1.4e-45;
Matches 351; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
Qy 1175 ACAGTTTCAAGAAAAACCCCTAGTGAATTTATCTCCAGTGCAAAATTCAGTCAGCTCCT 1234
Db 1 ACAGTTTCAAGAAAAACCCCTAGTGAATTTATCTCCAGTGCAAAATTCAGTCAGCTCCT 60
Qy 1235 GCACCTGTTATTTATTTGTCCTTTAAAGAAATGGTGCTCAACTATAGCAGAGTGATTT 1294
Db 61 GCACCTGTTATTTATTTGTCCTTTAAAGAAATGGTG-CAACTATAGCAGAGTGATTT 119
Qy 1295 GTCAATACATTTGACTACTTTTAAATGATTTGTTTACAAAATGAAATATTTGAAAGCA 1354
Db 120 GTCAATACATTTGACTACTTTTAAAGAAATGGTGTTTACAAAATGAAATATTTGAAAGCA 179
Qy 1355 AATTAAATTCATTTTGTCTGATGGTGCTAATAACAACTGGGAAGAAAGTCTGGAGTA 1414
Db 180 AATTAAATTCATTTTGTCTGATGGTGCTAATAACAACTGGGAAGAAAGTCTGGAGTA 239
Qy 1415 GCTCAAAATTTGTAGAAAATTTTCTGAAATCATCATTTGGAATCTGTTTAAATCATCGA 1474
Db 240 GCTCAAAATTTGTAGAAAATTTTCTGAAATCATCATTTGGAATCTGTTTAAATCATCGA 299
Qy 1475 TTCAATTTGCTCATTGATGATTTCTATATCCGAAATATAAACAATAATTAATCATTTA 1528
Db 300 TTCAATTTG-CACITGATGATTTCTATATCCGAAATATAAACAATAATTAATCATTTA 352

RESULT 14
LOCUS AX419136 4999 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 1 from Patent WO0216426.
ACCESSION AX419136
VERSION AX419136.1 GI:21523894
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS Dechering,K.J. and Mosselman,S.
TITLE Coactivation of nuclear receptors
JOURNAL Patent: WO 0216426-A 1 28-FEB-2002;
Akzo Nobel N.V. (NL)
FEATURES
source 1. 4999
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 20.7%; Score 317.6; DB 6; Length 4999;
Best Local Similarity 90.9%; Pred. No. 8.9e-44;
Matches 360; Conservative 0; Mismatches 34; Indels 2; Gaps 2;
Qy 1 AGAGAAAGAGGCTCCGGGAGATACCGGACCAAGTGGGCTCCCTCTTTTGAAGCGGT 60
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Db 16 AGAGAAAGCGGCTCCGGGGGATAGCGGGGAGTAAGGGGCGCTCTCTCTTTGAAGAGGT 75

Qy 61 TTT-CGTCTCTTTCCGCGAGTGGCTCCAGCTCACGACAGGGGGGCTCCCGGTAGCGCG 119

Db 76 TTTGCGTCTCTTTCCGCGGTTGGCGTCCGCGCTCACGACGGGGGCGTCCCGGTAGCGCC 135

Qy 120 AGGCGGTGCGAGGGGGGAGAGGGAGTGTGGCGGCTCGCGGAG-TAGGGACAGCAGGAGC 178

Db 136 AGGCGGTGCGAGGGGGGAGAGGGAGTGTGGCGGAGCGGCGGCGGAGGAGCAGCAGGAGC 195

Qy 179 AGTGGTGTGTCAGCGCGGCGTCCGAGAGATGGAGACCGGGGTCCGGAATAATAGAA 238

Db 196 AGTGGTGTGTCAGCGCGGCGTCCGAGAGATGGAGACCGGGGTCCGAGATAATAGAA 255

Qy 239 TCTGTCTCTCCAGCTGGCGCTTCCGAGCATCTGAGTCAACAACGGATGAAATGAAGACGAC 298

Db 256 TCTGTCTCTCCAGCTGGCGCTTCCGAGCATCTGAGTCAACAACGGATGAAATGAAGACGAC 315

Qy 299 ATTCACTTTGTCAGTGAAGACCATCGAGACCTCTTCTTGAATACATCGATCTGGTCTGT 358

Db 316 ATTCACTTTGTCAGTGAAGACCATCGAGACCTCTTCTTGAATACATCGATCTGGTCTGT 375

Qy 359 GGTGATGATGAACACCTAGCGCTTATATAGTAT 394

Db 376 AGTATGATGAAGACCTAGCACCTCTTATACTGAT 411

RESULT 15

LOCUS AX419137 4999 bp DNA linear PAT 18-JUN-2002

DEFINITION Sequence 2 from Patent WO0216426.

ACCESSION AX419137

VERSION AX419137.1 GI:21523895

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Dechering, K.J. and Mosselman, S.

TITLE Coactivation of nuclear receptors

JOURNAL Patent: WO 0216426-A 2 28-FEB-2002;

Akzo Nobel N.V. (NL)

FEATURES

source Location/Qualifiers

1. 4999

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 20.7%; Score 317.6; DB 6; Length 4999;

Best Local Similarity 90.9%; Pred. No. 8.9e-44;

Matches 360; Conservative 0; Mismatches 34; Indels 2; Gaps 2;

Qy 1 AGAGAAAGAGGCTCCGGGGAGATAGCGGAGTGAAGGCTGCCCTCTTTTGAAGCGGT 60

Db 16 AGAGAAAGCGGCTCCGGGGGATAGCGGGGAGTAAGGGGCGCTCTCTCTTTGAAGAGGT 75

Qy 61 TTT-CGTCTCTTTCCGCGAGTGGCTCCAGCTCACGACAGGGGGGCTCCCGGTAGCGCG 119

Db 76 TTTGCGTCTCTTTCCGCGGTTGGCGTCCGCGCTCACGACGGGGGCTCCCGGTAGCGCC 135

Qy 120 AGGCGGTGCGAGGGGGGAGAGGGAGTGTGGCGGCTCGCGGAG-TAGGGACAGCAGGAGC 178

Db 136 AGGCGGTGCGAGGGGGGAGAGGGAGTGTGGCGGAGCGGCGGAGGAGCAGCAGGAGC 195

Qy 179 AGTGGTGTGTCAGCGCGGCGTCCGAGAGATGGAGACCGGGGTCCGGAATAATAGAA 238

Db 196 AGTGGTGTGTCAGCGCGGCGTCCGAGAGATGGAGACCGGGGTCCGAGATAATAGAA 255

Qy 239 TCTGTCTCTCCAGCTGGCGCTTCCGAGCATCTGAGTCAACAACGGATGAAATGAAGACGAC 298

Db 256 TCTGTCTCTCCAGCTGGCGCTGAGGCGATCTGAGTCAACAACGGATGAATAAGACGAC 315

Qy 299 ATTCACTTTGTCAGTGAAGACCATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGT 358

Db 316 ATTCACTTTGTCAGTGAAGACCATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGT 375

Qy 359 GGTGATGATGAACACCTAGCGCTTATATAGTAT 394

Db 376 AGTATGATGAAGACCTAGCACCTCTTATACTGAT 411

RESULT 16

LOCUS AY055204 4999 bp mRNA linear PRI 01-APR-2002

DEFINITION Homo sapiens COASTER mRNA, complete cds.

ACCESSION AY055204

VERSION AY055204.1 GI:19879435

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Heldens, I.M. and Dechering, K.J.

TITLE Isolation of a novel coactivator for steroid receptors that alters the intrinsic activity of the estrogen receptor alpha liganded with SERMs

JOURNAL Unpublished

2 (bases 1 to 4999)

AUTHORS Heldens, I.M. and Dechering, K.J.

TITLE Direct Submission

JOURNAL Submitted (10-SEP-2001) Target Discovery, N.V. Organon, Molenstraat 110, Oss 5340 BH, The Netherlands

FEATURES

source Location/Qualifiers

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/notes="coactivator for steroid receptors"

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/db_xref="GI:19879436"

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Query Match 20.7%; Score 317.6; DB 8; Length 4999;

Best Local Similarity 90.9%; Pred. No. 8.9e-44;

Matches 360; Conservative 0; Mismatches 34; Indels 2; Gaps 2;

Qy 1 AGAGAAAGAGGCTCCGGGGAGATAGCGGAGTGAAGGCTGCCCTCTTTTGAAGCGGT 60

Db 16 AGAGAAAGCGGCTCCGGGGGATAGCGGGGAGTAAGGGGCGCTCTCTCTTTGAAGAGGT 75

QY 61 TTT-CGTCTCTTTCCGCGAGTGGCTCCAGCTCAGCAGGAGGGGCTCCCGGTAGCGG 119
DB 76 TTTGGCTCTCTTTCCGCGGTGGCTCGGCGCTCAGCAGGAGGGGCTCCCGGTAGCGG 135
QY 120 AGGCGGTGAGGCGGGAAGGGAGTGGTGGCGGTGCGGAG-TAGGGACAGCAGGAGC 178
DB 136 AGGCGGTGAGGCGGGAAGGGAGTTCGTGGCGACGCGGCGGCAAGGAGCAGCAGGAGC 195
QY 179 AGTGGTGTCTCAGCGCGGCGCTCGGAGACATGGGAGACCGGGGTCCGAAATATAGAA 238
DB 196 AGTGGTGTCTCAGCGCGGCGCTCGGAGACATGGGAGACCGGGGTCCGAGATATAGNA 255
QY 239 TCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAACGAGTGAATAATGAAGACGAC 298
DB 256 TCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAACGAGTGAATAATGAAGACGAC 315
QY 299 ATTCAAGTTGTCAAGTGAAGGACATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGT 358
DB 316 ATTCAAGTTGTCAAGTGAAGGACATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGT 375
QY 359 GGTGATGATGAACCCCTAGCCCTATTATAGTAT 394
DB 376 AGTGAATGATGAAGAGCCTAGCACCTCTTATCTGAT 411

RESULT 17
AX419138
LOCUS AX419138 5144 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 3 from Patent WO0216426.
ACCESSION AX419138
VERSION AX419138.1 GI:21523896
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Dechering, K.J. and Mosselman, S.
TITLE Coactivation of nuclear receptors
JOURNAL Patent: WO 0216426-A 3 28-FEB-2002;
Akzo Nobel N.V. (NL)
FEATURES
Location/Qualifiers
source
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/organism="Homo sapiens"
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Query Match 20.7%; Score 317.6; DB 6; Length 5144;
Best Local Similarity 90.9%; Pred. No. 8.9e-44;
Matches 360; Conservative 0; Mismatches 34; Indels 2; Gaps 2;

QY 1 AGAGAAAGAGGCTCCGGGAGATAGCGACAGTGAAGGCTCCCGCTCTTTTGAAGCGGT 60
DB 16 AGAGAAAGCGGCTCCGGGGCATAGCGGCGAGTAAGGCGCTCTCTTTGAAGAGGT 75
QY 61 TTT-CGTCTCTTTCCGCCAGTGGCTCCAGTCAACGAGGCGGGTCCCGGTAGCGG 119
DB 76 TTTGGCTCTCTTTCCGCGGTGGCGTCCGCGCTCAGCAGGCGGGTCCCGGTAGCGG 135
QY 120 AGGCGGTGAGGCGGGAAGGGAGTGGTGGCGGTGCGGAG-TAGGGACAGCAGGAGC 178
DB 136 AGGCGGTGAGGCGGGAAGGGAGTTCGTGGCGACGCGGCGGCAAGGAGCAGCAGGAGC 195
QY 179 AGTGGTGTCTCAGCGCGGCGCTCGGAGACATGGGAGACCGGGGTCCGAAATATAGAA 238
DB 196 AGTGGTGTCTCAGCGCGGCGCTCGGAGACATGGGAGACCGGGGTCCGAGATATAGNA 255
QY 239 TCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAACGAGTGAATAATGAAGACGAC 298
DB 256 TCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAACGAGTGAATAATGAAGACGAC 315

QY 299 ATTCAAGTTGTCAAGTGAAGGACCATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGT 358
DB 316 ATTCAAGTTGTCAAGTGAAGGACCATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGT 375
QY 359 GGTGATGATGAACCCCTAGCCCTATTATAGTAT 394
DB 376 AGTGAATGATGAAGAGCCTAGCACCTCTTATCTGAT 411

RESULT 18
AX419139
LOCUS AX419139 5144 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 4 from Patent WO0216426.
ACCESSION AX419139
VERSION AX419139.1 GI:21523897
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Dechering, K.J. and Mosselman, S.
TITLE Coactivation of nuclear receptors
JOURNAL Patent: WO 0216426-A 4 28-FEB-2002;
Akzo Nobel N.V. (NL)
FEATURES
Location/Qualifiers
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ORIGIN
Query Match 20.7%; Score 317.6; DB 6; Length 5144;
Best Local Similarity 90.9%; Pred. No. 8.9e-44;
Matches 360; Conservative 0; Mismatches 34; Indels 2; Gaps 2;

QY 1 AGAGAAAGAGGCTCCGGGAGATAGCGACAGTGAAGGCTCCCGCTCTTTTGAAGCGGT 60
DB 16 AGAGAAAGCGGCTCCGGGGCATAGCGGCGAGTAAGGCGCTCTCTTTGAAGAGGT 75
QY 61 TTT-CGTCTCTTTCCGCCAGTGGCTCCAGTCAACGAGGCGGGTCCCGGTAGCGG 119
DB 76 TTTGGCTCTCTTTCCGCGGTGGCGTCCGCGCTCAGCAGGCGGGTCCCGGTAGCGG 135
QY 120 AGGCGGTGAGGCGGGAAGGGAGTGGTGGCGGTGCGGAG-TAGGGACAGCAGGAGC 178
DB 136 AGGCGGTGAGGCGGGAAGGGAGTTCGTGGCGACGCGGCGGCAAGGAGCAGCAGGAGC 195
QY 179 AGTGGTGTCTCAGCGCGGCGCTCGGAGACATGGGAGACCGGGGTCCGAAATATAGAA 238
DB 196 AGTGGTGTCTCAGCGCGGCGCTCGGAGACATGGGAGACCGGGGTCCGAGATATAGNA 255
QY 239 TCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAACGAGTGAATAATGAAGACGAC 298
DB 256 TCTGTCCCTCCAGCTGGCCCTGAGGCATCTGAGTCAACAACGAGTGAATAATGAAGACGAC 315
QY 299 ATTCAAGTTGTCAAGTGAAGGACCATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGT 358
DB 316 ATTCAAGTTGTCAAGTGAAGGACCATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGT 375
QY 359 GGTGATGATGAACCCCTAGCCCTATTATAGTAT 394
DB 376 AGTGAATGATGAAGAGCCTAGCACCTCTTATCTGAT 411

RESULT 19
BC021712
LOCUS BC021712 3420 bp mRNA linear PRI 28-JUL-2005
DEFINITION Homo sapiens zinc finger protein 451, mRNA (cDNA clone MGC:26701
IMAGE:4821000), complete cds.
ACCESSION BC021712
VERSION BC021712.2 GI:34193451

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KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
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EGETLPSSTLTDNLANKPSALITVLDHSPANSRPRGKOCRIKCDMFDSDQYKQH
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Best Local Similarity 92.4%; Pred. No. 1.4e-38;
Matches 302; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
Qy 68 TCTTTCGGCCAGTGGCTCCAGCTCAGCAGGAGGGGGTCCCGGTAGCGGAGGGCGTG 127
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Qy 128 CAGGCGGGGAAGGGAGTGGTGGCGCTGCGGAGTAGGAGCAGCAGGAGCAGTGGTGCT 187
Db 61 CAGGCGGGGAAGGGAGTGGTGGCGAGTGGGAGACCGGGGTAGGAGTCTGTCCCT 120
Qy 188 GTCAGCGCGCCCTCGGAGACATGGGAGACCGGGGTGCGAAATAATAGATTCGTCCCT 247
Db 121 GTCAGCGCGCCCTCGGAGACATGGGAGACCGGGGTGCGAGATAATAGATTCGTCCCT 180
Qy 248 CGAGCTGGCCCTCAGGACATCTGATCAACACGATGAAATAGACGACATTCAGTTT 307
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Qy 308 GTCAGTGAAGGACCATCGAGACCTGTTCTTGAATACATCGATCTGGTCTGTGTGATGAT 367
Db 241 GTCAGTGAAGGACCATTCAGACCTGTTCTTGAATACATTCATCTGGTCAGCATGAT 300
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Db 301 GAAGAGCCTAGCACCTCTTATCTGAT 327
RESULT 20
BD025398 274 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD025398
VERSION BD025398.1 GI:22566621
KEYWORDS JP 2001269182-A/1644.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 274)
Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 1644 02-OCT-2001;
GENSET
OS Homo sapiens (human)
PN JP 2001269182-A/1644
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES
PI JORDAN
MGC.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 3420)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Datchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 3420)
NIH MGC Project
Direct Submission
Submitted (14-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 25, 2003 this sequence version replaced gi:20987289.
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbio.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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Location/Qualifiers
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PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
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PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40

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FH Key Location/Qualifiers
PT CDS 108..272.

FEATURES

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ORIGIN

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Best Local Similarity 97.1%; Pred. No. 18-35; Mismatches 0; Indels 0; Gaps 0;

Matches 266; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCGGGTCCCGTAGCGGAGCGGTGCGAGCGGGGAGGGGAGTGGTGGCGGCRKGGGR 60

QY 162 GTAGGACAGCAGGAGCAGTGGTGTGTCAGCGCGCGCGTCGGAGACATGGGAGACCCGG 221

DB 61 GTAGGACAGCAGGAGCAGTGGTGTGTCAGCGCGCGCGTCGGAGACATGGGAGACCCGG 120

QY 222 GGTGGAAATATAGATCTGCTCCCTCAGCTGGCCCTGAGGCATCTGAGTCAACAACGG 281

DB 121 GGTGGARATATAGATCTGCTCCCTCAGCTGGCCCTGAGGCATCTGAGTCAACAACGG 180

QY 282 ATGAAATGAAGACGACATTCAGTTGTGTCAGTGAAGGACCATCGAGACCTGTTCTTGAAT 341

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DB 241 ACATCGATCTGCTGTGTCGATGATGAAACCC 274

RESULT 21

AX885788

LOCUS

AX885788 Sequence 1651 from Patent EP1033401. linear PAT 18-DEC-2003

DEFINITION

AX885788

ACCESSION

AX885788.1 GI:40042299

VERSION

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

Genset (FR)

FEATURES

source

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ORIGIN

Query Match

Best Local Similarity

Matches

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C12N5/10

PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC

G06F15/40

CC

FH Key Location/Qualifiers

PT CDS 108..272.

FEATURES

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Location/Qualifiers

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Best Local Similarity 97.1%; Pred. No. 18-35; Mismatches 0; Indels 0; Gaps 0;

Matches 266; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 102 GCGGGTCCCGTAGCGGAGCGGTGCGAGCGGGGAGGGGAGTGGTGGCGGCTCGGGCA 161

DB 1 GCGGGTCCCGTAGCGGAGCGGTGCGAGCGGGGAGGGGAGTGGTGGCGGCRKGGGR 60

QY 162 GTAGGACAGCAGGAGCAGTGGTGTGTCAGCGCGCGCGTCGGAGACATGGGAGACCCGG 221

DB 61 GTAGGACAGCAGGAGCAGTGGTGTGTCAGCGCGCGCGTCGGAGACATGGGAGACCCGG 120

QY 222 GGTGGAAATATAGATCTGCTCCCTCAGCTGGCCCTGAGGCATCTGAGTCAACAACGG 281

DB 121 GGTGGARATATAGATCTGCTCCCTCAGCTGGCCCTGAGGCATCTGAGTCAACAACGG 180

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DB 181 ATGAAATGAAGACGACATTCAGTTGTGTCAGTGAAGGACCATCGAGACCTGTTCTTGAAT 240

QY 342 ACATCGATCTGCTGTGTCGATGATGAAACCC 375

DB 241 ACATCGATCTGCTGTGTCGATGATGAAACCC 274

RESULT 21

AX885788

LOCUS

AX885788 Sequence 1651 from Patent EP1033401. linear PAT 18-DEC-2003

DEFINITION

AX885788

ACCESSION

AX885788.1 GI:40042299

VERSION

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

Genset (FR)

FEATURES

source

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ORIGIN

Query Match

Best Local Similarity

Matches

QY 102 GCGGGTCCCGTAGCGGAGCGGTGCGAGCGGGGAGGGGAGTGGTGGCGGCTCGGGCA 161

DB 1 GCGGGTCCCGTAGCGGAGCGGTGCGAGCGGGGAGGGGAGTGGTGGCGGCRKGGGR 60

QY 162 GTAGGACAGCAGGAGCAGTGGTGTGTCAGCGCGCGCGTCGGAGACATGGGAGACCCGG 221

DB 61 GTAGGACAGCAGGAGCAGTGGTGTGTCAGCGCGCGCGTCGGAGACATGGGAGACCCGG 120

QY 222 GGTGGAAATATAGATCTGCTCCCTCAGCTGGCCCTGAGGCATCTGAGTCAACAACGG 281

DB 121 GGTGGARATATAGATCTGCTCCCTCAGCTGGCCCTGAGGCATCTGAGTCAACAACGG 180

QY 282 ATGAAATGAAGACGACATTCAGTTGTGTCAGTGAAGGACCATCGAGACCTGTTCTTGAAT 341

DB 181 ATGAAATGAAGACGACATTCAGTTGTGTCAGTGAAGGACCATCGAGACCTGTTCTTGAAT 240

QY 342 ACATCGATCTGCTGTGTCGATGATGAAACCC 375

DB 241 ACATCGATCTGCTGTGTCGATGATGAAACCC 274

RESULT 22

HS808227

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

AUTHORS

CONSRM

TITLE

JOURNAL

COMMENT

This clone (DKFZp686M03226) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further

information about the clone and the sequencing project is available

at http://mips.gsf.de/proj/cDNA/.

FEATURES

Location/Qualifiers

1..5100

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFZp686M03226"

/tissue_type="human small intestine"

/clone_lib="686 (synonym: hicc3). Vector pSport1_sfi; host

DL10B; sites SfiIA + SfiIB"

/dev_stage="adult"

5087

polyA_site

ORIGIN

Query Match

Best Local Similarity

Matches

14.5%; Score 222.4; DB 8; Length 5100;

91.8%; Pred. No. 1.1e-27;

0; Mismatches 21; Indels 0; Gaps 0;

QY 139 GGGGAGTGGTGGCGGCTGGGCGAGTAGGACAGCAGGAGCAGTGGTGTGTGTCAGCGCGGC 198

DB 1 GGGGATCTGTGACGACGCGCGCGGCGGACGAGGACAGTGGTGTGTGTCAGCGCGGC 60

```
Qy 199 CGTGGAGACATGGAGACCGGGGTCGGAATAATAGAAATCTCTCCCTCAGCTGCCCC 258
Db 61 CGTGGAGACATGGAGACCGGGGTCGGAATAATAGAAATCTCTCCCTCAGCTGCCCC 120
Qy 259 TGAGGCATCTGAGTCAACAACGGATGAATAAATGAAGACGACATTCAGTTGTCAGTGAAG 318
Db 121 TGAGGCATCTGAGTCAACAACGGATGAATAAATGAAGACGACATTCAGTTGTCAGTGAAG 180
Qy 319 ACCATCGAGACCTGTTCTTGAATACATCGATCTCGTCTGTGGTGATGATGAACACCTAG 378
Db 181 ACCATTAGACCTGTTCTTGAATACATTCATCTGTCAGCAGTGTATGATGAAGACCTAG 240
Qy 379 CGCCTATTATAGTAT 394
Db 241 CACCTCTTATAGTAT 256

RESULT 23
BC098382 3247 bp mRNA linear PRI 03-AUG-2005
LOCUS Homo sapiens zinc finger protein 451, mRNA (CDNA clone MGC:104563
DEFINITION IMAGE:5295845), complete cds.
ACCESSION BC098382
VERSION BC098382.1 GI:58534646
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 3247)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,B., Moore,T., Max,S.I., Wang,J., Haieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schaez,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramsen,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Heiton,E., Kettner,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywicki,M.I., Skaleka,U., Smalilus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J., and Marra,M.A.
Mammalian Gene Collection Program Team
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
1247932
2 (bases 1 to 3247)

NIH MGC Project
Direct Submission
Submitted (01-JUL-2005) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-roman@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Tohiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 198 Row: e Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 20127147.

FEATURES

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Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="MGC:104563 IMAGE:5295845"
/tissue_type="Testis"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
/notes="Vector: pBluescriptR"

gene
1..3247
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/notes="synonyms: COASTER, dj41711.1, KIAA0576"
/db_xref="GeneID:26036"
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YIDLVSDDEPSTYDENIRKSDHIQYOKVVALTLARLARHVEVEKQKEKNRA
FREKIDFOAHGQLELEFIRKSDHIQYOKVVALTLARLARHVEVEKQKEKNRA
HTVSGKPIICPIHCKNKPFDNGHLLGLKRFDPHSPCDPTITLHGPFSSFCVGV
KFWTQOQVLDHLFDKENTDGHNNLLPOLIOCFACPNCLFLLPSRKEECSKMSGCN
HFQSPFKIGNKGIAPISPPSPFAKLLISLCKDVPFQVCKVACHKTLRSHMELTAHF
RVHCRNAGPVSAEKSQVVKTFECNQRPESDVEKHVFSANTMGYKCVGCKVD
SVESVLLYCHVSEGNKDPSSDLHLLDQSFSLKRTMSIKESSELECIATPKKWN
LKDQHEGVACVQKEKSVVKTWFECNQRPESDVEKHVFSANTMGYKCVGCKVD
DSGVIHLMSRIHGAHLNLFLEWCTKKEKTRKDTIMAHVTFFNHGRHYFVEMDEV
EGTLPSSSTLNLNTANKPSSATVVIDHSPANSRPGKQCRICEDMPDFOEYVHOH
CMLSHAEHRYSCAHCCKPFIKELIYRHCQEDHNEIKLYFCGLDLIFVBEAF
LSHYEHSIDYVYSEKTSITKEDDFPIVTEQSDHNEIKLYFCGLDLIFVBEAF
CLQIMLDKGLKFWKCSLQATQNLDMNTHIQVHKESDDEEQQVYIKGCTKAF
HDPEAQOHFKRHKCFLOKPSVAHFGSEKSNLYKTASASHTERRLKQAINYSKSLDM
EKGVENTLSYONIEEIVELPDLDTMTHTVFDVDFNWSNFFGLPHGLNQLFTW
FGOGNTNWKPLNCKIYNYLNRIQGFLLHPRCSKRDADFAICMHAGLDELQLPQ
IPTIILSGDQGFLELENOFKKTORPAILNPHILEGDMMCALLNSISDTTKGTLQSQ
CKPPKRRRLHC"
```

ORIGIN

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Query Match 14.4%; Score 221.2; DB 8; Length 3247;
Best Local Similarity 92.8%; Pred. No. 1.8e-27;
Matches 232; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 145 TGGTGGCGCTGCGGAGTAGGACACAGAGCAGTGGTGTCTGTACGCGCGCGCTCGG 204
Db 4 TCGTGGCGAGCGGCGGCGGAGGACAGCAGCAGTGGTGTCTGTACGCGCGCGCTCGG 63

Qy 205 AGACATGGAGACCGCGGTCGGAATAATAGAAATCTCTCCCTCAGTGCCTGAGGC 264
Db 64 AGACATGGAGACCGCGGTCGGAATAATAGAAATCTCTCCCTCAGTGCCTGAGGC 123

Qy 265 ATCTGAGTCAACACGATGAATAAATGAAGACGACATTCAGTTTGTAGTGAAGACCATC 324
Db 124 ATCTGAGTCAACACGATGAATAAATGAAGACGACATTCAGTTTGTAGTGAAGACCATC 183

Qy 325 GAGACCTGTTCTTGAATACATCGATCTGGTCTGTGGTGATGATGAACACCTAGCGCTA 384
Db 184 ACGACCTGTTCTTGAATACATTCATCTGGTCTGGTCTGGTCTGGTCTGGTCTGGTCTGGT 243

Qy 385 TTATAGTAT 394
Db 244 TTATAGTAT 253
```


RESULT 24
CQ861506
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Sequence 139 from Patent WO2004072265.
CQ861506
CQ861506.1 GI:51982495
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL

Burczynski, M., Twine, N., Dorner, A.J. and Trepicchio, W.L.
METHODS FOR MONITORING DRUG ACTIVITIES IN VIVO / I
Patent: WO 2004072265-A 139 26-AUG-2004;
Wyeth (US); Burczynski, Michael E. (US); Twine, Natalie C. (US);
Dorner, Andrew J. (US); Trepicchio, William L. (US)

FEATURES
Source

1. 4961
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 13.6%; Score 208.2; DB 6; Length 4961;
Best Local Similarity 94.3%; Pred. No. 2.7e-25;
Matches 216; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 166 GCACAGCAGGAGCAGTGTCTGTCTGAGCGCGCGCTCGGAGACATCGGAGACCCGGGTC 225
DB 1 GCACAGCAGGAGCAGTGTCTGTCTGAGCGCGCGCTCGGAGACATCGGAGACCCGGGTC 60

QY 226 GGAATAATAGAAATCTGCTCCAGCTGGCGCTGAGGACATCTGAGTCAACACGATGA 285
DB 61 GGAGATAATAGAAATCTGCTCCAGCTGGCGCTGAGGACATCTGAGTCAACACGATGA 120

QY 286 AAATGAGACGACATCTGCTCCAGCTGGCGCTGAGGACATCTGAGTCAACACGATGA 345
DB 121 AAATGAGACGACATCTGCTCCAGCTGGCGCTGAGGACATCTGAGTCAACACGATGA 180

QY 346 CGATCTGCTGTGGTGATGATGAACCCCTAGCGCTATTATAGTAT 394
DB 181 TGATCTGCTGAGCAGTGTGATGATGAACCCCTAGCGCTATTATAGTAT 229

RESULT 25
AB011148
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AB011148
Homo sapiens mRNA for KIAA0576 protein, partial cds.
AB011148
AB011148.1 GI:3043675
KIAA0576 protein.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL

FEATURES
source

1. 4961
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HJ0261"
/sex="male"
/tissue type="brain"
/clone lib="pBluescriptII SK plus"

gene
CDS

1. 4961
/gene="KIAA0576"
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/protein_id="BAA25502.1"
/db_xref="GI:3043675"

ORIGIN

Query Match 13.6%; Score 208.2; DB 8; Length 4961;
Best Local Similarity 94.3%; Pred. No. 2.7e-25;
Matches 216; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 166 GCACAGCAGGAGCAGTGTCTGTCTGAGCGCGCGCTCGGAGACATCGGAGACCCGGGTC 225
DB 1 GCACAGCAGGAGCAGTGTCTGTCTGAGCGCGCGCTCGGAGACATCGGAGACCCGGGTC 60

QY 226 GGAATAATAGAAATCTGCTCCAGCTGGCGCTGAGGACATCTGAGTCAACACGATGA 285
DB 61 GGAGATAATAGAAATCTGCTCCAGCTGGCGCTGAGGACATCTGAGTCAACACGATGA 120

QY 286 AAATGAGACGACATCTGCTCCAGCTGGCGCTGAGGACATCTGAGTCAACACGATGA 345
DB 121 AAATGAGACGACATCTGCTCCAGCTGGCGCTGAGGACATCTGAGTCAACACGATGA 180

QY 346 CGATCTGCTGTGGTGATGATGAACCCCTAGCGCTATTATAGTAT 394
DB 181 TGATCTGCTGAGCAGTGTGATGATGAACCCCTAGCGCTATTATAGTAT 229

RESULT 26
AC157307/c
LOCUS
DEFINITION

Bos taurus clone CH240-69E15, *** SEQUENCING IN PROGRESS ***, 20
unordered pieces.
AC157307
AC157307.2 GI:68302732
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Bos taurus
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.

REFERENCE
1 (bases 1 to 249308)

AUTHORS

Muzny,D,Marie., Metzker,M, Lee., Abramson,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Ayoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Cesar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cres,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,I., Fan,C., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabis,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregiorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Rulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpachy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorenshewa,L., Louissegh,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartine,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaakemeleh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L., L., Puazo,M., Quiroz,J., Rachin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojao,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajd,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Taber,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villalana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhauser,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE

JOURNAL
REFERENCE

AUTHORS

TITLE

Submitted (11-FEB-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 249308)

REFERENCE

AUTHORS

JOURNAL

COMMENT

On Jun 29, 2005 this sequence version replaced gi:59276112. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole

genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: FDWU
Center clone name: CH240-69E15
----- Summary Statistics

Assembly program: Atlas 3.0;
Consensus quality: 240953 bases at least Q40
Consensus quality: 242833 bases at least Q30
Consensus quality: 244182 bases at least Q20
Estimated insert size: 247434; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
* 1 23245: contig of 23245 bp in length
* 23246 23295: gap of 50 bp
* 23296 43048: contig of 19753 bp in length
* 43049 43098: gap of 50 bp
* 43099 45405: contig of 2307 bp in length
* 45406 45455: gap of 50 bp
* 45456 53285: contig of 7830 bp in length
* 53286 53335: gap of 50 bp
* 53336 63919: contig of 10584 bp in length
* 63920 71469: gap of 50 bp
* 71470 71586: contig of 7500 bp in length
* 71587 80912: contig of 9326 bp in length
* 80913 80962: gap of 50 bp
* 80963 100854: contig of 19892 bp in length
* 100855 101277: gap of 423 bp
* 101278 103192: contig of 1915 bp in length
* 103193 103982: gap of 790 bp
* 103983 113223: contig of 9241 bp in length
* 113224 113398: gap of 175 bp
* 113399 122799: contig of 9400 bp in length
* 122800 122849: gap of 50 bp
* 122850 130140: contig of 7242 bp in length
* 130141 130140: gap of 50 bp
* 130141 195238: contig of 65098 bp in length
* 195239 195288: gap of 50 bp
* 195289 196693: contig of 1405 bp in length
* 196694 196743: gap of 50 bp
* 196744 199736: contig of 2943 bp in length
* 199737 199736: gap of 50 bp
* 199737 206065: contig of 6329 bp in length
* 206066 206115: gap of 50 bp
* 206116 237389: contig of 31274 bp in length
* 237390 237439: gap of 50 bp
* 237440 244436: contig of 6997 bp in length
* 244437 244536: gap of unknown length
* 244537 245708: contig of 1172 bp in length
* 245709 245808: gap of unknown length
* 245809 249308: contig of 3500 bp in length.

FEATURES

source

1. .249308
/organism="Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:9913"


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Qy 209 ATGGGAGACCCGGGTCGGAATAATAGAAATCTGTCCCTCCAGCTGGCCCTGAGGCATCT 268
Db 1 ATGGGAGACCCGGGTCGGAATAATAGAAATCTGTCCCTCCAGCTGGCCCTGAGGCATCT 60

Qy 269 GAGTCAACAACGGATGAAATGAAGACGACATTCAGTTTGTTCAGTGAAGGACCATCGAGA 328
Db 61 GAGTCAACAACGGATGAAATGAAGACGACATTCAGTTTGTTCAGTGAAGGACCATCGAGA 120

Qy 329 CCTGTTCTTGAATACATCGATCTGGTCTGTGGTGATGATGAAAAACCCCTAGCGCCTATTAT 388
Db 121 CCTGTTCTTGAATACATCGATCTGGTCTGGTCAAGCATGATGAAGAGCCCTAGCACCTCTTAT 180

Qy 389 AGTGAT 394
Db 181 ACTGAT 186

RESULT 29
AX419144
LOCUS AX419144 3183 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 9 from Patent WO0216426.
ACCESSION AX419144
VERSION AX419144.1 GI:21523900
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Dechering, K.J. and Mosselman, S.
TITLE Coactivation of nuclear receptors
JOURNAL Patent: WO 0216426-A 9 28-FEB-2002;
Akzo Nobel N.V. (NL)
FEATURES
source
1..3183
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 10.8%; Score 165.2; DB 6; Length 3183;
Best Local Similarity 93.0%; Pred. No. 5.2e-18;
Matches 173; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Hominidae; Homo.
REFERENCE 1
AUTHORS Dechering, K.J. and Mosselman, S.
TITLE Coactivation of nuclear receptors
JOURNAL Patent: WO 0216426-A 10 28-FEB-2002;
Akzo Nobel N.V. (NL)
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c 156	30.6	2.3	2215	6	US-10-750-185-62186	Sequence 62186, A	c 229	29.8	2.3	1637	7	US-11-065-943-68	Sequence 68, Appl
c 157	30.6	2.3	2822	7	US-11-112-908-7	Sequence 7, Appl	c 230	29.8	2.3	1637	7	US-11-065-943-70	Sequence 70, Appl
c 158	30.6	2.3	3671	6	US-10-131-826A-141	Sequence 141, App	c 231	29.8	2.3	1637	7	US-11-065-943-72	Sequence 72, Appl
c 159	30.6	2.3	3379	6	US-10-750-185-35238	Sequence 35238, A	c 232	29.8	2.3	1637	7	US-11-065-943-74	Sequence 74, Appl
c 160	30.6	2.3	4084	6	US-10-750-185-51348	Sequence 51348, A	c 233	29.8	2.3	1637	7	US-11-065-943-76	Sequence 76, Appl
c 161	30.6	2.3	4745	6	US-10-909-125-837	Sequence 837, App	c 234	29.8	2.3	1637	7	US-11-065-943-80	Sequence 80, Appl
c 162	30.6	2.3	7762	6	US-10-750-185-41139	Sequence 41139, A	c 235	29.8	2.3	1637	7	US-11-065-943-82	Sequence 82, Appl
c 163	30.6	2.3	10494	8	US-11-174-186-40	Sequence 40, Appl	c 236	29.8	2.3	1637	7	US-11-065-943-84	Sequence 84, Appl
c 164	30.4	2.3	273	6	US-10-467-657-3589	Sequence 3589, Ap	c 237	29.8	2.3	1637	7	US-11-065-943-86	Sequence 86, Appl
c 165	30.4	2.3	273	6	US-10-467-657-6439	Sequence 6439, Ap	c 238	29.8	2.3	1637	7	US-11-065-943-88	Sequence 88, Appl
c 166	30.4	2.3	558	6	US-10-750-185-35711	Sequence 35711, A	c 239	29.8	2.3	1637	7	US-11-065-943-90	Sequence 90, Appl
c 167	30.4	2.3	600	6	US-10-750-185-21841	Sequence 21841, A	c 240	29.8	2.3	1637	7	US-11-065-943-94	Sequence 94, Appl
c 168	30.4	2.3	1194	6	US-10-750-185-44388	Sequence 44388, A	c 241	29.8	2.3	1637	7	US-11-065-943-96	Sequence 96, Appl
c 169	30.4	2.3	1212	6	US-10-467-657-6325	Sequence 6325, Ap	c 242	29.8	2.3	1637	7	US-11-065-943-98	Sequence 98, Appl

243	29.8	2.3	1682	6	US-10-850-816-1	Sequence 1, Appl	C 316	29.2	2.2	1467	6	US-10-750-185-35694	Sequence 35694, A
244	29.8	2.3	1682	6	US-10-850-816-3	Sequence 3, Appl	C 317	29.2	2.2	1600	6	US-10-750-185-29159	Sequence 29159, A
245	29.8	2.3	1682	6	US-10-850-816-5	Sequence 5, Appl	C 318	29.2	2.2	1627	6	US-10-750-185-46094	Sequence 46094, A
246	29.8	2.3	1688	7	US-11-065-943-21	Sequence 21, Appl	C 319	29.2	2.2	1642	6	US-10-750-185-61235	Sequence 61235, A
247	29.8	2.3	1688	7	US-11-065-943-23	Sequence 23, Appl	C 320	29.2	2.2	1805	6	US-10-821-234-212	Sequence 212, App
248	29.8	2.3	1688	7	US-11-065-943-25	Sequence 25, Appl	C 321	29.2	2.2	1821	6	US-10-750-185-29962	Sequence 29962, A
249	29.8	2.3	1688	7	US-11-065-943-29	Sequence 29, Appl	C 322	29.2	2.2	1866	6	US-10-821-234-534	Sequence 524, App
250	29.8	2.3	1688	7	US-11-065-943-31	Sequence 31, Appl	C 323	29.2	2.2	2849	6	US-10-131-826A-371	Sequence 371, App
251	29.8	2.3	1688	7	US-11-065-943-33	Sequence 33, Appl	C 324	29.2	2.2	2959	6	US-10-750-185-36103	Sequence 36103, A
252	29.8	2.3	1688	7	US-11-065-943-35	Sequence 35, Appl	C 325	29.2	2.2	3797	6	US-10-750-185-44659	Sequence 44659, A
253	29.8	2.3	1688	7	US-11-065-943-37	Sequence 37, Appl	C 326	29.2	2.2	3824	6	US-10-131-826A-341	Sequence 341, App
254	29.8	2.3	1750	6	US-10-750-185-57403	Sequence 57403, A	C 327	29.2	2.2	4982	6	US-10-276-233A-17	Sequence 17, Appl
255	29.8	2.3	1904	6	US-10-131-826A-99	Sequence 99, Appl	C 328	29.2	2.2	150450	7	US-11-112-908-54	Sequence 54, Appl
256	29.8	2.3	1967	6	US-10-750-185-26228	Sequence 26228, A	C 329	29.2	2.2	155515	7	US-11-112-908-42	Sequence 42, Appl
257	29.8	2.3	2496	6	US-10-750-185-61573	Sequence 61573, A	C 330	29.2	2.2	157224	7	US-11-112-908-51	Sequence 51, Appl
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262	29.8	2.3	5073	6	US-10-909-125-827	Sequence 827, App	C 335	29	2.2	170189	7	US-11-112-908-50	Sequence 50, Appl
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264	29.8	2.3	157230	7	US-11-112-908-64	Sequence 64, Appl	C 337	29	2.2	605	6	US-10-750-185-20765	Sequence 20765, A
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266	29.8	2.3	173115	7	US-11-112-908-65	Sequence 65, Appl	C 339	29	2.2	843	6	US-10-793-628-3193	Sequence 3193, Ap
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271	29.6	2.3	1547	6	US-10-750-185-56974	Sequence 56974, A	C 344	29	2.2	1609	6	US-10-750-185-30217	Sequence 30217, A
272	29.6	2.3	1719	6	US-10-848-724-4	Sequence 4, Appl	C 345	29	2.2	1705	6	US-10-750-185-36545	Sequence 36545, A
273	29.6	2.3	1737	6	US-10-858-730-174	Sequence 174, App	C 346	29	2.2	1979	6	US-10-750-185-62238	Sequence 62238, A
274	29.6	2.3	1786	6	US-10-750-185-41582	Sequence 41582, A	C 347	29	2.2	2148	6	US-10-821-234-29	Sequence 29, Appl
275	29.6	2.3	1958	7	US-11-087-227-1	Sequence 1, Appl	C 348	29	2.2	2823	6	US-10-131-826A-63	Sequence 63, Appl
276	29.6	2.3	2167	6	US-10-131-826A-159	Sequence 159, App	C 349	29	2.2	2823	6	US-10-750-185-30725	Sequence 30725, A
277	29.6	2.3	2270	6	US-10-750-185-50019	Sequence 50019, A	C 350	29	2.2	2922	6	US-11-099-691-22	Sequence 22, Appl
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279	29.6	2.3	2332	6	US-10-750-185-31968	Sequence 31968, A	C 352	29	2.2	3081	6	US-10-793-626-3435	Sequence 3435, Ap
280	29.6	2.3	2496	6	US-10-750-185-36044	Sequence 36044, A	C 353	29	2.2	3088	6	US-10-793-626-3859	Sequence 3859, Ap
281	29.6	2.3	2551	6	US-10-750-185-40726	Sequence 40726, A	C 354	29	2.2	3318	6	US-10-793-626-4149	Sequence 4149, Ap
282	29.6	2.3	2556	6	US-10-467-657-5003	Sequence 5003, Ap	C 355	29	2.2	3343	6	US-10-793-626-4149	Sequence 4149, Ap
283	29.6	2.3	2815	6	US-10-821-234-165	Sequence 165, App	C 356	29	2.2	3597	6	US-10-793-626-3810	Sequence 3810, Ap
284	29.6	2.3	3016	6	US-10-793-626-4292	Sequence 4292, Ap	C 357	29	2.2	3607	6	US-10-793-626-4297	Sequence 4297, Ap
285	29.6	2.3	3062	6	US-10-793-626-4009	Sequence 4009, Ap	C 358	29	2.2	3840	6	US-10-793-626-4015	Sequence 4015, Ap
286	29.6	2.3	3137	6	US-10-793-626-3473	Sequence 3473, Ap	C 359	29	2.2	3926	6	US-10-793-626-4015	Sequence 4015, Ap
287	29.6	2.3	3413	6	US-10-750-185-51161	Sequence 51161, A	C 360	29	2.2	4244	6	US-10-793-626-4256	Sequence 4256, Ap
288	29.6	2.3	3601	6	US-10-793-626-3515	Sequence 3515, Ap	C 361	29	2.2	4402	7	US-11-077-712-2	Sequence 2, Appl
289	29.6	2.3	8424	6	US-10-821-234-47	Sequence 47, Appl	C 362	29	2.2	149419	7	US-11-112-908-49	Sequence 49, Appl
290	29.6	2.3	191343	7	US-11-112-908-53	Sequence 53, Appl	C 363	29	2.2	161726	7	US-11-112-908-48	Sequence 48, Appl
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292	29.4	2.2	623	6	US-10-750-185-59858	Sequence 59858, A	C 365	29	2.2	166111	7	US-11-112-908-47	Sequence 47, Appl
293	29.4	2.2	694	6	US-10-750-185-38044	Sequence 38044, A	C 366	28.8	2.2	403	6	US-10-750-185-2176	Sequence 2176, Ap
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296	29.4	2.2	1200	6	US-10-131-826A-273	Sequence 273, App	C 369	28.8	2.2	600	6	US-10-750-185-281	Sequence 281, App
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301	29.4	2.2	2729	6	US-10-750-185-64217	Sequence 64217, A	C 374	28.8	2.2	1188	6	US-10-750-185-59537	Sequence 59537, A
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306	29.4	2.2	8651	6	US-10-432-483-48	Sequence 48, Appl	C 379	28.8	2.2	1348	6	US-10-750-185-35880	Sequence 35880, A
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308	29.2	2.2	598	6	US-10-750-185-21101	Sequence 21101, A	C 381	28.8	2.2	1384	6	US-10-750-185-47997	Sequence 47997, A
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310	29.2	2.2	647	6	US-10-750-185-48154	Sequence 48154, A	C 383	28.8	2.2	1590	7	US-10-632-150-43	Sequence 43, Appl
311	29.2	2.2	763	6	US-10-750-185-40941	Sequence 40941, A	C 384	28.8	2.2	1590	7	US-11-073-457-43	Sequence 43, Appl
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Best Local Similarity 61.0%; Pred. No. 0.53;
Matches 64; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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QY 169 AGCGCGCGCGCTCGCGCGCCCAAGCAGCACAGCGCGAGGAGGA 213
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RESULT 8
US-10-821-234-749
; Sequence 749, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 749
; LENGTH: 2543
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-749

Query Match 2.9%; Score 38.4; DB 6; Length 2543;
Best Local Similarity 45.8%; Pred. No. 1;
Matches 132; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

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RESULT 9
US-10-821-234-836
; Sequence 836, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
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; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 836
; LENGTH: 2584
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-836

Query Match 2.9%; Score 38.4; DB 6; Length 2584;
Best Local Similarity 51.8%; Pred. No. 1;
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RESULT 10
US-11-112-908-37/c
; Sequence 37, Application US/11112908
; Publication No. US2005026059A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37
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; ORGANISM: Homo sapiens
US-11-112-908-37

Query Match 2.9%; Score 38.4; DB 7; Length 150481;
Best Local Similarity 48.2%; Pred. No. 10;
Matches 108; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 78 GGAAGCAGCGTGAAGAGCGGCTTTTGGGGGACCTTCGGCGATGGCGCTCTGGCAGCA 137
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 133848 GGACGGGAGGACGGGGCCAGGGGCTGCACCGCGGGGGGGGGTGC 133789
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 138 GTTCCGATCGGCGGAGCCCGCAGGGCCCGGCGGCGCGGTTCGGCGCCCGAAGCAG 197
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 133788 GGAGCGGCGCGCGGCTCCCGGGCGCGGAGGGCGGGCGTGGGGCGGACGGA 133729
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 198 CACAGCGGAGGAGGACCGGTGAAGAGCGGCGGCTTCAGTGCCTTGGCGTTGG 257
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 133728 CCACCGGGCGGGGTGGGAGGTAAACGGGACCGGCGGACCATGGCGGTGAGGAGCGG 133669
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 258 TGGGGGATGCGACCCACGATGTTCCCGAGCGTCTCTGCGGGAG 301
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Db 133668 GGGTGGGATCGGTCCGGGGAGGCGCTGAGGCCGCTGGCTTGTG 133625

RESULT 11
US-11-112-908-39/c
; Sequence 39, Application US/11112908
; Publication No. US2005026059A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39
; LENGTH: 179892
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-39

Query Match 2.9%; Score 38.4; DB 7; Length 179892;
Best Local Similarity 48.2%; Pred. No. 11;
Matches 108; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 78 GGAAGCAGCGTGAAGAGCGGGTGTGTTGAGGGGACCTCGCGCGATGGCTGTGCAGCA 137
Db 55837 GGACGGGAGGAGCGGGCCAGGGACTGCAGGGCGGTGCACCGCCCGGGCGGGGTGC 55778

QY 138 GTTCCGATCGCGGAGCCCGCAGGGCGCGGCGCGCTCGGCGCCCGCAAGCAG 197
Db 55777 GGAGCGGGCGCGGCTCCCGGGCGGGCGGAGGGCGGGCGTGGGGCGGACGAA 55718

QY 198 CACAGCGGAGGAGACCGGGTGAAGAGCGCGGCTTCAGTGCCTGGGCTTGGTGG 257
Db 55717 CCACCGGGCGGGTGGGAGGTAAACGGGACCGGGCGGACCATGGCGCGGTGAGGAGCGG 55658

QY 258 TGGGGGATGCGACCCACGATGGTCCCGCAGCGTCTCGGGGAG 301
Db 55657 GGGTGGGATCGGTCCGGGGAGGCGCTGAGGCCGCTGGCTTGTG 55614

RESULT 12
US-10-821-234-698
; Sequence 698, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Ton
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 698
; LENGTH: 1398
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-821-234-698

Query Match 2.9%; Score 37.8; DB 6; Length 1398;
Best Local Similarity 49.7%; Pred. No. 1;
Matches 96; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 109 GGACCTCGCGCGATGGCTGTGGCAGCAGTTCCGATGCGGCGGAGCCCGCAGGCGCGGC 168
Db 18 GGACCGCTGCCCGGCTGCAGTCGGGGCGGAGCTGAGCGGAGGCTGACGAGAGGC 77

QY 169 AGGGCGGCGCGCTCGCGCCCGAAGCAGCAGCAGCGGAGGAGACCGGGTGAAGAGCG 228
Db 78 GGATCCCGCGCGCTCAGATCTGCCGACACCCAGGCCATCGAGCCCGCAGGCATCGTGA 137

QY 229 CGGGCTTCAGTGCCTGGGCTTTGGTTGGTGGGGGATGCGACCCACGATGCTCCCGAG 288
Db 138 GCAGGTCCACGCCCGCAGTCGAATGCAGATCCCGAGGGAAACCCGCTGCTGTGCCA 197

QY 289 CGTCTCGGGGAG 301
Db 198 CACCTGCAGGAG 210

RESULT 13
US-11-112-908-61
; Sequence 61, Application US/11112908
; Publication No. US2005026059A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 159497
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-61

Query Match 2.8%; Score 37.2; DB 7; Length 159497;
Best Local Similarity 49.5%; Pred. No. 23;
Matches 96; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 71 GAGGGCGGGAAGCAGCGTGAAGAGCGGGTGTGTTGAGGGGACCTTCGCGCGATGGCGTCT 130
Db 69361 GAGCGCGGGAGCGCGCGGGCGGGCGGCCCGCCAGAGCGGCGCTCGCTCGGAGCGGGC 69420

QY 131 GCGACAGTTCGATCGCGCGAGCCCGCAGAGGCGCGGCGGCGCGGCGGTGCGCGCCC 190
Db 69421 GCGAGGGCGGGCGGAGCGGAGCGCGCGGGCGGCGAGTAGCGCAGTGAAGTTTGGCGGC 69480

QY 191 GAAGCAGCAGCGGGAGGAGACCGGGTGAAGAGCGGCGGCTTCAGTGGCTGGGCTTT 250
Db 69481 GGAGGGCGGGCGGTCCCGGGTCCGAGGAGGCGGCGGCGGCGGCGCGGACCGGGGCCAT 69540

QY 251 GCGTTGGTGGGGG 264
Db 69541 GGGGCGGCGCGG 69554

RESULT 14
US-10-909-125-833/c


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US-10-821-234-40
; Sequence 40, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 40
; LENGTH: 4564
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-821-234-40

Query Match      2.8%; Score 36.2; DB 6; Length 4564;
Best Local Similarity 54.0%; Pred. No. 5.7;
Matches 74; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 78 GGAAGCAGCGTGAAGAGCGGGTGTGTTGAGGGGACCTTGGCGCGATGCGGCTTGGCAGCA 137
Db 4235 GGGGGCGGAGCGGGAGCGCGCTCATGTGGCTCCGGGACGCGGGCGGTGTCAGGC 4294

QY 138 GTTCGATCGCGCGGAGCCCGCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 197
Db 4295 CCGCAGCTCGGGGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4354

QY 198 CACAGCGGAGGAGGAC 214
Db 4355 GCCTGGCGGAGGCTGCC 4371

RESULT 18
US-10-979-821-13
; Sequence 13, Application US/10979821
; Publication No. US20050244937A1
; GENERAL INFORMATION:
; APPLICANT: ABRAHAM, TIMOTHY W.
; APPLICANT: CAMERON, DOUGLAS C.
; APPLICANT: HICKS, PAULA M.
; APPLICANT: MCFARLAN, SARA C.
; APPLICANT: MILLIS, JIM
; APPLICANT: ROSAZZA, JACK
; APPLICANT: WEINER, DAVID P.
; APPLICANT: ZHAO, LISHAN
; TITLE OF INVENTION: POLYPEPTIDES AND BIOSYNTHETIC PATHWAYS FOR THE
; PRODUCTION OF MONATIN AND ITS PRECURSORS
; FILE REFERENCE: 023829-0390
; CURRENT APPLICATION NUMBER: US/10/979,821
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: 10/422,366
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/374,831
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 13
; LENGTH: 1413
; TYPE: DNA
; ORGANISM: Rhodobacter sphaeroides
US-10-979-821-13

Query Match      2.7%; Score 35.4; DB 6; Length 1413;
Best Local Similarity 50.9%; Pred. No. 4.8;
Matches 84; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

US-10-858-730-160
; Sequence 160, Application US/10858730
; Publication No. US2005025558A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 1587
; TYPE: DNA
; ORGANISM: Mycobacterium leprae
US-10-858-730-160

Query Match      2.7%; Score 35.4; DB 6; Length 1587;
Best Local Similarity 56.4%; Pred. No. 5.2;
Matches 66; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 138 GTTCGATCGCGGAGCGCCGCGCAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 197
Db 875 GTACTGATGTGGCCGAAGCGTGGCGCTGGCGCTGGCGGAGTTTGTGCTTACCGCGG 934

QY 198 CACAGCGGAGGAGGACCGGGTGAAGAGCGCGCGCGGCTTCAGTGCCTGGGCTTTGCGT 254
Db 935 TCACGTGGACGGGGCGGTGCTCAACGAGAGGTGGTCCCTCGCTGAGACTTGGTGT 991

RESULT 20
US-10-750-185-28195
; Sequence 28195, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
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; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28195
; LENGTH: 2738
; TYPE: DNA
; ORGANISM: Bovine 1986880642784
US-10-750-185-28195

Query Match      2.7%; Score 35.4; DB 6; Length 2738;
Best Local Similarity 47.7%; Pred. No. 7.1;
Matches 134; Conservative 0; Mismatches 146; Indels 1; Gaps 1;

QY 71 GAGGGCGGAAGCAGCGTGAAGAGCGGGTGTGTTAGGGAGACCTCGCGCGATGCGGTCT 130
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1721 GAGCTGAGAGAGCGTGAAGAGCGGGTGTGTTAGGGAGACCTCGCGCGATGCGGTCT 1780

QY 131 G-GCAGCAGTTCGATCGCGCGGAGCCCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCC 189
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1781 GAGCGCGCGCTTGGCGCGCGCAGCGCGCGCGCTTGGCGCTGAGGGGGCGCGCTGCGGCGC 1840

QY 190 CGAAGCAGCACAGCGCGGAGGAGACCGCGGTGAAGAGCGCGCGCGCTTCACTGCTGGCTT 249
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1841 GCGCGCGCGCATGAGCAGCGGAGCGCGGTGTGAGCAGCGCGCGCGCTGCTCGCGCACCGCAG 1900

QY 250 TGGCTTGTGGGGGATGCGACCCACAGATGTTCCCGAGCGTCTCGGGGAGAACACTG 309
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1901 GGGGATGAGTACGGGCTGTAGCGCAGCGCGCGCGCATGTTGTTCAAGTTTCAGGAAGG 1960

QY 310 GCAGACGCGAAGACCCCTGAGCGCCCTACTTTCGAGCTGCCAG 350
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1961 GTGGCGGTGACGCGAGCTGAGGCTGCGCGCGGAGGCGCG 2001

RESULT 21
US-10-276-233A-6/c
; Sequence 6, Application US/10276233A
; Publication No. US20050260572A1
; GENERAL INFORMATION:
; APPLICANT: DNA Chip Research Inc.
; APPLICANT: Hitachi Software Engineering Co., Ltd.
; TITLE OF INVENTION: A method of predicting cancer condition
; FILE REFERENCE: PH-1533-PCT
; CURRENT APPLICATION NUMBER: US/10/276,233A
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: JP 2001-73063
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: JP 2001-108503
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: JP 2001-234807
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 79528
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-233A-6

Query Match      2.7%; Score 35.4; DB 6; Length 79528;
Best Local Similarity 56.4%; Pred. No. 48;
Matches 66; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 149 GCGGAGCCCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 208
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 33198 GCGAGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 33139

QY 209 GAGGACCGGTGAAGAGCGCGCGCTTCACTGCTCGGCTTTCGTTGTTGGTGGGGGGA 265
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 33138 GAAGCGCGCGGAGTGGCGCGGAGCGCGCTAGACGAGCGGTTGAGGCGAGGA 33082
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RESULT 22
US-11-112-908-22/c
; Sequence 22, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 172147
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-22

Query Match      2.7%; Score 35; DB 7; Length 172147;
Best Local Similarity 50.3%; Pred. No. 95;
Matches 86; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 66 GGCACGAGGGCGGAGCAGCGTGAAGAGCGGGTGTGTTGAGGGGACCCCTCGCGCGATGG 125
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 88662 GGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGG 88603

QY 126 CGTCTGGCAGCAGTTCGATGCGGGGAGCCCGCAGGGCGGGCGGGCGGGCGGGCGGGCTCGG 185
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 88602 GGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGG 88543

QY 186 CGCCCGAAGCAGCAGCAGCGCGGAGGACCCGGGTGAAGAGCGGGCGGGCGGGCGGGCTTC 236
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 88542 GGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCTC 88492

RESULT 23
US-11-112-908-23/c
; Sequence 23, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 188682
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-23

Query Match      2.7%; Score 35; DB 7; Length 188682;
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 11:01:36 ; Search time 1105.9 Seconds
(without alignments)
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Title: US-10-757-745-3
Perfect score: 1312
Sequence: 1 agctattaatgatgaatt.....tctcaacorttcaggacatc 1312

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1312	100.0	1312	9	US-10-757-745-3
2	668.2	50.9	1920	9	US-10-757-745-1
3	668.2	50.9	1948	5	US-10-037-270-889
4	668.2	50.9	1948	5	US-10-117-722-889
5	668.2	50.9	1948	9	US-10-122-851-889
6	668.2	50.9	3152	3	US-09-981-353-88
7	667	50.8	1296	3	US-09-925-299-170
8	666.6	50.8	1296	3	US-09-925-299-170
9	666.6	50.8	1940	9	US-10-783-271-28
10	493.2	37.6	1088	9	US-10-450-763-22058
11	490	37.3	1079	3	US-09-745-288-63
12	490	37.3	1079	7	US-10-453-919-63
13	461.6	35.2	674	5	US-10-066-543-1067
14	436.4	33.3	644	5	US-10-066-543-1070
15	428.4	32.7	625	5	US-10-066-543-1031
16	428.4	32.7	633	5	US-10-066-543-1084
17	418	31.9	625	5	US-10-066-543-548
18	385.8	29.4	553	5	US-10-066-543-983
19	230.2	22.1	401	5	US-10-066-543-1363
20	227.2	17.3	400	7	US-10-242-535A-8082
21	227.2	17.3	400	7	US-10-085-783A-8082
22	198.2	15.1	1227	9	US-10-450-763-22059
23	140.8	10.7	391	5	US-10-066-543-826
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Sequence 889, App					
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Sequence 88, Appl					
Sequence 170, App					
Sequence 170, App					
Sequence 28, Appl					
Sequence 22058, A					
Sequence 63, Appl					
Sequence 63, Appl					
Sequence 1067, Ap					
Sequence 1070, Ap					
Sequence 1031, Ap					
Sequence 1084, Ap					
Sequence 548, App					
Sequence 983, App					
Sequence 1363, App					
Sequence 8082, Ap					
Sequence 22059, A					
Sequence 826, App					

10.2	134.4	24	3	176	3	US-09-878-722-121	Sequence 121, App
10.2	134.4	c 25	3	176	3	US-09-878-178-50	Sequence 50, Appl
10.2	134.4	26	3	176	3	US-09-904-456-121	Sequence 121, App
10.2	134.4	c 27	5	176	5	US-10-046-935-50	Sequence 50, Appl
10.2	134.4	28	5	176	5	US-10-146-502-50	Sequence 50, Appl
10.2	134.4	c 29	5	176	5	US-10-060-036-1367	Sequence 1367, Ap
8.3	108.4	30	4	606	4	US-09-925-065A-783537	Sequence 783537, Sequence 783536,
8.3	108.4	31	4	634	4	US-09-876-889-312	Sequence 312, App
7.7	101.4	32	3	268	3	US-09-864-761-16762	Sequence 16762, A
5.7	74.6	33	3	444	3	US-09-864-761-33229	Sequence 33229, A
5.7	74.6	34	3	691	3	US-10-115-831-61	Sequence 61, Appl
5.7	65	35	6	499	6	US-10-404-460-149	Sequence 149, App
4.9	63.8	36	7	696	7	US-10-404-460-154	Sequence 154, App
4.8	63.2	37	7	704	7	US-10-404-460-105	Sequence 105, App
4.8	63.2	38	7	704	7	US-10-093-045-5	Sequence 5, Appli
4.7	62.2	39	5	1549	5	US-10-093-246-5	Sequence 5, Appli
4.7	62.2	40	5	1549	5	US-10-404-460-121	Sequence 121, App
4.7	62.2	41	7	701	7	US-10-404-460-201	Sequence 201, App
4.7	61.6	42	7	682	7	US-10-404-460-201	Sequence 201, App
4.7	61.4	43	7	682	7	US-10-404-460-201	Sequence 201, App
4.7	61.4	44	7	1775	5	US-10-098-841-26	Sequence 26, Appl
4.7	61.2	45	7	956	2	US-08-816-011-52	Sequence 52, Appl
4.7	61.2	46	7	956	2	US-10-870-492-52	Sequence 52, Appl
4.6	60.4	47	7	706	7	US-10-404-460-231	Sequence 231, App
4.6	60.2	48	7	657	7	US-10-404-460-209	Sequence 209, App
4.6	60.2	49	7	686	7	US-10-404-460-138	Sequence 138, App
4.5	59	50	7	691	7	US-10-404-460-24	Sequence 24, Appl
4.5	59	51	7	691	7	US-10-404-460-169	Sequence 169, App
4.5	58.8	52	7	627	7	US-10-404-460-201	Sequence 201, App
4.5	58.8	53	7	688	7	US-10-404-460-214	Sequence 214, App
4.5	58.6	54	9	382	9	US-10-756-149-4637	Sequence 4637, Ap
4.5	58.6	55	7	631	7	US-10-404-460-129	Sequence 129, App
4.5	58.6	56	7	705	7	US-10-404-460-155	Sequence 155, App
4.5	58.6	57	5	846	5	US-10-198-846-9716	Sequence 9716, Ap
4.5	58.4	58	5	422	5	US-10-198-846-9716	Sequence 12993, A
4.4	58.2	59	9	519	9	US-10-756-149-4511	Sequence 4511, App
4.4	58	60	7	633	7	US-10-404-460-264	Sequence 264, App
4.4	58	61	7	666	7	US-10-404-460-6	Sequence 6, Appli
4.4	57.8	62	7	670	7	US-10-404-460-27	Sequence 27, Appl
4.4	57.8	63	7	670	7	US-10-404-460-207	Sequence 207, App
4.4	57.8	64	7	671	7	US-10-404-460-93	Sequence 93, Appl
4.4	57.8	65	7	671	7	US-10-404-460-196	Sequence 196, App
4.4	57.8	66	7	689	7	US-10-404-460-187	Sequence 187, App
4.4	57.6	67	7	615	7	US-10-152-319A-915	Sequence 915, App
4.4	57.6	68	7	708	7	US-10-404-460-221	Sequence 221, App
4.4	57.6	69	7	728	7	US-10-404-460-137	Sequence 137, App
4.4	57.4	70	7	663	7	US-10-404-460-166	Sequence 166, App
4.4	57.4	71	7	705	7	US-10-404-460-163	Sequence 163, App
4.4	57.2	72	7	422	7	US-10-404-460-150	Sequence 150, App
4.4	57.2	73	7	690	7	US-10-404-460-123	Sequence 123, App
4.4	57.2	74	7	719	7	US-10-404-460-230	Sequence 230, App
4.4	57.2	75	8	3232	8	US-10-357-930-24319	Sequence 24319, A
4.3	57.2	76	7	684	7	US-10-404-460-164	Sequence 164, App
4.3	57	77	7	769	7	US-10-404-460-174	Sequence 174, App
4.3	56.8	78	3	488	3	US-09-801-574-66	Sequence 66, Appl
4.3	56.8	79	3	627	3	US-10-404-460-197	Sequence 197, App
4.3	56.8	80	7	639	7	US-10-404-460-245	Sequence 245, App
4.3	56.8	81	7	688	7	US-10-404-460-63	Sequence 63, Appl
4.3	56.8	82	7	693	7	US-10-404-460-216	Sequence 216, App
4.3	56.8	83	7	705	7	US-10-404-460-132	Sequence 132, App
4.3	56.8	84	7	717	7	US-10-404-460-172	Sequence 172, App
4.3	56.8	85	7	659	7	US-10-404-460-171	Sequence 171, App
4.3	56.6	86	7	682	7	US-10-404-460-215	Sequence 215, App
4.3	56.6	87	7	698	7	US-10-404-460-16	Sequence 16, Appl
4.3	56.6	88	9	736	9	US-10-493-047-7	Sequence 7, Appli
4.3	56.6	89	5	1842	5	US-09-814-353-21079	Sequence 21079, A
4.3	56.6	90	5	1842	5	US-10-198-846-9679	Sequence 9679, Ap
4.3	56.4	91	7	665	7	US-10-404-460-167	Sequence 167, App
4.3	56.4	92	7	688	7	US-10-404-460-35	Sequence 35, Appl
4.3	56.4	93	7	705	7	US-10-404-460-141	Sequence 141, App
4.3	56.2	94	7	655	7	US-10-404-460-233	Sequence 233, App
4.3	56.2	95	7	667	7	US-10-404-460-54	Sequence 54, Appl
4.3	56.2	96	7	686	7	US-10-404-460-101	Sequence 101, App

97	56.2	4.3	689	7	US-10-404-460-145	Sequence 145, App	170	54.8	4.2	654	7	US-10-404-460-235	Sequence 235, App
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99	56.2	4.3	693	7	US-10-404-460-193	Sequence 199, App	172	54.8	4.2	657	7	US-10-404-460-222	Sequence 222, App
100	56.2	4.3	698	7	US-10-404-460-1109	Sequence 103, App	c 173	54.8	4.2	665	7	US-10-404-460-8	Sequence 8, Appli
101	56.2	4.3	700	7	US-10-404-460-227	Sequence 227, App	174	54.8	4.2	667	9	US-10-404-460-219	Sequence 219, App
102	56.2	4.3	701	7	US-10-404-460-64	Sequence 64, Appl	175	54.8	4.2	667	9	US-10-928-465-113	Sequence 113, App
103	56.2	4.3	768	9	US-10-960-235-4	Sequence 4, Appli	176	54.8	4.2	675	7	US-10-404-460-220	Sequence 220, App
104	56	4.3	665	7	US-10-404-460-202	Sequence 202, App	177	54.8	4.2	676	7	US-10-404-460-234	Sequence 234, App
105	56	4.3	690	7	US-10-404-460-188	Sequence 188, App	178	54.8	4.2	680	7	US-10-404-460-181	Sequence 181, App
106	56	4.3	704	7	US-10-404-460-255	Sequence 255, App	179	54.8	4.2	686	7	US-10-404-460-111	Sequence 111, App
107	56	4.3	724	7	US-10-404-460-68	Sequence 68, Appl	180	54.8	4.2	688	7	US-10-404-460-106	Sequence 106, App
108	55.8	4.3	565	3	US-09-827-669-56	Sequence 56, Appl	181	54.8	4.2	688	7	US-10-404-460-243	Sequence 243, App
109	55.8	4.3	565	3	US-10-236-006-56	Sequence 56, Appl	182	54.8	4.2	689	7	US-10-404-460-18	Sequence 18, Appl
c 110	55.8	4.3	609	5	US-10-198-846-8289	Sequence 8289, Ap	183	54.8	4.2	691	7	US-10-404-460-118	Sequence 118, App
c 111	55.8	4.3	631	3	US-09-814-353-21588	Sequence 21588, A	184	54.8	4.2	692	7	US-10-404-460-173	Sequence 173, App
112	55.8	4.3	667	7	US-10-404-460-212	Sequence 212, App	185	54.8	4.2	692	7	US-10-404-460-210	Sequence 210, App
113	55.8	4.3	676	7	US-10-404-460-170	Sequence 170, App	186	54.8	4.2	694	7	US-10-404-460-36	Sequence 36, Appl
114	55.8	4.3	689	7	US-10-404-460-185	Sequence 185, App	187	54.8	4.2	694	7	US-10-404-460-86	Sequence 86, Appl
115	55.8	4.3	691	7	US-10-404-460-161	Sequence 161, App	188	54.8	4.2	694	7	US-10-404-460-157	Sequence 157, App
116	55.8	4.3	693	7	US-10-404-460-240	Sequence 240, App	189	54.8	4.2	695	7	US-10-404-460-70	Sequence 70, Appl
117	55.8	4.3	693	7	US-10-404-460-251	Sequence 251, App	190	54.8	4.2	696	7	US-10-404-460-99	Sequence 99, Appl
118	55.8	4.3	694	7	US-10-404-460-135	Sequence 135, App	191	54.8	4.2	696	7	US-10-404-460-191	Sequence 191, App
119	55.8	4.3	694	7	US-10-404-460-217	Sequence 217, App	c 192	54.8	4.2	698	7	US-10-404-460-241	Sequence 241, App
120	55.8	4.3	697	7	US-10-404-460-146	Sequence 146, App	193	54.8	4.2	699	7	US-10-404-460-122	Sequence 122, App
121	55.8	4.3	701	7	US-10-404-460-228	Sequence 228, App	194	54.8	4.2	699	7	US-10-404-460-229	Sequence 229, App
122	55.8	4.3	703	7	US-10-404-460-179	Sequence 179, App	195	54.8	4.2	700	7	US-10-404-460-114	Sequence 114, App
123	55.8	4.3	704	7	US-10-404-460-142	Sequence 142, App	196	54.8	4.2	701	7	US-10-404-460-177	Sequence 177, App
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125	55.8	4.3	704	7	US-10-404-460-265	Sequence 265, App	198	54.8	4.2	702	7	US-10-404-460-125	Sequence 125, App
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127	55.8	4.3	705	7	US-10-404-460-151	Sequence 151, App	200	54.8	4.2	703	7	US-10-404-460-184	Sequence 184, App
128	55.8	4.3	711	7	US-10-404-460-73	Sequence 73, Appl	201	54.8	4.2	704	7	US-10-404-460-159	Sequence 159, App
129	55.8	4.3	712	7	US-10-404-460-148	Sequence 148, App	202	54.8	4.2	704	7	US-10-404-460-223	Sequence 223, App
130	55.8	4.3	719	7	US-10-404-460-178	Sequence 178, App	203	54.8	4.2	707	7	US-10-404-460-134	Sequence 134, App
131	55.8	4.3	721	7	US-10-404-460-190	Sequence 190, App	204	54.8	4.2	707	7	US-10-404-460-153	Sequence 153, App
132	55.8	4.3	727	7	US-10-404-460-160	Sequence 160, App	c 205	54.8	4.2	707	7	US-10-404-460-366	Sequence 266, App
133	55.8	4.3	751	7	US-10-404-460-211	Sequence 211, App	c 206	54.8	4.2	715	7	US-10-404-460-90	Sequence 90, Appl
134	55.8	4.3	2885	6	US-10-405-877-36	Sequence 36, Appl	207	54.8	4.2	717	7	US-10-404-460-51	Sequence 51, Appl
135	55.8	4.3	2885	6	US-10-405-877-56	Sequence 56, Appl	208	54.8	4.2	719	7	US-10-404-460-143	Sequence 143, App
136	55.6	4.2	633	7	US-10-404-460-26	Sequence 26, Appl	209	54.8	4.2	723	7	US-10-404-460-180	Sequence 180, App
137	55.6	4.2	672	7	US-10-404-460-254	Sequence 254, App	210	54.8	4.2	725	7	US-10-404-460-19	Sequence 19, Appl
138	55.6	4.2	691	7	US-10-404-460-14	Sequence 14, Appl	211	54.8	4.2	727	7	US-10-404-460-158	Sequence 158, App
139	55.6	4.2	692	7	US-10-404-460-218	Sequence 218, App	212	54.8	4.2	727	7	US-10-404-460-176	Sequence 176, App
140	55.6	4.2	694	7	US-10-404-460-89	Sequence 89, Appl	213	54.8	4.2	766	7	US-10-404-460-193	Sequence 193, App
141	55.6	4.2	702	7	US-10-404-460-224	Sequence 224, App	214	54.8	4.2	980	6	US-10-367-978-7	Sequence 7, Appli
142	55.6	4.2	705	7	US-10-404-460-204	Sequence 204, App	215	54.8	4.2	1060	3	US-09-910-151-1	Sequence 1, Appli
143	55.4	4.2	693	7	US-10-404-460-31	Sequence 31, Appl	216	54.8	4.2	1166	5	US-10-198-846-13477	Sequence 13477, A
144	55.4	4.2	750	7	US-10-404-460-162	Sequence 162, App	217	54.4	4.1	1611	5	US-10-928-465-115	Sequence 115, App
c 145	55.2	4.2	558	5	US-10-066-543-3342	Sequence 3342, Ap	218	54.4	4.1	1611	5	US-10-198-846-11262	Sequence 11262, A
c 146	55.2	4.2	582	5	US-10-066-543-2635	Sequence 2635, Ap	219	54.2	4.1	723	7	US-10-404-460-152	Sequence 152, App
c 147	55.2	4.2	587	5	US-10-066-543-2681	Sequence 2681, Ap	220	54.2	4.1	814	6	US-10-291-285-123	Sequence 123, App
c 148	55.2	4.2	607	5	US-10-066-543-2932	Sequence 2932, Ap	221	54.2	4.1	1033	8	US-10-788-792-108	Sequence 108, App
149	55.2	4.2	633	7	US-10-404-460-194	Sequence 194, App	222	54	4.1	3092	8	US-10-357-930-24592	Sequence 24592, A
150	55.2	4.2	636	7	US-10-404-460-205	Sequence 205, App	c 223	53.6	4.1	659	7	US-10-767-701-4135	Sequence 4135, Ap
151	55.2	4.2	657	7	US-10-404-460-175	Sequence 175, App	224	53.4	4.1	928	9	US-10-450-763-21774	Sequence 21774, A
152	55.2	4.2	686	7	US-10-404-460-237	Sequence 237, App	c 225	53.4	4.1	2068	3	US-09-767-770A-1	Sequence 1, Appli
153	55.2	4.2	691	7	US-10-404-460-192	Sequence 192, App	226	53.2	4.1	692	7	US-10-404-460-4	Sequence 4, Appli
154	55.2	4.2	700	9	US-10-928-465-114	Sequence 114, App	c 227	53.2	4.1	700	7	US-10-404-460-3	Sequence 3, Appli
155	55.2	4.2	703	7	US-10-404-460-247	Sequence 247, App	228	53.2	4.1	721	7	US-10-404-460-144	Sequence 144, App
156	55.2	4.2	707	7	US-10-404-460-120	Sequence 120, App	c 229	53	4.0	511	7	US-10-191-803-897	Sequence 897, App
157	55.2	4.2	709	7	US-10-404-460-113	Sequence 113, App	c 230	53	4.0	589	7	US-10-191-803-450	Sequence 450, App
158	55.2	4.2	719	7	US-10-404-460-136	Sequence 136, App	c 231	53	4.0	589	7	US-10-152-319A-1149	Sequence 1149, Ap
159	55	4.2	684	7	US-10-404-460-226	Sequence 226, App	232	53	4.0	647	6	US-10-291-285-230	Sequence 230, App
160	55	4.2	703	6	US-10-291-265-28	Sequence 28, Appl	233	53	4.0	722	7	US-10-404-460-147	Sequence 147, App
c 161	54.8	4.2	61	8	US-10-199-820-142	Sequence 142, App	234	52.8	4.0	720	7	US-10-404-460-182	Sequence 182, App
c 162	54.8	4.2	444	8	US-10-723-860-4554	Sequence 4554, Ap	235	52.2	4.0	1355	7	US-10-729-807-20	Sequence 20, Appl
163	54.8	4.2	508	7	US-10-404-460-140	Sequence 140, App	236	52.2	4.0	1979	5	US-10-037-270-838	Sequence 838, App
164	54.8	4.2	629	7	US-10-404-460-32	Sequence 32, Appl	237	52.2	4.0	1979	5	US-10-117-722-838	Sequence 838, App
165	54.8	4.2	633	7	US-10-404-460-195	Sequence 195, App	238	52.2	4.0	1979	9	US-10-122-851-838	Sequence 838, App
166	54.8	4.2	637	7	US-10-404-460-206	Sequence 206, App	c 239	51.8	3.9	757	7	US-10-767-701-1518	Sequence 1518, Ap
167	54.8	4.2	638	7	US-10-404-460-156	Sequence 156, App	c 240	51.6	3.9	1545	8	US-10-425-115-182663	Sequence 182663, A
168	54.8	4.2	641	7	US-10-404-460-198	Sequence 198, App	241	51.2	3.9	440	5	US-10-184-644-202	Sequence 202, App
169	54.8	4.2	654	7	US-10-404-460-213	Sequence 213, App	242	51.2	3.9	440	5	US-10-184-634-202	Sequence 202, App

243	51.2	3.9	440	6	US-10-063-685-52	Sequence 52, Appl	316	45.4	3.5	641	5	US-10-037-270-954	Sequence 954, App
244	51	3.9	580	6	US-10-291-265-126	Sequence 126, App	317	45.4	3.5	641	6	US-10-117-722-954	Sequence 954, App
245	51	3.9	2954	5	US-10-164-278-2	Sequence 2, Appl	318	45.4	3.5	641	9	US-10-122-851-954	Sequence 954, App
246	51	3.9	2954	5	US-10-164-278-2	Sequence 2, Appl	319	45.4	3.5	972	8	US-10-425-115-17653	Sequence 17653, A
247	50.8	3.9	578	6	US-10-115-831-60	Sequence 60, Appl	320	45.4	3.5	2213	7	US-10-437-963-11899	Sequence 11899, A
248	50.8	3.9	647	7	US-10-115-831-59	Sequence 59, Appl	321	45.4	3.5	3324	7	US-10-437-963-69380	Sequence 69380, A
249	50.8	3.9	789	5	US-10-125-237-25	Sequence 25, Appl	C 322	45.4	3.5	9025608	6	US-10-156-761-1	Sequence 1, Appl
250	50.8	3.9	789	5	US-10-105-891-25	Sequence 25, Appl	C 323	45.2	3.4	458	7	US-10-437-963-3998	Sequence 3998, App
C 251	50.6	3.9	520	8	US-10-123-860-1213	Sequence 1213, App	324	45.2	3.4	720	9	US-10-818-066-21	Sequence 21, Appl
C 252	50.6	3.9	645	7	US-10-767-701-3807	Sequence 3807, App	325	45.2	3.4	735	8	US-10-723-860-7172	Sequence 7172, App
C 253	50.4	3.8	669	7	US-10-404-460-87	Sequence 87, Appl	326	45.2	3.4	2499	7	US-10-097-034A-10	Sequence 10, Appl
C 254	50	3.8	1883	8	US-10-357-930-23221	Sequence 23221, A	C 327	45	3.4	560	9	US-10-450-763-14101	Sequence 14101, A
C 255	50	3.8	1883	8	US-10-357-930-29093	Sequence 29093, A	328	45	3.4	825	7	US-10-437-963-60378	Sequence 60378, A
C 256	49.6	3.8	583	8	US-10-425-115-84442	Sequence 84442, A	329	45	3.4	1360	6	US-10-256-113-3	Sequence 3, Appl
C 257	49.6	3.8	639	7	US-10-404-460-203	Sequence 203, App	C 330	45	3.4	1395	7	US-10-437-963-102411	Sequence 102411, A
C 258	49.6	3.8	1347	7	US-10-767-701-11203	Sequence 11203, A	331	45	3.4	2012	8	US-10-357-930-20122	Sequence 20122, A
C 259	49.6	3.8	1975	5	US-10-098-841-310	Sequence 310, App	332	45	3.4	2012	8	US-10-357-930-20649	Sequence 20649, A
C 260	49.4	3.8	975	7	US-10-282-122A-11290	Sequence 11290, A	333	45	3.4	2012	8	US-10-357-930-20706	Sequence 20706, A
C 261	49.4	3.8	4351	6	US-10-251-186-10	Sequence 10, Appl	334	45	3.4	2012	8	US-10-357-930-21843	Sequence 21843, A
C 262	48.8	3.7	1370	5	US-10-037-270-680	Sequence 680, App	335	45	3.4	2012	8	US-10-357-930-22617	Sequence 22617, A
C 263	48.8	3.7	1370	6	US-10-117-722-680	Sequence 680, App	336	45	3.4	2012	8	US-10-357-930-22737	Sequence 22737, A
C 264	48.8	3.7	1370	9	US-10-122-851-680	Sequence 680, App	337	45	3.4	2012	8	US-10-357-930-22765	Sequence 22765, A
C 265	48.6	3.7	420	7	US-10-021-323-5998	Sequence 5998, App	338	45	3.4	2012	8	US-10-357-930-24853	Sequence 24853, A
C 266	48.4	3.7	1110	7	US-10-425-114-19204	Sequence 19204, A	339	45	3.4	2012	8	US-10-357-930-25853	Sequence 25853, A
C 267	48.4	3.7	1228	8	US-10-425-115-21367	Sequence 21367, A	340	45	3.4	2012	8	US-10-357-930-25985	Sequence 25985, A
C 268	48.2	3.7	820	3	US-09-814-353-19899	Sequence 19899, A	341	45	3.4	2012	8	US-10-357-930-26489	Sequence 26489, A
C 269	48	3.7	54	3	US-09-938-744-11	Sequence 11, Appl	342	45	3.4	2012	8	US-10-357-930-26546	Sequence 26546, A
C 270	48	3.7	448	5	US-10-125-237-66	Sequence 66, Appl	343	45	3.4	2012	8	US-10-357-930-27692	Sequence 27692, A
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Query Match 100.0%; Score 1312; DB 9; Length 1312;

ALIGNMENTS

RESULT 1

US-10-757-745-3
; Sequence 3, Application US/10757745
; Publication No. US20050101769A1
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut Voor Biotechnologie VZW
; TITLE OF INVENTION: CD-40 INTERACTING AND TRAF-INTERACTING PROTEINS
; FILE REFERENCE: 2676-4555US
; CURRENT APPLICATION NUMBER: US/10/757,745
; CURRENT FILING DATE: 2004-01-15
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; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1312
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (122)..(1234)
; OTHER INFORMATION:
US-10-757-745-3


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RESULT 3

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; Publication No. US20030104529A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feiyang

```
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghast, John
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt FL_genes Version 1.0
; SEQ ID NO 889
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(1127)
```

US-10-037-270-889

Query Match 50.9%; Score 668.2; DB 5; Length 1948;

Best Local Similarity 75.6%; Pred. No. 9.2e-180;

Matches 858; Conservative 0; Mismatches 268; Indels 9; Gaps 2;

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QY      131 GGCAGCAGTTCCGATCGCGGAGCCCGCAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 190
Db      15 GCCAAGAATTCGGCACGAGGGAAGATGGAGTTGGGAGTTCCCTGGAGGGCGGAGGAG 74
QY      191 GAAGCAGCACAGGCGGAGGAGGACCGGGTGAAGAGCGCGGCGGCGGCGGCGGCGGCGGCGG 250
Db      75 GCGGCGGAGGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 134
QY      251 GCGTGTGGGGGAGATGCGACCCACAGATGTGTCGCCAGCGTCTCGCGGGAGAACGACTGG 310
Db      135 GCCTCGGTGCGAAAGTGCAGTCCGCGAGTGGCTCAGTGTCTTCTCGCGCGAGAACGACTGG 194
QY      311 CAGAGCGAAGAACCCCTGAGCGCCTACTTTCAGAGCTCCAGAGACGACCAAGGTTGGCGG 370
Db      195 GAGATGGAAGAGGCGTCTGAACTCTCTACTTTCAGAGCCTCCGTTGGAGAGAGCGCTTGGAA 254
QY      371 GCGCAGCCTCCACAGCTCTTCAAGTCCGAGGCGTATGTTGATCTTAACCAACGAGGATGCA 430
Db      255 GCGCGACCTGAAACCATCTCTGAGCGCCCAAGACCTATGTTGACCTAACCAATGAAGAA 314
QY      431 AATGATACAAACATTTTGAAGCCAGTCCATCTGGA---ACTCTCTTAGAGATAGCAGC 487
Db      315 ACTGATTCACACCTTCTTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAAATGGCAGC 374
QY      488 ACTATTTCTTTCATTTACCTGGNAATATGATGGATAGATGGAATGCAATCTGCCGAGAGG 547
Db      375 ATGTTCTCTCTCATTTACCTGGNAATATGATGGATAGATCTTAAACATCTGTCTCAGAGAG 434
QY      548 GCTCAGGCGGTGTGTTCTCTGCTAGCTTTGTATAGTCCAGATGTGGTATTTCTACAGGAA 607
Db      435 GCTCAGGCGGTGTGTTCTCTACTTACTTGTAGCTTTGACAGCCAGATGTGATTTCTACAG 494
QY      608 GTTATCCCCCATACTGTGCGCTTACTTAAGAGAGAGAGAGCAGGTTACAAATATTATACA 667
Db      495 GTTATTTCCCATATTTATAGCTTACCTAAAGAGAGATCAAGTAAATATGAGATTTATACA 554
QY      668 GGTATGAAGAGGATATTTTACAGCTATATCTATTGAAGAAAGGAGAGTGAATTTAAA 727
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Db 555 GGTGATGAAGAGGATATTTACAGCTATATATGTTGAGAAATCAAGAGTGAATTAATA 614
Qy 728 AGTCAGAGATATTCCTTTTCCAAATACAAATGATGAGAACTGCTATGCGTAAT 787
Db 615 AGCCAAAGAGATATTCCTTTTCCAAATGATGAGAACTTTTATGTGTCAT 674
Qy 788 GTGAGTTGGTGGAAATGAAATTTTGGCTTATGACATCCATTTGGAGAGCACCAGAA 847
Db 675 GTGAATGTGTACAGAAATGAGCTTTGCTTTATGACATCCATTTGGAGAGCACCAGAGG 734
Qy 848 CATTTCTGCGAAGCAATTAAGCAATTAATAAATGTTCTTGGAAATGCAAGAGGCTCCA 907
Db 735 CATGCTGCGAAGCAATGATGATGATTAATAATGTTTAAAGAAATGCAAGAGGCTCCA 794
Qy 908 GATTTCAACCAAGGTTATATTTGAGAGATACAAATTTAAGAGATCAAGAGTTATCAAA 967
Db 795 GAGTCAGCTACAGTTATATTTGAGAGATACAAATCTAAGGATCGAGAGGTTACACAG 854
Qy 968 TGTGGTGGTTTACTGACACAGTTTGTGATGCTGGGATTTTGTAGGCAACCTAAACAT 1027
Db 855 TGTGGTGGTTTACTGACACAGTTTGTGATGCTGGGATTTTGTAGGCAACCTAAACAT 914
Qy 1028 TGCAGGTATACATGAGATACAAAGCAATTAACAACTCAGGATCCTGCTGCTTATAAG 1087
Db 915 TGCAGGTATACATGAGGATACAAATGAACTCTAATCTTGAATTAATGCTGCTGTGTA 974
Qy 1088 CATCGTTTGTGATCGAATATTTTTCAG-----AGCAGAGAGGGGACCTTATTCCTCAA 1141
Db 975 CTTTCGTTTGTGATCGAATATTTTTCAGAGCAGCAGCAGAGAGGACACATTAATTCCTCGA 1034
Qy 1142 AGTTTACAGCTGTTGGTGGTGGAAATCTGGACTGTGATGATTTCCGAGTATCACTGG 1201
Db 1035 AGTTTACAGCTGTTGGTGGTGGAAATCTGGACTGTGATGATTTCCGAGTATCACTGG 1094
Qy 1202 GGCCTCTGTGACCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 1256
Db 1095 GGTCTCTGTGCAACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1149

RESULT 4

US-10-117-722-889
; Sequence 889, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219744A1 Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2BCIP
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_Fl_genes Version 1.0
; SEQ ID NO 889
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(1127)
US-10-117-722-889

Query Match

50.9%; Score 668.2; DB 6; Length 1948;

Best Local Similarity 75.6%; Pred. No. 9.2e-180;
Matches 858; Conservative 0; Mismatches 268; Indels 9; Gaps 2;
Qy 131 GGCAGAGATTCGATCGCGCGAGACCCGCGAGCGCGCGAGCGCGCGCGCGCGCGCGCC 190
Db 15 GCCAAGAAATCGCGCAGAGGAAATGGAATTTGGGAGTTGCTTGGAGGCGGAGGGAG 74
Qy 191 GAAGCAGACACGCGCGAGGAGGACCGGGTGAAGAGCGCGCGCTTCAGTGCCTTGGGCTTT 250
Db 75 GCGCGGAGAAAGAGCGCGAGCTGAGGTGAANAAGCGCGAGCTTCTGTGTGTGGAGTTT 134
Qy 251 GCGTTGGTGGGGGATGCGACCCCGACGATGGTCCCAGCGCTCTGCGGGAGAAACGACTGG 310
Db 135 GCTCGGTGCGAAGCTGCGATGCGCGAGTGGCTCAGTGTCTCTGCGCGAGAACGACTGG 194
Qy 311 CAGACGCAAAAGCCCTGAGCGCTACTTTCGAGCTCCAGAGAACACACCAAGGGTGGCCG 370
Db 195 GAGATGAAAGGGCTCTGAACCTCTACTTCGAGCGCTCCGGTGGAGAGAGCGCTTTGAA 254
Qy 371 CGCGAGCCTCCGAGCTCTTCAAGTCCGAGGCTATGTTGATCTAAACCAACGAGGATGCA 430
Db 255 CGCGAGCTGAAACCAATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACA 314
Qy 431 AATGATACCAACCAATTTTGAAGCCAGTCCATCTGGA---ACTCTCTAGAGATAGCAGC 487
Db 315 ACTGATTCACCACTCTTAAATCAGCCCATCTGAAGATACTCAGCAAGAAATGGCAGC 374
Qy 488 ACTATTTCTTCAATACCTGGGAATATGATGGAATGAGATGGATGCAATCTGCCGAGAGG 547
Db 375 ATGTTCTCTCTATTAACCTGGAAATATGATGGAATAGATCTAAACAATCTGTGAGAGAG 434
Qy 548 GCTCGAGGGGTGTGTTCTGCTAGCTTTGATGATGATGATGATGATGATGATGATGATGAT 607
Db 435 GCTCGAGGGGTGTGTTCTGCTAGCTTTGATGATGATGATGATGATGATGATGATGATGAT 494
Qy 608 GTTATCCCCCCTACTGTGCTTACCTTAAAGAGAGAGCAGCCAGTTTACACAATATTATACA 667
Db 495 GTTATCCCCCCTACTGTGCTTACCTTAAAGAGAGATCAAGTAATTTATGAGATTTATACA 554
Qy 668 GGTAAATGAAGAGGATATTTTACAGCTATATCTATTTGAAGAGAGAGTGAATTTTAA 727
Db 555 GGTATGAAGAGGATATTTTACAGCTATATTTTGAAGAGAAATCAAGAGTGAATTTTAA 614
Qy 728 AGTCAGAGATTTTCTCTTCCAAATACCAATGATGAGAACTGCTATGCTGTAAT 787
Db 615 AGCCAAAGAGATTTTCTCTTCCAAATGATGAGAACTTTTATGTGTCAT 674
Qy 788 GTGAGTTGGGTGGAATGAAATTTTGCCTTATGACATCCCATTGGAGAGCACCAGAGAA 847
Db 675 GTGAATGTGTGAGAAATGAGCTTTGCTTATGACATCCCATTGGAGAGCACCAGAGGG 734
Qy 848 CATTTCTGCGAAGCAATAGACAAATTAATAAATCTTTGGAATAATGCAAGAGGCTCCA 907
Db 735 CATGCTGCGAAGCAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 794
Qy 908 GATTTCAACCAAGGTTATTTTTCAGAGATACAAATTTTGAAGATCAAGAGTATTATCAA 967
Db 795 GAGTCAGCTACAGTTATATTTTTCAGAGATACAAATCTAAGGATCGAGAGTTACACAG 854
Qy 968 TGTGGTGGTTTACTGACAACTGTTTGTGCTGGGAAATTTTGTAGGCAACCTTAAACAT 1027
Db 855 TGTGGTGGTTTACTGACAACTGTTTGTGCTGGGAAATTTTGTAGGCAACCTTAAACAT 914
Qy 1028 TGCAGGTATACATGAGGATACAAAGCAATTAACAACTCAGGATCCTGCTGCTTATAAG 1087
Db 915 TGCAGGTATACATGAGGATACAAATGAACTCTAATCTTGAATTAATGCTGCTGTGTA 974
Qy 1088 CATCGTTTGTGATCGAATATTTTTCAG-----AGCAGAGAGGGGACCTTATTCCTCAA 1141
Db 975 CTTTCGTTTGTGATCGAATATTTTTCAGAGCAGCAGCAGAGAGGACACATTAATTCCTCGA 1034
Qy 1142 AGTTTACAGCTGTTGGTGGTGGAAATCTGGACTGTGATGATTTCCGAGTATCACTGG 1201

Db 1035 AGTTTGACCTCTTGGATTAGAAAACCTGGACTGTGTGTAGATTTCTTAGTGATCACTGG 1094
QY 1202 GGGCTCTGTGACCTTGAATGTAGTATTTGTGAAAAGCTTCCACCTTGCAGCTTT 1256
Db 1095 GGTCTCTGTGCAACTTAGATATAATTTGTAAAAATGCTTTTCAAGTGTGGGTTT 1149

RESULT 5

US-10-122-851-889
; Sequence 889, Application US/10122851
; Publication No. US20050239060A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Felyan
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: Polyptides
; CURRENT APPLICATION NUMBER: US/10/122,851
; CURRENT FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 889
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(1127)
US-10-122-851-889

Query Match 50.9%; Score 668.2; DB 9; Length 1948;

Best Local Similarity 75.6%; Pred. No. 9.2e-180;

Matches 858; Conservative 0; Mismatches 268; Indels 9; Gaps 2;

QY 131 GCAGCAGTTCGATCGCGCGAGCCCGCAGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCC 190
Db 15 GCCAAGAATTCGGCAGCGAGGGAAGATGGAGTTGGGAGTTGCCCTGGAGGGCGGGAGGAG 74
QY 191 GAAGCAGCACAGCGCGAGGAGGACCGGGTGAAGAGCGCGCGCTTCAGTGCCTGGGCTTT 250
Db 75 GCGCGGAGGAGAGCGCGAGCGCTGAGGTGAAGAGCGCGACTTCTGTGTGGAGTTT 134
QY 251 GCGTTGGTGGGGATGCGACCCCGACGATGGTCCCGCGCTCTCGCGGAGAACGACTGG 310
Db 135 GCCTGGTGCAGCTGCGATGCGCGAGTGGCTCAGTGTCTTCTGGCCGAGAACGACTGG 194
QY 311 CAGACGAGAAAGCCCTGAGCGCTACTTCGAGCTGCCAGAAACGACCAAGGGTGGCG 370
Db 195 GAGATGGAAGGGCTCTGAACCTCTACTTCGAGCGCTCCGGTGGAGGAGCGCCCTGGAA 254
QY 371 GCGAGCCTCCACGCTCTCAAGTCCGAGGCGTATGTTGATCTAACCAACGAGGATGCA 430
Db 255 GCGCGACCTGAACCACTCTCGAGCCCAAGACTATGTTGACCTTAACCAATGAAGAAC 314
QY 431 AATGATACACCAATTTAGAACCGAGTCCATCTGGA---ACTCCTCTAGAAATAGCAGC 487
Db 315 ACTGATTCACCACTTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAAATGCGAGC 374
QY 488 ACTATTTCTTCTATCTACCTGGATATTGATGATGATGATGATGATGATGATGATGATGAT 547
Db 375 ATGTTCTCTCTATTAACCTGGAAATATTGATGATGATGATGATGATGATGATGATGATGAT 434
QY 548 GCTCGAGGGGTGTGTTCTCCCTAGCTTTGTATAGTCCAGATGTGGTATTTCTTACAGGAA 607

Db 435 GCTCGAGGGGTGTGTTCTCTAGCTTTGTACAGCCAGATGTGATATTTCTTACAGGAA 494
QY 608 GTTATCCCCCATACTGTGCTTACTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667
Db 495 GTTATCCCCCATATTTATAGCTACTTAAGAGAGAGATCAAGTAATTTATGAGATTTATTA 554
QY 668 GGTAAATGAAGAGGATATTTCAAGCTATATCTATTGAAGAAAGGAGAGTGAATTTAAA 727
Db 555 GGTATGAGAGAGGATATTTCAAGCTATATTTGAAGAAATCAAGAGTGAATTTAAA 614
QY 728 AGTCAGGAGATTTATCTCTTTTCCAAATACCAAAATGATGAGAAACCTCTATGCTTAAT 787
Db 615 AGCCAAGAGATTTATCTCTTTTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTCAT 674
QY 788 GTGAGTTGGGTGGAATTTTTCCTTTATGACATCCCATTTGGAGAGCACCAGAGAA 847
Db 675 GTGAATGTGCAGGAATGAGCTTTTGCCTTATGATCCCATTTGGAGAGCACCAGAGGG 734
QY 848 CATTCTCGGGAACGAATAAGACAAATTAATAAACTGTTCTTGGAAAAATCAAGAGGCTCCA 907
Db 735 CATGCTCGGGAACGAATGATCAGTTAAAAATGGTTTAAAGAAAAATGCAAGAGGCTCCA 794
QY 908 GATTCAACCCAGGTTATATTTTCAGGAGATACAAATTTAAGAGATCAAGAAAGTTATCAAA 967
Db 795 GAGTCAGCTACAGTTATATTTTCAGGAGATACAAATCTAAGGGATCGAGAGGTTACCAGA 854
QY 968 TGTGGTGTGTACCTGACAAAGCTTTTTCATGCTGGGAAATTTTAGGCAACCTTAACAT 1027
Db 855 TGTGGTGTGTACCCCAACAACTTGTGATGTCTGGGAGTTTTCGGGCAACCTTAACAT 914
QY 1028 TGCCAGTATACATGGGATACGAAGCAATTAACAACCTTCAGGATCCCTGCTGCTTATAAG 1087
Db 915 TGCCAGTATACATGGGATACCAATGAACTCTAATCTTGGAAATAACTGCTGCTGTGAAA 974
QY 1088 CATCGTTTGTATCGAATATTTTTCAG-----AGCAGAGAGGGGCACTTATTCCTCAA 1141
Db 975 CTTTCGTTTGTATCGAATATTTTTCAGAGCAGCAGCAGAGAGGAGACATTTATTCCTCGA 1034
QY 1142 AGTTTAGACCTTGTGGGTTGGAAAACTGGAGCTGTGTAGATTTCCGAGTGATCACTGG 1201
Db 1035 AGTTTGGACCTTCTTGGATTAGAAAACTGGAGCTGTGTAGATTTCTTAGTGATCACTGG 1094
QY 1202 GGGCTCTTGTGCACCTTGAATGTAGTATTTGAAAAAGCTTCCCACTTGCAGCTTT 1256
Db 1095 GGTCTCTGTGCACTTAGATATAATATTGTAATAATGCTTTTCAAGTGTGGGTTT 1149

RESULT 6

US-09-981-353-88
; Sequence 88, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 88
; LENGTH: 3152
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 232992.1
; NAME/KEY: unsure
; LOCATION: 1171
; OTHER INFORMATION: a, t, c, g, or other
US-09-981-353-88

Query Match

50.9%; Score 668.2; DB 3; Length 3152;

Db 1060 GATTTCTAGTATCTAGGGGCTCTCTGCACTTAGATATATATTGTAATGCTT 1119
Qy 1242 CCACCTTGCAGCTTT 1256
Db 1120 TTCAAGTGTGGGTTT 1134

RESULT 9

US-10-783-271-28
; Sequence 28, Application US/10783271
; Publication No. US20050186577A1
; GENERAL INFORMATION:
; APPLICANT: Veridex, LLC
; APPLICANT: Wang, Yixin
; TITLE OF INVENTION: BREAST CANCER PROGNOSTICS
; FILE REFERENCE: VDX-5003 USNP
; CURRENT APPLICATION NUMBER: US/10/783,271
; CURRENT FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 1940
; TYPE: DNA
; ORGANISM: human
US-10-783-271-28

Query Match 50.8%; Score 666.6; DB 9; Length 1940;
Best Local Similarity 76.9%; Pred. No. 2.6e-179;
Matches 842; Conservative 0; Mismatches 244; Indels 9; Gaps 2;

Qy 171 GCGGGGGGCTCGGCGCCGAGACGACGAGCGGAGGAGGACCGGCTGAGAGCGGC 230
Db 42 GCCTGAGGGCGGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 101
Qy 231 GCGTTCAGTCCCTGGGCTTTGCTGTGGGGGATGCGACCCCGACGATGGTCCCGAGCG 290
Db 102 GACTTCTGTGTGGAGTTTGCTCGGTGCGAAGTGGCGATGCGGAGTGGCTCAGTGCT 161
Qy 291 TCCTGGGGGAGACGACTGCGCAGACGCGAGAAAGCCCTGAGCGGCTACTTCGAGCTGCCAG 350
Db 162 TCCTGGCGGAGACGACTGGGAGATGGAAGGGCTCTGAACTCTACTTCGAGCTCCGG 221
Qy 351 AGAACGACCAAGGGTGGCGCGCGAGCTCCGAGCTCTCAAGTCCGAGGCTATGTTG 410
Db 222 TGGAGGAGAGCGGCTTGGAAACGCGGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTG 281
Qy 411 ATCTAACCAAGGAGATGCAAAATGATACCAACATTTTGAAGCGAGTCCATCTGGA--A 467
Db 282 ACCTAACCAATGAAGAACAACTGATTCACCACTTCTAAATCAGCCCATCTGAAGATA 341
Qy 468 CTCCTCTAGAAGATAGCAGCACTATTTCCTTCAATTAACCTGGAATATTGATGATGATG 527
Db 342 CTCAGCAAGAAATGGCAGCATGTTCTCTCTATTACCTGGAATATTGATGATGATGATC 401
Qy 528 GATGCAATCTCCGAGAGGGCTCGAGGGGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 587
Db 402 TAAACCAATCTCTCAGAGAGGGCTCGAGGGGTGTCTCTGCTGCTGCTGCTGCTGCTGCTG 461
Qy 588 ATGTGGTATTCTTACAGAAAGTTATCCCCCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 647
Db 462 ATGTGATATTCTTACAGAAAGTTATCCCCCATATTATAGTACTTAAAGAGAGATCAA 521
Qy 648 CCAAGTACAAATATTACAGGTAATGAAGAGGATATTTTACAGCTTATCTATTGGAAGA 707
Db 522 GTAATTATGATATTATTACAGGTCATGAAGAGGATATTTTACAGCTTATTAATGTTGAAGA 581
Qy 708 AAGGAAGAGTGAATTTTAAAGTCAGGATATTTCCTTTTCCAAATACCAATATGATGA 767
Db 582 AATCAAGAGTGAATTTTAAAGGCCAAGAGATTTATTCCTTTTCCAAAGTACCAATATGATGA 641
Qy 768 GAAACCTGCTATGCGTAAATCTGAGTTTGGGTGGAATGAATTTTGGCTTATGACATCCC 827

Db 642 GAAACCTTTTATGTGTGCATGTGAACGTGTGAGGAAATGAGCTTTGCCCTTATGACATCCC 701
Qy 828 ATTTGGAGAGCACCAGAGAACTTCTGCGGAAACGAATAGACAAATTAATAAATCTGTTCTTG 887
Db 702 ATTTGGAGAGCACCAGAGGGCATGCTGCGGAAACGAATGATGATGATGATGATGATGATG 761
Qy 888 GAAAAATGCAAGAGGCTCCAGATTCAACCAACCGGTTATATTTTCAGAGAGATACAAATTTAA 947
Db 762 AGAAATGCAAGAGGCTCCAGAGTCCAGAGTACAGTTATATTTTCAGAGAGATACAAATCTAA 821
Qy 948 GAGATCAAGAGATTATCAAAATGT 1007
Db 822 GGGATCGAGAGGTTTACCAAGT 881
Qy 1008 TTTTAGGCAACCTAAACATTCGCCAGTATACATGGGATACGAAAGCAAAATACAACTCA 1067
Db 882 TTTTGGGCAACCTAAACATTCGCCAGTATACATGGGATACCAAAATGAACTCTAAATCTTG 941
Qy 1068 GGATCCCTGCTCTTATTAAGCATCGTTTTGTGATCGAATATTTTTCAG-----AGCAGAAG 1121
Db 942 GAATAACTGCTGCTTGTAACTTCGTTTTGTATCGAATATTTTTCAGAGCAGCAGAGAAG 1001
Qy 1122 AGGGGCACTTATTCCTCAAGTTTAGACCTTGTGGGTGGGAACTGGAGCTGGTA 1181
Db 1002 AGGGACACATTTATCCCGAAGTTTGGACCTTCTTGGATTAGAAAACTGGAGCTGGTA 1061
Qy 1182 GATTTCCGAGTGCATCACTGGGGCTCTTGTGCACTTGAATGTAGTATTGTGAAAAAGCTT 1241
Db 1062 GATTTCTTAGTGCATCACTGGGTCTTCTGTGCACTTAGATATATATTGTAAATGCTT 1121
Qy 1242 CCCACTTGCAGCTTT 1256
Db 1122 TTCAAGTGTGGGTTT 1136

RESULT 10

US-10-450-763-22058
; Sequence 22058, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22058
; LENGTH: 1088
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1)..(687)
; OTHER INFORMATION: 98% homologous to Homo sapiens dJ30M3.3 (novel protein
; OTHER INFORMATION: similar to C. elegans Y63D3A.4), accession number AL031775, Smith-
; OTHER INFORMATION: Waterman Score=1199.
US-10-450-763-22058

Query Match 37.6%; Score 493.2; DB 9; Length 1088;
Best Local Similarity 82.9%; Pred. No. 7.7e-130;
Matches 577; Conservative 0; Mismatches 113; Indels 6; Gaps 1;
Qy 548 GCTCGAGGGGTGTGTTCTCGCTAGCTTTGTATAGTCCAGATGTTGTTTCTTACAGAA 607
Db 1 GCTCGAGGGGTGTGTTCTCTACTTAGCTTTGTACAGCCAGATGTGATATTCTTACAGAA 60


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; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1070
; LENGTH: 644
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-066-543-1070

Query Match      33.3%; Score 436.4; DB 5; Length 644;
Best Local Similarity 83.3%; Pred. No. 1e-113;
Matches 510; Conservative 0; Mismatches 96; Indels 6; Gaps 1;

QY 548 GCTCAGGGGTGTCTCTGCTAGCTTTGTATGTCCAGATGTGGTATTCTACAGAA 607
Db 32 GCTCAGGGGTGTCTCTGCTAGCTTTGTATGTCCAGCCAGATGTGATATTCTACAGAA 91
QY 608 GTTATCCCCCATCTACTGTGCTTACCTAAAGAGAGAGCAGCCAGTTACAAATTATTACA 667
Db 92 GTTATCCCCCATATATAGCTTACCTTAAGAGAGAGATCAAGTAATTATGAGATTATTACA 151
QY 668 GGTAAATGAAGAGGATATTTCACAGCTATATCTATTGAAGAAAGGAGAGTGAATTTAAA 727
Db 152 GGTCAATGAAGAGGATATTTCACAGCTATATCTATTGAAGAAATCAAGAGTGAATTTAAA 211
QY 728 AGTCAGGAGATTAATTCCTTTTCCAAATACCAAAATGATGAGAAACCTGCTATGCTTAAT 787
Db 212 AGCCAAGAGATTAATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCAT 271
QY 788 GTGAGTTGGGTGGAAATGAATTTTGCCTTATGACATCCATTTTGAGAGACACAGAGAA 847
Db 272 GTGAATGTGTCAAGAAATGAGCTTTTGCCTTATGACATCCATTTTGAGAGACACAGAGGG 331
QY 848 CATTCTGCGGAACGAATAGACAAATTAATAAAGTCTTTTGGAAAAATGCAAGAGGCTCCA 907
Db 332 CATGCTGCGGAACGAATGAATCAGTTTAAATAATGGTTTTTAAAGAAATGGAAGAGGCTCCA 391
QY 908 GATTCAACACAGGTATATTTCGAGGAGATACAAATTTAAGAGATCAAGAAGTTATCAA 967
Db 392 GAGTCAGCTACAGTTATATTTCGAGGAGATACAAATCTAAGGGATCGAGAGGTTACCAGA 451
QY 968 TGTGGTGGTTTACCTGACAAAGTTTTGTGCTGGGAATTTTATAGGCAAACTTAAACAT 1027
Db 452 TGTGGTGGTTTACCCACAAACATTTGTGGATGTCTGGGAGTTTTTGGGCAAACTTAAACAT 511
QY 1028 TGCCAGTATACATGGGATACGAAGCAAAATAACAACCTCAGGATCCCTGCTCTTATAG 1087
Db 512 TGCCAGTATACATGGGATACGAAGTAACTCTAATCTTTGGAATAACTGCTGCTGTGAAA 571
QY 1088 CATCGTTTGTATCGAATATTTTTCAG-----AGCAGAGAGGGGACCTTATTCCTCAA 1141
Db 572 CTTGCTTTTGTATCGAATATTTTTCAGAGCAGCAGAGAGAGGGACACATTTATCCCCGA 631
QY 1142 AGTTTAGACCTT 1153
Db 632 AGTTTGGACCTT 643

RESULT 15
US-10-066-543-1031
; Sequence 1031, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.

; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1031
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 10
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-1031

Query Match      32.7%; Score 428.4; DB 5; Length 625;
Best Local Similarity 84.1%; Pred. No. 2e-111;
Matches 483; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 548 GCTCAGGGGTGTCTCTGCTAGCTTTGTATGTCCAGATGTGGTATTCTACAGAA 607
Db 42 GCTCAGGGGTGTCTCTGCTAGCTTTGTATGTCCAGCCAGATGTGATATTCTACAGAA 101
QY 608 GTTATCCCCCATCTACTGTGCTTACCTAAAGAGAGAGCAGCCAGTTACAAATTATTACA 667
Db 102 GTTATCCCCCATATATATAGCTTACCTAAAGAGAGATCAAGTAATTATGAGATTATTACA 161
QY 668 GGTAAATGAAGAGGATATTTCACAGCTATATCTATTGAAGAAAGGAGAGTGAATTTAAA 727
Db 162 GGTCAATGAAGAGGATATTTCACAGCTATATCTATTGAAGAAATCAAGAGTGAATTTAAA 221
QY 728 AGTCAGGAGATTAATTCCTTTTCCAAATACCAAAATGATGAGAAACCTGCTATGCTTAAT 787
Db 222 AGCCAAGAGATTAATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCAT 281
QY 788 GTGAGTTGGGTGGAAATGAATTTTGCCTTATGACATCCATTTTGAGAGACACAGAGAA 847
Db 282 GTGAATGTGTCAAGAAATGAGCTTTTGCCTTATGACATCCATTTTGAGAGACACAGAGGG 341
QY 848 CATTCTGCGGAACGAATAGACAAATTAATAAAGTCTTTTGGAAAAATGCAAGAGGCTCCA 907
Db 342 CATGCTGCGGAACGAATGAATCAGTTTAAATAATGGTTTTTAAAGAAATGCAAGAGGCTCCA 401
QY 908 GATTCAACACAGGTATATTTCGAGGAGATACAAATTTAAGAGATCAAGAAGTTATCAA 967
Db 402 GAGTCAGCTACAGTTATATTTCGAGGAGATACAAATCTAAGGGATCGAGAGGTTACCAGA 461
QY 968 TGTGGTGGTTTACCTGACAAAGTTTTGTGCTGGGAATTTTATAGGCAAACTTAAACAT 1027
Db 462 TGTGGTGGTTTACCCCAACAAACATTTGTGGATGTCTGGGAGTTTTTGGGCAAACTTAAACAT 521
QY 1028 TGCCAGTATACATGGGATACGAAGCAAAATAACAACCTCAGGATCCCTGCTCTTATAG 1087
Db 522 TGCCAGTATACATGGGATACCAAAATGAATCTTAATCTTTGGAATAACTGCTGCTGTGAAA 581
QY 1088 CATCGTTTGTATCGAATATTTTTCAGAGCAGAGAAAG 1121
Db 582 CTTGCTTTTGTATCGAATATTTTTCAGAGCAGCAG 615

RESULT 16
US-10-066-543-1084
; Sequence 1084, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
```



```
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 1084
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 3
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-1084
```

```
Query Match 32.7%; Score 428.4; DB 5; Length 633;
Best Local Similarity 84.1%; Pred. No. 2e-111;
Matches 483; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 548 GCTCGAGGGGTGTTCTCTGCTGCTTGTATAGTCCAGATGGGTATTTCTACAGGAA 607
DB 34 GCTCGAGGGGTGTTCTCTGCTGCTTGTATAGTCCAGATGGGTATTTCTACAGGAA 93

QY 608 GTTATCCCCCATCTGCTGCTTGTATAGTCCAGATGGGTATTTCTACAGGAA 667
DB 94 GTTATCCCCCATCTGCTGCTTGTATAGTCCAGATGGGTATTTCTACAGGAA 153

QY 668 GGTAAATGAAGAGGATATTTTACAGCTATATCTTGAAGAAAGAGGATGAATTTAA 727
DB 154 GGTAAATGAAGAGGATATTTTACAGCTATATCTTGAAGAAAGAGGATGAATTTAA 213

QY 728 AGTCAGGAGATTAATCTCTTTTCCAAATACCAAAATGATGAGAAACCTGCTATCGTAAAT 787
DB 214 AGCCAGAGATTAATCTCTTTTCCAAATACCAAAATGATGAGAAACCTTTTATGTGTCAT 273

QY 788 GTGAGTTGGGTGGAATGAATTTTGGCTTATGACATCCCATTTGGAGAGCACCAGAGAA 847
DB 274 GTGAGTTGGGTGGAATGAATTTTGGCTTATGACATCCCATTTGGAGAGCACCAGAGGG 333

QY 848 CATCTCGGGAACGAATGAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAG 907
DB 334 CATCTCGGGAACGAATGAATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 393

QY 908 GATTCAACACCGGTATATTTTGGAGGAGATACAAATTTAAGAGATCAAGAGGTTATCAAA 967
DB 394 GAGTCAGCTACAGTTATATTTGAGGAGATACAAATTTAAGAGATCAAGAGGTTATCAAA 453

QY 968 TGTGGTGGTTTACTGCAACAGTTTGTGCTGCTGGGAAATTTTGGGCAAACTTAACAT 1027
DB 454 TGTGGTGGTTTACTGCAACAGTTTGTGCTGCTGGGAAATTTTGGGCAAACTTAACAT 513

QY 1028 TGCAGATATACATGGGATACGAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 1087
DB 514 TGCAGATATACATGGGATACGAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 573

QY 1088 CATCGTTTGTGATCGAATATTTTTCAGAGCAGAAG 1121
DB 574 CTTCTGTTTGTGATCGAATATTTTTCAGAGCAGAAG 607
```

RESULT 17

```
US-10-066-543-548
; Sequence 548, Application US/10066543
; Publication NO. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 548
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 19, 71
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-548
```

```
Query Match 31.9%; Score 418; DB 5; Length 625;
Best Local Similarity 84.0%; Pred. No. 1.8e-108;
Matches 483; Conservative 0; Mismatches 91; Indels 1; Gaps 1;
```

```
QY 548 GCTCGAGGGGTGTTCTCTGCTGCTTGTATAGTCCAGATGGGTATTTCTACAGGAA 607
DB 26 GCTCGAGGGGTGTTCTCTGCTGCTTGTATAGTCCAGATGGGTATTTCTACAGGAA 85

QY 608 GTTATCCCCCATCTGCTGCTTGTATAGTCCAGATGGGTATTTCTACAGGAA 667
DB 86 GTTATCCCCCATCTGCTGCTTGTATAGTCCAGATGGGTATTTCTACAGGAA 145

QY 668 -GTAATGAAGAGGATATTTTACAGCTATATCTTGAAGAAAGAGGATGAATTTAA 726
DB 146 GGTCTCATGAAGAGGATATTTTACAGCTATATCTTGAAGAAAGAGGATGAATTTAA 205

QY 727 AAGTCAGGAGATTAATTTCTCTTTTCCAAATACCAAAATGATGAGAAACCTGCTATCGTAA 786
DB 206 AAGTCAGGAGATTAATTTCTCTTTTCCAAATACCAAAATGATGAGAAACCTTTTATGTGTC 265

QY 787 TGTGAGTTGGGTGGAATGAATTTTGGCTTATGACATCCCATTTGGAGAGCACCAGAGA 846
DB 266 TGTGAGTTGGGTGGAATGAATTTTGGCTTATGACATCCCATTTGGAGAGCACCAGAGG 325

QY 847 ACATTTCTCGGGAACGAATGAAGCAATTTAAAGCAATTTTGGGAAATGCAAGAGGCTCC 906
DB 326 GCATGCTCGGGAACGAATGAATGAAGCAATTTTAAAGCAATTTTGGGAAATGCAAGAGGCTCC 385

QY 907 AGATTCAACACCGGTATATTTTGGAGGAGATACAAATTTAAGAGATCAAGAGGTTATCAA 966
DB 386 AGAGTCAGCTACAGTTATATTTTGGAGGAGATACAAATTTAAGGAGATCGAGAGGTTACCA 445

QY 967 ATCTGTTGGTTTACCTGACAAACGTTTGTGATGCTGGGAAATTTTGGGCAAACTTAACA 1026
DB 446 ATCTGTTGGTTTACCTGACAAACGTTTGTGATGCTGGGAAATTTTGGGCAAACTTAACA 505

QY 1027 TTGCCAGTATACATGGGATACGAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 1086
DB 506 TTGCCAGTATACATGGGATACGAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT 565
```

QY 1087 GCATCGTTTGTGATCGAATATTTTTCAGAGCAGAAG 1121
Db 566 ACTTCGTTTGTGATCGAATATTTTTCAGAGCAGAG 600

RESULT 18

US-10-066-543-983
; Sequence 983, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 983
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; LOCATION: 6, 35
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-983

Query Match 29.4%; Score 385.8; DB 5; Length 553;
Best Local Similarity 84.9%; Pred. No. 2.8e-99;
Matches 432; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 548 GCTCAGGGGTGTGTCCTGCTAGCTTTGTATAGTCCAGATGTGTTTCTACAGAA 607
Db 42 GCTCAGGGGTGTGTCCTGCTAGCTTTGTATAGTCCAGATGTGTTTCTACAGAA 101
QY 608 GTTATCCCCCCTACTGTGCTTACCTAAAGAGAGAGCAGCGATTACAAATTATTACA 667
Db 102 GTTATCCCCCCTACTGTGCTTACCTAAAGAGAGATCAAGTAATTATGAGATTATTACA 161
QY 668 GGTATGAAGAAGGATATTTCACAGTATACCTATTTGAAGAAAGGAGAGTGAAATTTAAA 727
Db 162 GGTATGAAGAAGGATATTTCACAGTATACCTATTTGAAGAAATCAAGAGTGAAATTTAAA 221
QY 728 AGTCAGGAGATTTATTCCTTTCCAAATACCAATGATGAGAAACCTGCTATCGCTAAT 787
Db 222 AGCCAAAGAGATTTATTCCTTTCCAAATGATGAGAAACCTTTTATGTGTGCAT 281
QY 788 GTGAGTTTGGGTGGAATGAATTTTCCCTTTATGACATCCCATTTGGAGAGCACCAGAGAA 847
Db 282 GTGATGTGTGAGGAATGTGCTTTGCTTTATGACATCCCATTTGGAGAGCACCAGAGGG 341
QY 848 CATTTCTGCGGAACGAATAGACAAATTTAAAACCTGTTTGGAAAAATGCAAGAGGCTCCA 907
Db 342 CATGCTGCGGAACGAATGAATCAGTTTAAAAATGGTTTAAAGAAAAATGCAAGAGGCTCCA 401
QY 908 GATTCAACACCGGTTATATTTCAGGAGATACAAATTTAAGAGATCAAGAAGTTATCAAA 967
Db 402 GAGTCAGCTACAGTTATATTTCAGGAGATACAAATCTAAGGAGATCAGAGGTTACCAGA 461
QY 968 TGTGTTGGTTTACCTGACAAACGTTTTTGTATGCTGGGAAATTTTATAGGCAAACTTAACAT 1027
Db 462 TGTGTTGGTTTACCCCAACAACTTGTGGATGCTGGGAGTTTGTGGCAAACTTAACAT 521

QY 1028 TGCCAGTATACATGGGATACGAAAGCAA 1056
Db 522 TGCCAGTATACATGGGATACACAATGAA 550

RESULT 19

US-10-066-543-1363
; Sequence 1363, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1363
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-066-543-1363

Query Match 22.1%; Score 290.2; DB 5; Length 401;
Best Local Similarity 84.9%; Pred. No. 5.2e-72;
Matches 325; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 548 GCTCAGGGGTGTGTCCTGCTAGCTTTGTATAGTCCAGATGTGTTTCTACAGAA 607
Db 19 GCTCAGGGGTGTGTCCTGCTAGCTTTGTATAGTCCAGATGTGTTTCTACAGAA 78
QY 608 GTTATCCCCCCTACTGTGCTTACCTAAAGAGAGAGCAGCGATTACAAATTATTACA 667
Db 79 GTTATCCCCCCTACTGTGCTTACCTAAAGAGAGATCAAGTAATTATGAGATTATTACA 138
QY 668 GGTATGAAGAAGGATATTTCACAGTATACCTATTTGAAGAAAGGAGAGTGAAATTTAAA 727
Db 139 GGTATGAAGAAGGATATTTCACAGTATACCTATTTGAAGAAATCAAGAGTGAAATTTAAA 198
QY 728 AGTCAGGAGATTTATTCCTTTCCAAATACCAAAATGATGAGAAACCTGCTATCGCTAAT 787
Db 199 AGCCAAAGAGATTTATTCCTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCAT 258
QY 788 GTGAGTTTGGGTGGAATGAATTTTCCCTTTATGACATCCCATTTGGAGAGCACCAGAGAA 847
Db 259 GTGAATGTGTGAGGAATGAGCTTTGCTTTATGACATCCCATTTGGAGAGCACCAGAGGG 318
QY 848 CATTTCTGCGGAACGAATAGACAAATTTAAAACCTGTTTGGAAAAATGCAAGAGGCTCCA 907
Db 319 CATGCTGCGGAACGAATGAATCAGTTTAAAAATGGTTTAAAGAAAAATGCAAGAGGCTCCA 378
QY 908 GATTCAACACCGGTTATATTTCG 930
Db 379 GAGTCAGCTACAGTTTATATTTCG 401

RESULT 20

US-10-242-535A-8082
; Sequence 8082, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:

QY 971 GGTGTTTACCTGACAAAGCTTTTTCATGCTGGGAATTTTATAGGCAACCTAAACATTCG 1030
| | | | |
Db 674 GTCAGTTTGTGATGTTTGGAGACAGATTAATTGCTATGAGACTAAATTAGGTTCTCTTTTTCG 733
| | | | |
QY 1031 CAGTATACATGGGATACGAAAGCAATAACAACTCAGATCCCTGCTGCTTATAAGCAT 1090
| | | | |
Db 734 CAGTATACATGGGATACAAATGAATGACTCTATCTTGGAAATACCTGCTGTGTAACCTT 793
| | | | |
QY 1091 CTTTTCATCGAATATTTTTCAG-----AGCAGAAGAGGGGCACCTTATTCTCTCAAAAGT 1144
| | | | |
Db 794 CTTTTCATCGAATATTTTTCAGAGCAGCAGCAGAGAGGGACACATATTATCCCGGAAGT 853
| | | | |
QY 1145 TTAGACCTTGTGGGTGGAAAACTGGACTGTGTAGATTATTCAGAGTATCATCTGGGGG 1204
| | | | |
Db 854 TTGGACCTTCTGGATTAGAAAACTGGACTGTGTAGATTATTCCTAGTATCATCTGGGGT 913
| | | | |
QY 1205 CTCCTGTGCACCTTGAATCTAGTATTGTGMAAGCTTCCCA 1245
| | | | |
Db 914 CTCCTGTGCACTTAGATATAATATTGTAAAAATGCTTTTCA 954
| | | | |

RESULT 23

US-10-066-543-826/c
; Sequence 826, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 826
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 373
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-826

Query Match 10.7%; Score 140.8; DB 5; Length 391;
Best Local Similarity 69.6%; Pred. No. 2.9e-29;
Matches 206; Conservative 0; Mismatches 87; Indels 3; Gaps 1;
QY 262 GGGATGCGACCCACGATGGTCCCGAGCGTCTGCGGGAGAACGACTGGCAGACGAGAA 321
| | | | |
Db 338 GAGCTGCGATGCGGACGTGGCTCAGTGCTTCTTGGCCGAGACGACTGGGAGATGGAAG 279
| | | | |
QY 322 AGCCCTGACGGCTACTTCGAGTGCAGAGAACCAAGGGTGGCCGCGCAGCTCC 381
| | | | |
Db 278 GGCCTGGAATCTTACTTCGAGCTCCGCTGGGAGAGCGCTTGGACGCGGACCTGA 219
| | | | |
QY 382 CAGCTCCTTCAAGTCGAGGCTATGTTGATCTTAACCAACGAGGATGCAATATGATACAC 441
| | | | |
Db 218 AACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAACTGATTCAC 159
| | | | |
QY 442 CATTATTAGAGCCAGTCCATCTGGA---ACTCCTCTAGAGATAGCAGCACTATTCTTTT 498
| | | | |

Db 158 CACTTCTAAATCAGCCATCTGAAGATACTCAGCAAGAAAATGCAGCATGTTCTCTCT 99
| | | | |
QY 499 CATTACCTGGAATATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 554
| | | | |
Db 98 CATTACCTGGAATATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 43
| | | | |
RESULT 24
US-09-878-722-121
; Sequence 121, Application US/09878722
; Publication No. US20020040127A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Hepler, William T.
; APPLICANT: Clapper, Jonathan
; APPLICANT: Wang, Aijun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.524
; CURRENT APPLICATION NUMBER: US/09/878,722
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-878-722-121

Query Match 10.2%; Score 134.4; DB 3; Length 176;
Best Local Similarity 85.2%; Pred. No. 1.2e-27;
Matches 150; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 579 ATAGTCCAGATGTGTGATTTCTACAGGAAGTTATCCCCCATCTACTGCTACCTAAAGA 638
| | | | |
Db 1 ACAGCCAGATGTGATATTTCTACAGGAAGTTATTTCCCATATTTATAGTACCTAAAGA 60
| | | | |
QY 639 AGAGAGCAGCAGTTACACATTTATCAGGTATGAAGAGGATATTTTCACAGCTATAC 698
| | | | |
Db 61 AGAGATCAAGTAATTTATGAGATTTATCAGGTATGAAGAGGATATTTTCACAGCTATAA 120
| | | | |
QY 699 TATTCAAGAAAGGAGAGTGAATTTAAAGTCAGGAGATTTCTCTTTTCCAAAT 754
| | | | |
Db 121 TGTGAAGAAATCAAGAGTGAATTTAAAGCCAGAGATTTATCTCTTTTCCAAAT 176
| | | | |

RESULT 25

US-09-878-178-50/c
; Sequence 50, Application US/09878178
; Patent No. US20020177552A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527
; CURRENT APPLICATION NUMBER: US/09/878,178
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 2237
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-878-178-50

Query Match 10.2%; Score 134.4; DB 3; Length 176;
Best Local Similarity 85.2%; Pred. No. 1.2e-27;
Matches 150; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 579 ATAGTCCAGATGTGTGATTTCTACAGGAAGTTATCCCCCATCTACTGCTACCTAAAGA 638
| | | | |

Db 176 ACAGCCAGATGATATTTCTACAGAGATTTATTTCCCATATATATAGCTACCTAAAGA 117
QY 639 AGAGACAGCCAGTTTACACAATTTATTTACAGGTAATGAAGAAGATATTTTACAGCTATAC 698
Db 116 AGAGATCAAGTAATTAATGAGATTTATTTACAGGTTCATGAAGAAGATATTTTACAGCTATAA 57
QY 699 TATTGAAGAAGGAAGTGAATTTAAAGTCAGAGATTTATTCCTTTTCCAAAT 754
Db 56 TGTGGAAGAAATCAAGAGTGAAATTTAAAGGCCAAGAGATTTATTCCTTTTCCAAGT 1

RESULT 26

US-09-904-456-121
; Sequence 121, Application US/09904456
; Publication No. US20030017167A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.524C1
; CURRENT APPLICATION NUMBER: US/09/904,456
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 247
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-904-456-121

Query Match 10.2%; Score 134.4; DB 3; Length 176;
Best Local Similarity 85.2%; Pred. No. 1.2e-27;
Matches 150; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 579 ATAGTCCAGATGGTATTTCTACAGAGTATTTCCCATCTGTGCTACCTAAAGA 638
Db 1 ACAGCCAGATGATATTTCTACAGAGATTTATTTCCCATATATATAGCTACCTAAAGA 60
QY 639 AGAGACAGCCAGTTTACACAATTTATTTACAGGTAATGAAGAAGATATTTTACAGCTATAC 698
Db 61 AGAGATCAAGTAATTAATGAGATTTATTTACAGGTTCATGAAGAAGATATTTTACAGCTATAA 120
QY 699 TATTGAAGAAGGAAGTGAATTTAAAGTCAGAGATTTATTCCTTTTCCAAAT 754
Db 121 TGTGGAAGAAATCAAGAGTGAAATTTAAAGGCCAAGAGATTTATTCCTTTTCCAAGT 176

RESULT 27

US-10-046-935-50/c
; Sequence 50, Application US/10046935
; Publication No. US20020156011A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527C1
; CURRENT APPLICATION NUMBER: US/10/046,935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2239
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-046-935-50

Query Match 10.2%; Score 134.4; DB 5; Length 176;
Best Local Similarity 85.2%; Pred. No. 1.2e-27;

Matches 150; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 579 ATAGTCCAGATGGTATTTCTACAGAGTATTTCCCATCTGTGCTACCTAAAGA 638
Db 176 ACAGCCAGATGATATTTCTACAGAGATTTATTTCCCATATATATAGCTACCTAAAGA 117
QY 639 AGAGACAGCCAGTTTACACAATTTATTTACAGGTAATGAAGAAGATATTTTACAGCTATAC 698
Db 116 AGAGATCAAGTAATTAATGAGATTTATTTACAGGTTCATGAAGAAGATATTTTACAGCTATAA 57
QY 699 TATTGAAGAAGGAAGTGAATTTAAAGTCAGAGATTTATTCCTTTTCCAAAT 754
Db 56 TGTGGAAGAAATCAAGAGTGAAATTTAAAGGCCAAGAGATTTATTCCTTTTCCAAGT 1

RESULT 28

US-10-146-502-50/c
; Sequence 50, Application US/10146502
; Publication No. US20030069180A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527C2
; CURRENT APPLICATION NUMBER: US/10/146,502
; CURRENT FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-502-50

Query Match 10.2%; Score 134.4; DB 5; Length 176;

Best Local Similarity 85.2%; Pred. No. 1.2e-27;
Matches 150; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 579 ATAGTCCAGATGGTATTTCTACAGAGTATTTCCCATCTGTGCTACCTAAAGA 638
Db 176 ACAGCCAGATGATATTTCTACAGAGATTTATTTCCCATATATATAGCTACCTAAAGA 117
QY 639 AGAGACAGCCAGTTTACACAATTTATTTACAGGTAATGAAGAAGATATTTTACAGCTATAC 698
Db 116 AGAGATCAAGTAATTAATGAGATTTATTTACAGGTTCATGAAGAAGATATTTTACAGCTATAA 57
QY 699 TATTGAAGAAGGAAGTGAATTTAAAGTCAGAGATTTATTCCTTTTCCAAAT 754
Db 56 TGTGGAAGAAATCAAGAGTGAAATTTAAAGGCCAAGAGATTTATTCCTTTTCCAAGT 1

RESULT 29

US-10-060-036-1367/c
; Sequence 1367, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0

GenCore version 5.1.6
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OM nucleic - nucleic search, using aw model

Run on: December 3, 2005, 09:59:45 ; Search time 237.195 Seconds
(without alignments)
9832.267 Million cell updates/sec

Title: US-10-757-745-3

Perfect score: 1312
Sequence: 1 agctataatgattcgatt.....tctcaacatttcaggacatc 1312

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1312	100.0	1312	3	US-09-697-863A-3
2	668.2	50.9	1920	3	US-09-697-863A-1
3	668.2	50.9	1948	3	US-09-620-312D-889
C 4	490	37.3	1079	3	US-09-118-554-63
C 5	490	37.3	1079	3	US-09-118-627-63
C 6	490	37.3	1079	3	US-09-602-877A-63
C 7	101.4	7.7	268	3	US-09-397-787-312
8	62.2	4.7	1549	3	US-09-444-336-5
9	62.2	4.7	1549	3	US-10-093-045-5
10	62.2	4.7	1549	3	US-10-093-045-5
11	56.2	4.3	768	3	US-09-530-219B-4
12	55.8	4.3	565	3	US-09-712-016-56
13	55.8	4.3	2885	3	US-09-232-200-36
14	55.8	4.3	2885	3	US-09-232-200-56
15	55.8	4.3	2885	3	US-09-232-197-36
16	55.8	4.3	2885	3	US-09-232-197-56
17	55.8	4.3	2885	3	US-09-232-201-36
18	55.8	4.3	2885	3	US-09-232-201-56
19	55.8	4.3	2885	3	US-09-232-195-36
20	55.8	4.3	2885	3	US-09-232-195-56
21	54.8	4.2	1055	3	US-09-215-131-3
22	54.8	4.2	1055	3	US-09-222-734-3
C 23	53.4	4.1	55	2	US-08-715-941-11
C 24	53.4	4.1	55	2	US-08-715-941-14

25	52.2	4.0	1979	3	US-09-620-312D-838
C 26	49.4	3.8	7218	2	US-08-232-463-14
27	49.4	3.8	4411529	3	US-09-103-840A-1
28	49.2	3.8	2846	3	US-09-613-182-5
C 29	48.8	3.7	1370	3	US-09-620-312D-680
30	47.2	3.6	906	3	US-09-206-166-4
31	47.2	3.6	1141	3	US-09-806-708B-22
C 32	47.2	3.6	1411	3	US-09-620-312D-535
C 33	47.2	3.6	2672	2	US-09-206-166-9
34	46.8	3.6	296	2	US-08-713-941-4
35	46.4	3.5	234	3	US-08-906-156A-21
C 36	46.2	3.5	426	3	US-09-252-991A-7105
37	46.2	3.5	1479	3	US-09-252-991A-7048
C 38	46.2	3.5	4236	3	US-09-252-991A-7057
39	46.2	3.5	10023	3	US-09-252-991A-6997
40	46	3.5	1794	3	US-09-620-312D-988
41	46	3.5	2241	3	US-09-342-353-9
42	45.4	3.5	600	3	US-09-023-942A-9
43	45.4	3.5	641	3	US-09-620-312D-954
44	45.4	3.5	1752	3	US-09-902-540-3466
45	45.4	3.5	4427	3	US-09-342-353-2
46	45.4	3.5	12277	3	US-09-902-540-1018
47	45.2	3.4	4403765	3	US-09-103-840A-2
48	44.6	3.4	1028	3	US-08-118-200-1
49	44.6	3.4	1028	3	US-08-438-745-1
C 50	44.6	3.4	2339	3	US-09-495-050A-26
51	44.2	3.4	6611	2	US-08-402-282-2
52	44.2	3.4	6611	2	US-08-508-004-2
53	44.2	3.4	6611	2	US-08-402-066-2
54	44.2	3.4	6611	2	US-08-402-068-2
C 55	42.8	3.3	700	3	US-09-735-271-843
56	42.8	3.3	1745	3	US-09-620-312D-711
57	42.6	3.2	4362	2	US-08-455-073A-1
C 58	42.4	3.2	2641	3	US-09-799-451-224
C 59	42.2	3.2	4403765	3	US-09-103-840A-2
C 60	42.2	3.2	4411529	3	US-09-103-840A-1
61	42	3.2	1845	3	US-09-902-540-7042
62	42	3.2	3471	3	US-09-902-540-8385
63	42	3.2	4087	3	US-09-902-540-825
64	42	3.2	7186	3	US-09-902-540-879
65	42	3.2	8865	3	US-09-949-016-4238
66	42	3.2	239527	3	US-09-949-016-15980
67	41.8	3.2	1493	3	US-09-620-312D-728
68	41.8	3.2	14382	3	US-09-902-540-1145
69	41.6	3.2	985	3	US-09-056-556-182
70	41.6	3.2	985	3	US-09-072-596-177
71	41.6	3.2	985	3	US-09-072-596-177
72	41.6	3.2	985	3	US-10-193-002-177
73	41.6	3.2	985	3	US-10-084-843-182
74	41.6	3.2	10178	3	US-09-902-540-977
C 75	41.4	3.2	2755	3	US-09-902-540-5035
C 76	41.4	3.2	30135	3	US-09-902-540-1249
C 77	41.4	3.2	640681	3	US-09-790-988-1
78	41.2	3.1	220	3	US-09-056-556-177
79	41.2	3.1	220	3	US-09-072-596-172
80	41.2	3.1	220	3	US-09-072-596-177
81	41.2	3.1	220	3	US-10-193-002-172
82	41.2	3.1	220	3	US-10-084-843-177
83	41.2	3.1	239	3	US-09-056-556-181
84	41.2	3.1	239	3	US-09-072-596-176
85	41.2	3.1	239	3	US-09-072-596-181
86	41.2	3.1	239	3	US-10-193-002-176
87	41.2	3.1	239	3	US-10-084-843-181
88	41.2	3.1	1395	3	US-09-902-540-4737
89	41.2	3.1	1471	3	US-09-620-312D-1099
90	41.2	3.1	2561	3	US-09-616-289-48
C 91	41.2	3.1	2561	3	US-09-976-740-48
92	41.2	3.1	28762	3	US-09-902-540-1232
93	41.2	3.1	8205	3	US-09-948-016-13430
94	41	3.1	1024	3	US-09-620-312D-91
95	41	3.1	1854	3	US-09-894-844-103
96	41	3.1	3765	3	US-07-705-490-1
97	41	3.1	3765	3	US-07-751-891B-1

98	41	3.1	154746	3	US-09-827-688-8	Sequence 8, Appli	171	39.2	3.0	601	3	US-09-949-016-139822	Sequence 139822,
C 99	41	3.1	154746	3	US-09-827-688-8	Sequence 8, Appli	172	39.2	3.0	1240	3	US-09-620-312D-414	Sequence 414, App
C 100	40.8	3.1	13534	3	US-09-902-540-1078	Sequence 1078, Ap	173	39.2	3.0	1765	3	US-10-237-551-225	Sequence 225, App
C 101	40.6	3.1	526	3	US-09-220-132-164	Sequence 164, App	174	39.2	3.0	3957	3	US-10-237-551-193	Sequence 193, App
102	40.6	3.1	789	3	US-09-902-540-7266	Sequence 7266, Ap	C 175	39.2	3.0	34621	3	US-09-949-002-700	Sequence 700, App
103	40.6	3.1	2456	2	US-07-882-711-1	Sequence 1, Appli	C 176	39.2	3.0	37875	3	US-09-949-016-13182	Sequence 13182, A
104	40.6	3.1	2456	2	US-08-462-174-1	Sequence 1, Appli	C 177	39.2	3.0	40653	3	US-09-949-002-640	Sequence 640, App
105	40.6	3.1	2457	2	US-08-723-4158-12	Sequence 12, Appl	C 178	39.2	3.0	72604	3	US-09-268-992-7	Sequence 7, Appli
106	40.6	3.1	2457	3	US-09-189-927A-12	Sequence 12, Appl	C 179	39.2	3.0	72604	3	US-09-657-474-7	Sequence 7, Appli
107	40.6	3.1	2457	3	US-09-710-861-12	Sequence 12, Appl	C 180	39.2	3.0	87352	3	US-09-949-016-12053	Sequence 12053, A
108	40.6	3.1	2486	3	US-09-949-016-4380	Sequence 4380, Ap	C 181	39.2	3.0	87352	3	US-09-949-016-12721	Sequence 12721, A
109	40.6	3.1	2492	2	US-08-139-937-13	Sequence 13, Appl	C 182	39.2	3.0	87352	3	US-09-949-016-15692	Sequence 15692, A
110	40.6	3.1	2492	3	US-09-023-655-1230	Sequence 1230, Ap	C 183	39.2	3.0	87352	3	US-09-949-016-15693	Sequence 15693, A
111	40.6	3.1	2492	6	PCT-US93-11310-13	Sequence 13, Appl	C 184	39	3.0	601	3	US-09-949-016-60191	Sequence 60191, A
112	40.6	3.1	2517	2	US-08-306-691B-18	Sequence 18, Appl	C 185	39	3.0	1124	3	US-09-949-016-2485	Sequence 2485, Ap
113	40.6	3.1	2517	2	US-08-385-142-2	Sequence 2, Appli	C 186	39	3.0	2091	3	US-10-237-551-78	Sequence 78, Appl
114	40.6	3.1	2517	2	US-08-481-814A-1	Sequence 1, Appli	C 187	39	3.0	2091	3	US-10-237-551-226	Sequence 226, App
115	40.6	3.1	2517	3	US-08-801-092-2	Sequence 2, Appli	C 188	39	3.0	2118	3	US-10-237-551-87	Sequence 87, Appl
116	40.6	3.1	2517	3	US-09-517-584A-3	Sequence 3, Appli	C 189	39	3.0	2211	3	US-10-237-551-86	Sequence 86, Appl
117	40.6	3.1	2517	3	US-09-315-113-2	Sequence 2, Appli	C 190	39	3.0	2539	3	US-09-620-312D-454	Sequence 454, App
118	40.6	3.1	2517	3	US-09-315-116-2	Sequence 2, Appli	C 191	39	3.0	6645	3	US-09-902-540-8819	Sequence 8819, Ap
119	40.6	3.1	4324	3	US-09-902-540-684	Sequence 684, App	C 192	39	3.0	8552	3	US-09-902-540-938	Sequence 938, App
120	40.6	3.1	14706	3	US-09-949-016-16122	Sequence 16122, A	C 193	39	3.0	10210	3	US-09-949-016-14227	Sequence 14227, A
C 121	40.4	3.1	18662	3	US-09-949-016-14655	Sequence 14655, A	C 194	39	3.0	30690	3	US-09-914-286-1	Sequence 1, Appli
C 122	40.4	3.1	50937	3	US-09-428-517-1	Sequence 1, Appli	C 195	39	3.0	54245	3	US-09-949-016-13499	Sequence 13499, A
123	40.2	3.1	319	3	US-09-165-264-8	Sequence 8, Appli	C 196	39	3.0	197336	3	US-09-949-016-12881	Sequence 12881, A
124	40.2	3.1	857	3	US-09-620-312D-391	Sequence 391, App	C 197	39	3.0	197337	3	US-09-949-016-14376	Sequence 14376, A
125	40.2	3.1	1752	3	US-09-620-312D-603	Sequence 603, App	C 198	39	3.0	197337	3	US-09-949-002-738	Sequence 738, App
126	40	3.0	320	3	US-09-165-264-7	Sequence 7, Appli	C 199	39	3.0	234287	3	US-09-949-002-687	Sequence 687, App
127	40	3.0	1200	3	US-09-495-050A-160	Sequence 160, App	C 200	39	3.0	234288	3	US-09-949-016-17272	Sequence 17272, A
128	40	3.0	1572	3	US-09-620-312D-664	Sequence 664, App	C 201	39	3.0	234288	3	US-09-949-002-841	Sequence 841, App
129	40	3.0	1926	3	US-09-249-585A-2	Sequence 2, Appli	C 202	38.8	3.0	461	3	US-09-620-312D-244	Sequence 244, App
130	40	3.0	1926	3	US-09-410-399-3	Sequence 3, Appli	C 203	38.8	3.0	843	3	US-09-724-797-33	Sequence 33, Appl
131	40	3.0	2398	3	US-09-620-312D-1056	Sequence 1056, Ap	C 204	38.8	3.0	1202	3	US-09-620-312D-97	Sequence 97, Appl
132	40	3.0	2437	3	US-09-620-312D-1055	Sequence 1055, Ap	C 205	38.8	3.0	2943	3	US-09-949-016-207	Sequence 207, App
133	40	3.0	2580	3	US-09-050-863-2	Sequence 2, Appli	C 206	38.8	3.0	24638	3	US-09-949-016-12087	Sequence 12087, A
134	40	3.0	2580	3	US-09-359-081-2	Sequence 2, Appli	C 207	38.8	3.0	24639	3	US-09-949-016-15749	Sequence 15749, A
C 135	40	3.0	3065	3	US-09-949-016-4249	Sequence 4249, Ap	C 208	38.6	2.9	1610	3	US-09-902-540-6105	Sequence 6105, Ap
C 136	40	3.0	3436	3	US-09-919-039-277	Sequence 277, App	C 209	38.6	2.9	1948	3	US-09-902-540-277	Sequence 277, App
C 137	40	3.0	4069	3	US-09-620-312D-174	Sequence 174, App	C 210	38.6	2.9	4826	3	US-09-949-016-898	Sequence 898, App
C 138	40	3.0	5452	2	US-09-130-114-1	Sequence 1, Appli	C 211	38.6	2.9	4826	3	US-09-772-304A-1	Sequence 1, Appli
C 139	40	3.0	8705	3	US-09-647-344A-14	Sequence 14, Appl	C 212	38.6	2.9	6253	3	US-09-949-016-12023	Sequence 12023, A
140	40	3.0	9600	3	US-08-910-647-1	Sequence 1, Appli	C 213	38.6	2.9	6253	3	US-09-949-016-16929	Sequence 16929, A
141	40	3.0	9600	3	US-09-620-925-1	Sequence 1, Appli	C 214	38.6	2.9	44377	2	US-08-804-227C-7	Sequence 7, Appli
142	40	3.0	10596	2	US-07-884-811-15	Sequence 15, Appl	C 215	38.6	2.9	44377	2	US-08-804-198-1	Sequence 1, Appli
143	40	3.0	10596	2	US-07-885-971-15	Sequence 15, Appl	C 216	38.4	2.9	336	3	US-09-902-540-6115	Sequence 6115, Ap
144	40	3.0	10596	2	US-08-087-783A-15	Sequence 15, Appl	C 217	38.4	2.9	1913	3	US-10-104-047-1636	Sequence 1636, Ap
145	40	3.0	10596	2	US-08-194-088B-15	Sequence 15, Appl	C 218	38.4	2.9	2234	3	US-09-902-540-280	Sequence 280, App
146	40	3.0	10596	2	US-08-194-087-15	Sequence 15, Appl	C 219	38.4	2.9	2594	3	US-09-949-016-568	Sequence 568, App
147	40	3.0	10596	6	PCT-US93-04648-15	Sequence 15, Appl	C 220	38.4	2.9	2584	3	US-09-949-016-1907	Sequence 1907, Ap
C 148	40	3.0	13535	3	US-09-949-016-15991	Sequence 15991, A	C 221	38.4	2.9	2584	3	US-09-949-016-1908	Sequence 1908, Ap
C 149	40	3.0	16080	3	US-09-734-566A-48	Sequence 48, Appl	C 222	38.4	2.9	2792	3	US-09-657-013-41	Sequence 41, Appl
C 150	40	3.0	16080	3	US-09-471-669A-48	Sequence 48, Appl	C 223	38.4	2.9	2792	3	US-09-949-016-1022	Sequence 1022, Ap
C 151	39.8	3.0	152331	3	US-09-128-155-16	Sequence 16, Appl	C 224	38.4	2.9	3740	3	US-09-949-016-3726	Sequence 3726, Ap
C 152	39.8	3.0	162841	3	US-09-949-016-13733	Sequence 13733, A	C 225	38.4	2.9	18159	3	US-09-949-016-12401	Sequence 12401, A
C 153	39.6	3.0	2436	3	US-09-902-540-8185	Sequence 8185, Ap	C 226	38.4	2.9	18159	3	US-09-949-016-13677	Sequence 13677, A
C 154	39.6	3.0	6583	3	US-09-902-540-841	Sequence 841, App	C 227	38.4	2.9	36228	3	US-09-949-016-12256	Sequence 12256, A
C 155	39.6	3.0	14862	3	US-09-949-016-14789	Sequence 14789, A	C 228	38.4	2.9	36228	3	US-09-949-016-15468	Sequence 15468, A
C 156	39.4	3.0	774	3	US-09-385-219A-39	Sequence 39, Appl	C 229	38.4	2.9	74550	3	US-09-949-016-12310	Sequence 12310, A
C 157	39.4	3.0	1146	3	US-08-911-853-26	Sequence 26, Appl	C 230	38.4	2.9	74550	3	US-09-949-016-12764	Sequence 12764, A
C 158	39.4	3.0	1146	3	US-09-479-409-26	Sequence 26, Appl	C 231	38.4	2.9	74550	3	US-09-949-016-13649	Sequence 13649, A
C 159	39.4	3.0	1146	3	US-09-479-453-26	Sequence 26, Appl	C 232	38.4	2.9	74550	3	US-09-949-016-13650	Sequence 13650, A
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C 161	39.4	3.0	7659	3	US-09-949-016-12695	Sequence 12695, A	C 234	38.2	2.9	408	3	US-09-252-991A-655	Sequence 655, App
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C 251	38.2	2.9	7001	2	US-08-458-076A-1	Sequence 1, Appli	C 324	37.2	2.8	2093	3	US-10-104-047-1666	Sequence 1666, App
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C 253	38.2	2.9	7001	2	US-08-761-258-6	Sequence 6, Appli	C 326	37.2	2.8	2109	3	US-09-854-133-153	Sequence 153, App
C 254	38.2	2.9	7001	2	US-08-729-214-1	Sequence 1, Appli	C 327	37.2	2.8	5097	3	US-09-902-540-745	Sequence 745, App
C 255	38.2	2.9	7001	2	US-08-977-306-6	Sequence 6, Appli	C 328	37.2	2.8	34662	3	US-09-902-540-1261	Sequence 1261, App
C 256	38.2	2.9	7001	2	US-09-028-934-1	Sequence 1, Appli	C 329	37.2	2.8	43267	3	US-09-949-016-17117	Sequence 17117, App
C 257	38.2	2.9	8438	2	US-07-945-283-1	Sequence 1, Appli	C 330	37.2	2.8	50186	3	US-09-949-016-14066	Sequence 14066, A
C 258	38.2	2.9	15271	3	US-09-902-540-1051	Sequence 1051, App	C 331	37.2	2.8	146095	3	US-09-949-016-12872	Sequence 12872, A
C 259	38.2	2.9	18187	3	US-09-949-016-14126	Sequence 14126, A	C 332	37.2	2.8	146104	3	US-09-949-016-13239	Sequence 13239, A
C 260	38.2	2.9	24984	3	US-09-949-016-14127	Sequence 14127, A	C 333	37	2.8	583	3	US-09-949-016-2863	Sequence 2863, App
C 261	38.2	2.9	24984	3	US-09-949-016-13288	Sequence 13288, A	C 334	37	2.8	645	3	US-09-902-540-7043	Sequence 7043, App
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C 264	38.2	2.9	75395	3	US-09-984-890-3	Sequence 3, Appli	C 337	37	2.8	1667	3	US-09-902-540-407	Sequence 10, Appl
C 265	38.2	2.9	75395	3	US-10-274-194-3	Sequence 3, Appli	C 338	37	2.8	1877	3	US-09-780-173A-10	Sequence 1868, App
C 266	38.2	2.9	75395	3	US-10-760-407-3	Sequence 3, Appli	C 339	37	2.8	3024	3	US-09-902-540-1868	Sequence 625, App
C 267	38.2	2.9	240157	3	US-09-949-016-16264	Sequence 16264, A	C 340	37	2.8	4087	3	US-09-902-540-833	Sequence 833, App
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C 281	37.8	2.9	9984	3	US-09-949-016-13283	Sequence 13283, A	C 354	36.8	2.8	945	3	US-09-902-540-3272	Sequence 3272, App
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C 286	37.6	2.9	1161	3	US-09-461-774-9	Sequence 9, Appli	C 359	36.8	2.8	4491	3	US-09-902-540-681	Sequence 681, App
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C 297	37.4	2.9	1141	3	US-09-806-708B-22	Sequence 22, Appl	C 370	36.8	2.8	12195	3	US-09-902-540-1194	Sequence 1194, App
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C 300	37.4	2.9	1943	3	US-09-620-312D-396	Sequence 396, App	C 373	36.8	2.8	14783	3	US-09-949-016-15127	Sequence 15127, A
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C 303	37.4	2.9	2581	3	US-09-902-540-472	Sequence 472, App	C 376	36.6	2.8	530	3	US-08-758-662-4	Sequence 4, Appli
C 304	37.4	2.9	4086	3	US-09-949-016-633	Sequence 633, App	C 377	36.6	2.8	601	3	US-09-949-016-46860	Sequence 46860, A
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C 310	37.4	2.9	68750	3	US-09-568-102-1	Sequence 1, Appli	C 383	36.6	2.8	3446	3	US-09-949-016-1033	Sequence 1033, App
C 311	37.4	2.9	68750	3	US-09-567-969-1	Sequence 1, Appli	C 384	36.6	2.8	3446	3	US-09-949-016-5776	Sequence 5776, App
C 312	37.4	2.9	68750	3	US-09-568-480-1	Sequence 1, Appli	C 385	36.6	2.8	3446	3	US-09-949-016-5776	Sequence 5776, App
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C 314	37.4	2.9	68750	3	US-09-568-472-1	Sequence 1, Appli	C 387	36.6	2.8	3715	3	US-09-041-886-10	Sequence 10, Appl
C 315	37.4	2.9	68750	3	US-09-567-899-1	Sequence 1, Appli	C 388	36.6	2.8	3899	3	US-09-902-540-573	Sequence 573, App
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RESULT 2
US-09-697-863A-1
; Sequence 1, Application US/09697863A
; Patent No. 6812203
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut Voor Biotechnologie VZW
; TITLE OF INVENTION: CD-40 INTERACTING AND TRAF-INTERACTING PROTEINS
; FILE REFERENCE: 2676-4555US
; CURRENT APPLICATION NUMBER: US/09/697,863A
; CURRENT FILING DATE: 2000-10-27
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; PRIOR FILING DATE: 1998-04-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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; ORGANISM: Homo sapiens
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; OTHER INFORMATION: N stands for any nucleotide.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1108)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1849)..(1849)
; OTHER INFORMATION: N stands for any nucleotide.
US-09-697-863A-1
Query Match 50.9%; Score 668.2; DB 3; Length 1920;
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Matches 843; Conservative 0; Mismatches 243; Indels 9; Gaps 2;
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DB 156 TCCTGGCCGAGAACGACTGGGAGATGGAAGAGGCTCTGAATCTCTACTTCGAGCTCCCG 215
QY 351 AGAACACCAAGGTCGCGCGCCGACCTCCACGCTCTTCAAGTCCGAGGCTATGTTG 410
DB 216 TGAAGAGAGCGCTTGGAAACCGCGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTG 275
QY 411 ATCTAACCAAGGAGTGAATGATAACCAATTTTAGAGCGCAGTCCATCTGGA---A 467
DB 276 ACCTAACCAATGAAGAAACAACTGATTCACCACTTCTAAATCAGCCCATCTGGAAGATA 335

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QY 468 CTCCTCTAGAGATAGCAGCACTATTCTTTTCATTACCTGGAAATATGATGGATTAGATG 527
Db 336 CTCAGCAAGAAATGGCAGCATGTTCTCTCATATTACCTGGAATATTGATGGATTAGATC 395
QY 528 GATGCAATCTGCCGAGAGGGCTCGAGGGGTGTGTTCTCTGCTAGCTTTGTATAGTCCAG 587
Db 336 TAAACAATCTGTACAGAGGGCTCGAGGGGTGTGTTCTCTACTTAGCTTTGTACAGCCAG 455
QY 588 ATGTGGTATTTCTACAGGAAGTTATCCCCCATACTGTGCCCTACTCTAAAGAAGAGAGAG 647
Db 456 ATGTGATATTTCTACAGGAAGTTATCCCCCATATTTAGCTACTCTAAAGAAGAGATCAA 515
QY 648 CCAAGTACAAATTTATACAGATTAATGAAGAGATTTTACAGCTATACATTTGAAGA 707
Db 516 GTAAATATGAGATTTATACAGTCTATGAAGAGGATATTTACAGCTATATATGTTGAAGA 575
QY 708 AAGGAAGAGTGAATTTAAAGTCCAGGAGATTTATCTTTTCCAAATACCAAAATGATGA 767
Db 576 AATCAAGAGTGAATTTAAAGCCCAAGAGATTTATCTTTTCCAAAGTACCAAAATGATGA 635
QY 768 GAAACCTGCTATCGCTAAATGTGAGTTTGGGTGGAATGAATTTTGCCTTTATGACATCCC 827
Db 636 GAAACCTTTTATGTGTGATGTGATGTGTGAGGAAATGAGCTTTTGCCTTTATGACATCCC 695
QY 828 ATTTGGAGACACAGAGAACATTTCTGCGGAACGAATAAGCAATTAATAAACTGTTCTTG 887
Db 696 ATTTGGAGACACAGAGGGCATGCTGCGGAACGAATGAATCAATGTTAAATAATGTTTAA 755
QY 888 GAAAAATGCAAGAGGCTCCAGATTCACACAGGTTATATTTGCGAGGATACAAATTTAA 947
Db 756 AGAAATGCAAGAGGCTCCAGATTCAGATTCAGATTCAGATTTATTTGCGAGGATACAAATCTAA 815
QY 948 GAGATCAAGAGTTATCAAAATGTGTGTTTACCTGACAACGTTTTCATGCTCGGGAAT 1007
Db 816 GGGATCGAGAGGTTACCAGATGTGTGTTTACCCCAACAACATTTGTGATGTCTGGGAGT 875
QY 1008 TTTTAGGCAACCTAAACATTTGCCAGTATACATGGGATACGAACCAATTAACAACCTCA 1067
Db 876 TTTTGGGCAACCTAAACATTTGCCAGTATACATGGGATACCAATGAACCTCTAATCTTG 935
QY 1068 GSATCCCTGCTCTTATAAGCATCGTTTGTGATCGAATATTTTCAG-----AGCAGAAG 1121
Db 936 GAATAACTGCTGCTGTAAACCTTCTGTTTGTGATCGAATATTTTTCAGACGACGACGAGAAG 995
QY 1122 AGGGGACCTTTATTCCTCAAGTTTTCAGCTTTGTTGGGTGGGAAACCTGGAATGTGTA 1181
Db 996 AGGGACACATTTATCCCCGAGTTTGGACCTTCTTTGGATTAGAAAAAAGCTGCTGTA 1055
QY 1182 GATTTCCAGATGATCACTGGGGGCTCTTGTGCACTTGAATGTAGTATTTGAAAGCTT 1241
Db 1056 GATTTCTAGTATCACTGGGGTCTCTGTGCACTTAGATATAATATTTGAAATGCTT 1115
QY 1242 CCCACTTCAGCTTT 1256
Db 1116 TTCAAGTGTGGGTTT 1130

```

RESULT 3

```

US-09-620-312D-889
; Sequence 889, Application US/09620312D
; Patent No. 659662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong

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; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yundong
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 659662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt FL_genes Version 1.0
; SEQ ID NO 889
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)...(1127)
US-09-620-312D-889

Query Match 50.9%; Score 668.2; DB 3; Length 1948;
Best Local Similarity 75.6%; Pred. No. 4.7e-174;
Matches 858; Conservative 0; Mismatches 268; Indels 9; Gaps 2;

QY 131 GCGAGCAGTTCGATCGGCGGAGCCGCGAGGCGCGAGGCGGGCGGCGGCGGCGGCC 190
Db 15 GCCAAGAAATTCGCGCACGAGGGAAGATGAGTGTGGGAGTTCCCTGGAGGGCGGAGGAG 74
QY 191 GAAGCAGCACAGCGGAGGAGGACCGGTGAAGAGGCGGCGGCTTCAGTGTCTGGGCTTT 250
Db 75 GCGGCGGAGGAGAGGCGGAGCTGAGTGAAAGCGGCGACTTCTGTGTGTGAGTTT 134
QY 251 GCCTGTGTGGGGGATGCGACCCCAAGATGTGTCGAGCTTCGCGGAGGAAACGACTGG 310
Db 135 GCCTCGGTGCGAAGCTGCGATGCGGAGTGGCTCAGTGTCTTCTGGCGAGAACGACTGG 194
QY 311 CAGAGCAGAAAGCCCTGAGGCGCTTTCAGTCCGAGGCTTATGTATCTAAACCAAGAGATGCA 430
Db 195 GAGATGGAAGAGGCTTGAACCTCTACTTCAGGCTTCGAGGAGGAGGAGCGCTTGGAA 254
QY 371 CGCCAGCCTCCACGTCCTTCAAGTCCGAGGCTTATGTATCTAAACCAAGAGATGCA 430
Db 255 CGCCAGCCTGAAACCACTCTGAGCCCAAGACCTATGTGACCTAAACCAATGAAGAAACA 314
QY 431 AATGATCAACCAATTTTAGAAGCCAGTCCATCTCGA---ACTCCTTAGAAGATAGCAGC 487
Db 315 ACTGATTCACCACTTCTTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGC 374
QY 488 ACTATTTCTTCATTACTGCAATATTGATGGATAGTATGATGCAATCTGCCGAGAGG 547
Db 375 ATGTTCTCTCTCATTAAGTGGATATTGATGGATTTAGATCTTAAACAATCTGTCTAGAGAG 434
QY 548 GCTCAGGGGTGTGTTCTCTGCTAGCTTGTATAGTCCAGATGTGGTATTTCTACAGGAA 607
Db 435 GCTCAGGGGTGTGTTCTCTACTTTAGCTTTGTGACGCCAGATGTGATATTTCTACAGGAA 494
QY 608 GTTATCCCCCATACTGTGCTTACTCTAAGAGAGAGCAGCCAGTTACACAAATTTATACA 667
Db 495 GTTATCCCCCATATATAGCTAGCTAGCTAGCAAGAGATCAAGTAAATTTATGAGATTTATACA 554
QY 668 GGTAAATGAGAGGATATTTTACAGCTATATCTATTGAGAGAGGAGAGTGAATTTTAAA 727
Db 555 GGTATGAGAGGAGATATTTTACAGCTATATCTATTGAGAGAGTGAATTTTAAA 614
QY 728 AGTCAGGAGATTTATCTCTTTTCCAAATACCAAAATGATGAGAAACCTCTATGCGTAAAT 787

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Db 615 AGCAAGAGATTATTCCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTGCAT 674
Qy GTGAGTTTGGTGGAAATGAAATTTTGCCTTATGACATCCATTTGGAGAGCACCAGAA 847
Db 675 GTGAATGTGTGACGAAATGAGCTTTGCCCTTATGACATCCATTTGGAGAGCACCAGGG 734
Qy 848 CATTTCTGCGGAACGAATAGACAAATTAATAAATCTGTTCTTGGAAAAATGCAAGAGGCTCA 907
Db 735 CATGCTGCGGAACGAATGATCAGTTTAAATATGTTTAAAGAAATGCAAGAGGCTCCA 794
Qy 908 GATTCACCAAGCTTTATTTTGCAGAGATACAAATTTAAGAGATCAAGAAGTTATCAAA 967
Db 795 GAGTCAGCTACAGTTATTTTGCAGAGATACAAATCTAAGGATCGAGAGGTTACCAGA 854
Qy 968 TGTGGTGGTTTACTGACAACTTTTGTGCTCGGAATTTTGGCAAACTTAACAT 1027
Db 855 TGTGGTGGTTTACCCCAACATTTGTGGATGCTGGGAGTTTGGGCAAACTTAACAT 914
Qy 1028 TGCAGTATACATGGGATACGAAGCAATAACAACTCAGGATCCCTGCTGCTTATAAG 1087
Db 915 TGCAGTATACATGGGATACGAATGAATCTTAATCTTGGATTAATCTGCTGTGTTAA 974
Qy 1088 CATCGTTTGTGATCGAATATTTTTCAG-----AGCAGAGAGGGGACCTTATTCCTCAA 1141
Db 975 CTTGCTTTGTGATCGAATATTTTTCAGAGCAGCAGCAGAGAGAGGACACATTTATCCCGA 1034
Qy 1142 AGTTTACCTTGTGGTGGTGGAAAACTGGACTGTGTAGATTTCCGAGTGTACTGCG 1201
Db 1035 AGTTTGGACCTTCTGGAATTAGAAAACTGGACTGTGTAGATTTCTTAGTGATCATCG 1094
Qy 1202 GGCTCTGTGCACTTGAATGTAGTATTGTGAAAAAGCTTCCCACTTGCAGCTTT 1256
Db 1095 GGTCTCTGTGCACTTGAATATATATTTGTAATAATGCTTTTCAAGTGTGGTTT 1149

RESULT 4

US-09-118-554-63/c

; Sequence 63, Application US/09118554A
; Patent No. 6365348
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jianshun
; TITLE OF INVENTION: COMPOUNDS FOR DIAGNOSIS OF BREAST CANCER AND
; TITLE OF INVENTION: METHODS FOR THEIR USE
; FILE REFERENCE: 210121.450C1
; CURRENT APPLICATION NUMBER: US/09/118,554A
; CURRENT FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 08/988,255
; EARLIER FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 1079
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-118-554-63

Query Match 37.3%; Score 490; DB 3; Length 1079;

Best Local Similarity 82.8%; Pred. No. 5.7e-125;

Matches 586; Conservative 0; Mismatches 115; Indels 7; Gaps 2;

Qy 555 GGGTGTGTTCTGCTAGCTTTGTATAGTCCAGATGGTATTTCTACAGAAAGTTATCC 614
Db 1079 GGGTGTGTTCTGCTAGCTTTGTATAGTCCAGATGGTATTTCTACAGAAAGTTATTC 1020
Qy 615 CCCCATCTGTGCTTACTTAAGAGAGAGCAGCAGTACACAAATTTATACAGGTAATG 674
Db 1019 CCCCATATTATAGTACTTAAGAGAGATCAAGTAATTATGAGATTATACAGGTCATG 960
Qy 675 AAGAAGGATATTTTACAGCTATACATTTGAAGAAAGGAGAGTGAATTTTAAAGTCAGG 734
Db 959 AAGAAGGATATTTTACAGCTATATATTTGAAGAAATCAAGAGTGAATTTTAAAGCCAG 900

Qy 735 AGATTATTCCTTTTCCAAATACCAAAATGATGAGAAACCTGCTATGCGTAAATGTGAGTT 794
Db 899 AGATTATTCCTTTTCCAAATACCAAAATGATGAGAAACCTTTATGTGTGATGTGAATG 840
Qy 795 TGGGTGGAATGAATTTTCCCTTATGACATCCATTTGGAGAGCACCAGAGAACATTTCTG 854
Db 839 TGTGAGGAATGAGCTTTGCCCTTATGACATCCATTTGGAGAGCACCAGAGGCGATGCTG 780
Qy 855 CGGAACGAATAGACAAATTAATAAATCTGTTCTTGGAAAAATGCAAGAGGCTCCAGATTCAA 914
Db 779 CGGAACGAATGAAATCAGTTTAAATAATGTTTAAAGAAATGCAAGAGGCTCCAGAGTCAG 720
Qy 915 CCACGGTTATATTTTCAGAGAGATACAAATTTAAGAGATCAAGAAGTTATCAAAATGTGGTG 974
Db 719 CTACAGTTATATTTTCAGAGAGATACAAATCTAAGGATCGAGAGGTTACAGATGTGGTG 660
Qy 975 GTTTACTGACAACTGTTTGTGATGCTGGGAATTTTATAGGCAAACTTAACATTTGCCACT 1034
Db 659 GTTTACCCCAACAACTTGTGGATGCTGGGAGTTTGGGCAAACTTAACATTTGCCAGT 600
Qy 1035 ATACATGGGATACGAAGCAATAACAACTCAGGATCCCTGCTGCTTATAAGCATCGTT 1094
Db 599 ATACATGGGATACAAATGAATCTTAATCTTGGAAATACTGCTGCTGTGTAACCTTCGTT 540
Qy 1095 TTGATCGAATATTTTTCAG-----AGCAGAGAGGGGACCTTATTCCTCAAAGTTTAG 1148
Db 539 TTGATCGAATATTTTTCAGAGCAGCAGCAGAGAGGACACATTTATCCCGAAGTTT-G 481
Qy 1149 ACCTTGTGGTGGTGGAAAACTGGACTGTGTAGATTTCCGAGTGTACTGCTGGGCTCT 1208
Db 480 ACCTTCTTGGATTAGAAAACTGGACTGTGTAGATTTCTTAGTGATCATCTGGGCTTTC 421
Qy 1209 TGTGCACTTGAATGTAGTATTGTGAAAAAGCTTCCCACTTGCAGCTTT 1256
Db 420 TGTGCACTTAGATATATATTTGTAATAATGCTTTTCAAGTGTGGTTT 373

RESULT 5

US-09-118-627-63/c

; Sequence 63, Application US/09118627A
; Patent No. 6379951
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jianshun
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF BREAST CANCER
; TITLE OF INVENTION: AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.446C1
; CURRENT APPLICATION NUMBER: US/09/118,627A
; CURRENT FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 1079
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-118-627-63

Query Match 37.3%; Score 490; DB 3; Length 1079;

Best Local Similarity 82.8%; Pred. No. 5.7e-125;

Matches 586; Conservative 0; Mismatches 115; Indels 7; Gaps 2;

Qy 555 GGGTGTGTTCTGCTAGCTTTGTATAGTCCAGATGGTATTTCTACAGAAAGTTATCC 614
Db 1079 GGGTGTGTTCTGCTAGCTTTGTATAGTCCAGATGGTATTTCTACAGAAAGTTATTC 1020
Qy 615 CCCCATCTGTGCTTACTTAAGAGAGAGCAGCAGTACACAAATTTATACAGGTAATG 674
Db 1019 CCCCATATTATAGTACTTAAGAGAGATCAAGTAATTATGAGATTATACAGGTCATG 960
Qy 675 AAGAAGGATATTTTACAGCTATACATTTGAAGAAAGGAGAGTGAATTTTAAAGTCAGG 734
Db 959 AAGAAGGATATTTTACAGCTATATATTTGAAGAAATCAAGAGTGAATTTTAAAGCCAG 900

142 AAATGCTTTTCAAGTGTGGGTTT 120
Dpb

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RESULT 8
US-09-444-336-5
; Sequence 5, Application US/09444336
; Patent No. 6410713
; GENERAL INFORMATION:
; APPLICANT: Guerriero, Vincent
; APPLICANT: Raynes, Deborah A
; TITLE OF INVENTION: DNA Encoding Proteins That Inhibit Hsp70 Function
; FILE REFERENCE: HspBP DNA and Protein Sequences
; CURRENT APPLICATION NUMBER: US/09/444,336
; CURRENT FILING DATE: 1999-11-19
; EARLIER APPLICATION NUMBER: 60/109,351
; EARLIER FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1549
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-444-336-5

```

Query Match	4.7%	Score 62.2;	DB 3;	Length 1549;
Best Local Similarity	95.5%;	Pred. No. 9.5e-07;		
Matches 64;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	19	TTTATACGACTC	CATATAGGGAATTTGGCCCTCGAGGCCAAGAAATTCGGCACGAGGCCG	78
dh	2	TTAATACGACTC	CATATAGGGAATTTGGCCCTCGAGGCCAAGAAATTCGGCACGAGGCCG	61

```

RESULT 9
US-10-093-045-5
; Sequence 5, Application US/10093045
; Patent No. 6903202
; GENERAL INFORMATION:
; APPLICANT: Guerriero, Vincent
; APPLICANT: Raynes, Deborah A
; TITLE OF INVENTION: DNA Encoding Proteins That Inhibit Hsp70 Function
; FILE REFERENCE: HspBP DNA and Protein Sequences
; CURRENT APPLICATION NUMBER: US/10/093,045
; CURRENT FILING DATE: 2002-03-07
; EARLIER APPLICATION NUMBER: 09/444,336
; EARLIER FILING DATE: 1999-11-19
; EARLIER APPLICATION NUMBER: 60/109,351
; EARLIER FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1549
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-093-045-5

```

```

Query Match      4.7%; Score 62.2; DB 3; Length 1549;
Best Local Similarity 95.5%; Pred. No. 9.5e-07;
Matches 64; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 19 TTTTATACGACTCATTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCAGAGGGCGG 78
      |||||
Db 2 TTAATACGACTCATTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCAGAGGGCGG 61
      |||||

Qy 79 GAAGCAG 85
      |||||
Db 62 CAAGCAG 68
      |||||

```

```

RESULT 10
US-10-093-246-5
; Sequence 5, Application US/10093246
; Patent No. 6908985
; GENERAL INFORMATION:
; APPLICANT: Guerriero, Vincent
; APPLICANT: Raynes, Deborah A
; TITLE OF INVENTION: DNA Encoding Proteins That Inhibit Hsp70 Function
; FILE REFERENCE: HspBP DNA and Protein Sequences
; CURRENT APPLICATION NUMBER: US/10/093,246
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 09/444,336
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/109,351
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1549
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-093-246-5

```

	Query Match	4.7%	Score 62.2;	DB 3;	Length 1549;
	Best Local Similarity	95.5%;	Pred. No. 9.5e-07;		
	Matches 64;	Conservative	0;	Mismatches 3;	Indels 0; Gaps 0;
Qy	19	TTTATACGACTCTACTATAGGCAATTTGGCCCTCGAGGCCAAGAAATTCGGCACGAGGCCG	78		
nb	2	TTTATACGACTCTACTATAGGCAATTTGGCCCTCGAGGCCAAGAAATTCGGCACGAGGCCG	61		

RESULT 11
US-09-530-219B-4
; Sequence 4, Application US/09530219B
; Patent No. 6844422
; GENERAL INFORMATION:
; APPLICANT: NIEHRS, CHRISTOF
; APPLICANT: GLINKA, ANDREI
; TITLE OF INVENTION: AN INHIBITOR PROTEIN OF THE WNT SIGNAL PATH
; FILE REFERENCE: RABG/40168
; CURRENT APPLICATION NUMBER: US/09/530,219B
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: PCT/DE98/03155
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: DE 197 47 418.7
; PRIOR FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-530-219B-4

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Query Match      4.3%; Score 56.2; DB 3; Length 768;
Best Local Similarity 95.1%; Pred. No. 3e-05;
Matches 58; Conservative 0; Mismatches 3; Indels 0; Gaps 0

QY      22 ATACGACTCTACTATAGGGAAATTTCGCCCTCGAGGCCAAGAATTTCGCACAGGGCGGGAA 81
         |||||
Db       1 ATACGACTCTACTATAGGGAAATTTCGCCCTCGAGGCCAAGAATTTCGCACAGGGTTCGGA 60

QY      82 G 82
         |
Db      61 G 61
```

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RESULT 12
US-09-712-016-56
; Sequence 56, Application US/09712016
; Patent No. 6468790
; GENERAL INFORMATION:
; APPLICANT: Giese, Klaus
; TITLE OF INVENTION: METASTATIC BREAST AND COLON CANCER
; TITLE OF INVENTION: REGULATED GENES
; FILE REFERENCE: 200130.460
; CURRENT APPLICATION NUMBER: US/09/712,016
; EARLIER FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US/09/417,615
; PRIOR FILING DATE: PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-712-016-56

Query Match          4.3%; Score 55.8; DB 3; Length 565;
Best Local Similarity 96.6%; Pred. No. 3.4e-05;
Matches 57; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 AATTATACGACTCACTATAGGAAATTTGGCCCTCGAGGCCAAGAAATTCGGCAGGAGG 75
Db 39 ATTTAATACGACTCACTATAGGAAATTTGGCCCTCGAGGCCAAGAAATTCGGCAGGAGG 97

RESULT 13
US-09-232-200-36
; Sequence 36, Application US/09232200A
; Patent No. 6288213
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WHI97-21p3MB
; CURRENT APPLICATION NUMBER: US/09/232,200A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 2885
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-232-200-36

Query Match          4.3%; Score 55.8; DB 3; Length 2885;
Best Local Similarity 96.6%; Pred. No. 7.7e-05;
Matches 57; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 AATTATACGACTCACTATAGGAAATTTGGCCCTCGAGGCCAAGAAATTCGGCAGGAGG 75
Db 150 ATTTAATACGACTCACTATAGGAAATTTGGCCCTCGAGGCCAAGAAATTCGGCAGGAGG 208

RESULT 14
US-09-232-200-56
; Sequence 56, Application US/09232200A
; Patent No. 6288213
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
```

```
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WHI97-21p3MB
; CURRENT APPLICATION NUMBER: US/09/232,200A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 2885
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-232-200-56

Query Match          4.3%; Score 55.8; DB 3; Length 2885;
Best Local Similarity 96.6%; Pred. No. 7.7e-05;
Matches 57; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 AATTATACGACTCACTATAGGAAATTTGGCCCTCGAGGCCAAGAAATTCGGCAGGAGG 75
Db 150 ATTTAATACGACTCACTATAGGAAATTTGGCCCTCGAGGCCAAGAAATTCGGCAGGAGG 208

RESULT 15
US-09-232-197-36
; Sequence 36, Application US/09232197A
; Patent No. 6300096
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WHI97-21p3MA
; CURRENT APPLICATION NUMBER: US/09/232,197A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 2885
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-232-197-36

Query Match          4.3%; Score 55.8; DB 3; Length 2885;
Best Local Similarity 96.6%; Pred. No. 7.7e-05;
Matches 57; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 AATTATACGACTCACTATAGGAAATTTGGCCCTCGAGGCCAAGAAATTCGGCAGGAGG 75
Db 150 ATTTAATACGACTCACTATAGGAAATTTGGCCCTCGAGGCCAAGAAATTCGGCAGGAGG 208

RESULT 16
US-09-232-197-56
; Sequence 56, Application US/09232197A
; Patent No. 6300096
; GENERAL INFORMATION:
```



```
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WHI97-21p3MA
; CURRENT APPLICATION NUMBER: US/09/232,197A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 2885
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-232-197-56

Query Match      4.3%; Score 55.8; DB 3; Length 2885;
Best Local Similarity 96.6%; Pred. No. 7.7e-05;
Matches 57; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 AATTATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCAGGAGG 75
Db 150 ATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCAGGAGG 208
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RESULT 17
US-09-232-201-36
; Sequence 36, Application US/09232201A
; Patent No. 6348321
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WHI97-21p3MC
; CURRENT APPLICATION NUMBER: US/09/232,201A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 2885
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-232-201-36

Query Match      4.3%; Score 55.8; DB 3; Length 2885;
Best Local Similarity 96.6%; Pred. No. 7.7e-05;
Matches 57; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 AATTATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCAGGAGG 75
Db 150 ATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCAGGAGG 208
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RESULT 18
US-09-232-201-56
; Sequence 56, Application US/09232201A
; Patent No. 6348321
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; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WHI97-21p3MC
; CURRENT APPLICATION NUMBER: US/09/232,201A
; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 2885
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-232-201-56
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Query Match      4.3%; Score 55.8; DB 3; Length 2885;
Best Local Similarity 96.6%; Pred. No. 7.7e-05;
Matches 57; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 AATTATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCAGGAGG 75
Db 150 ATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCAGGAGG 208
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RESULT 19
US-09-232-195-36
; Sequence 36, Application US/09232195A
; Patent No. 6657049
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WHI97-21p3MD
; CURRENT APPLICATION NUMBER: US/09/232,195A
; CURRENT FILING DATE: 1999-01-04
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 2885
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-232-195-36
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```
Query Match      4.3%; Score 55.8; DB 3; Length 2885;
Best Local Similarity 96.6%; Pred. No. 7.7e-05;
Matches 57; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 AATTATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCAGGAGG 75
Db 150 ATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCAAGAATTCGGCAGGAGG 208
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RESULT 20
US-09-232-195-56
; Sequence 56, Application US/09232195A
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; Patent No. 6657049
; GENERAL INFORMATION:
; APPLICANT: Stahl, Andreas
; APPLICANT: Hirsch, David J.
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Gimeno, Ruth E.
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
; FILE REFERENCE: WH197-21p3MD
; CURRENT APPLICATION NUMBER: US/09/232,195A
; CURRENT FILING DATE: 1999-01-04
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER FILING DATE: 1998-01-15
; EARLIER APPLICATION NUMBER: 60/093,491
; EARLIER FILING DATE: 1998-07-20
; EARLIER APPLICATION NUMBER: 60/110,941
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 2885
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-232-195-56

Query Match 4.3%; Score 55.8; DB 3; Length 2885;
Best Local Similarity 96.6%; Pred. No. 7.7e-05;
Matches 57; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 17 AATTATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCCAAGAAATTCGGCACGAGG 75
Db 150 ATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCCAAGAAATTCGGCACGAGG 208

RESULT 21
US-09-215-131-3
; Sequence 3, Application US/09215131
; Patent No. 6030834
; GENERAL INFORMATION:
; APPLICANT: Chu, Keting
; APPLICANT: Pot, David
; TITLE OF INVENTION: IKK Beta Regulates Transcription Factors
; FILE REFERENCE: 1449.002
; CURRENT APPLICATION NUMBER: US/09/215,131
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1055
; TYPE: DNA
; ORGANISM: human
US-09-215-131-3

Query Match 4.2%; Score 54.8; DB 3; Length 1055;
Best Local Similarity 96.6%; Pred. No. 8.7e-05;
Matches 56; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 17 AATTATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCCAAGAAATTCGGCACGAGG 74
Db 16 ATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCCAAGAAATTCGGCACGAGG 73

RESULT 22
US-09-222-734-3
; Sequence 3, Application US/09222734A
; Patent No. 6077701
; GENERAL INFORMATION:
; APPLICANT: Chu, Keting
; APPLICANT: Pot, David
; TITLE OF INVENTION: IKK-beta Regulates Transcription Factors
; FILE REFERENCE: 12441.78080
; CURRENT APPLICATION NUMBER: US/09/222,734A
; CURRENT FILING DATE: 1998-12-29

; EARLIER APPLICATION NUMBER: 09/215,131
; EARLIER FILING DATE: 1998-12-18
; EARLIER APPLICATION NUMBER: 60/068,954
; EARLIER FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1055
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-222-734-3

Query Match 4.2%; Score 54.8; DB 3; Length 1055;
Best Local Similarity 96.6%; Pred. No. 8.7e-05;
Matches 56; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 17 AATTATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCCAAGAAATTCGGCACGAGG 74
Db 16 ATTTAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCCAAGAAATTCGGCACGAGG 73

RESULT 23
US-08-715-941-11/c
; Sequence 11, Application US/08715941
; Patent No. 5846721
; GENERAL INFORMATION:
; APPLICANT: Soares, Marcelo B.
; APPLICANT: de Fatima Bonaldo, Maria
; TITLE OF INVENTION: AN EFFICIENT AND SIMPLER METHOD TO
; TITLE OF INVENTION: CONSTRUCT NORMALIZED cDNA LIBRARIES WITH IMPROVED
; TITLE OF INVENTION: REPRESENTATIONS OF FULL-LENGTH cDNAs.
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESS: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19-SEP-1996
; APPLICATION NUMBER: US/08/715,941
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 55 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-715-941-11

Query Match 4.1%; Score 53.4; DB 2; Length 55;
Best Local Similarity 98.2%; Pred. No. 4.7e-05;
Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 20 TTATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCCAAGAAATTCGGCACGAGG 74
Db 55 TAATACGACTCACTATAGGGAATTTGGCCCTCGAGGCCCAAGAAATTCGGCACGAGG 1

```

; APPLICANT: Drmanac, Radote T.
; TITLE OF INVENTION: No. 659662el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt FL_genes Version 1.0
; SEQ ID NO 838
; LENGTH: 1979
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (175)..(1053)
US-09-620-312D-838

Query Match      4.0%; Score 52.2; DB 3; Length 1979;
Best Local Similarity 87.7%; Pred.No. 0.00062;
Matches 57; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      24 ACACACTCACTATAGGAAATTGGCCCTCGAGGCCAAGAATTTCGGCACGAGGGCGGGAAGC 83
        |||
Db      5 ACACACTCACTATAGGAAATTGGCCCTCGAGGCCAAGAATTTCGGCACGAGGTGAGGTGAG 64
        |||

Qy      84 AGCGT 88
        |||
Db      65 AGAGT 69

RESULT 26
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEX: (703)683-4109
; TELEFAX: 899149

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Db 429 CCTACTTAGCTTGTACAGCCAGATGTGATATTTCTACAGGAAGTATTTCCCCCATATT 488
QY 492 ATAGCTTACTTAAGAGAGATCAAGCTAAATTATGAGATTTATACAGGTCAATGAGAGGAT 551
Db 489 ATAGCTTACTTAAGAGAGATCAAGCTAAATTATGAGATTTATACAGGTCAATGAGAGGAT 548
QY 552 ATTTCCACAGCTATAATGTGTTGAAGAAATCAAGAGTGAATTTAAAGACCAAGAGATTATTC 611
Db 549 ATTTCCACAGCTATAATGTGTTGAAGAAATCAAGAGTGAATTTAAAGACCAAGAGATTATTC 608
QY 612 CTTTTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAATGTGTGAGAA 671
Db 609 CTTTTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAACGTGTGAGAA 668
QY 672 ATGAGCTTTGCTTATGATCATCCCATTTTGGAGACCAAGAGGGCATGCTGGGACCA 731
Db 669 ATGAGCTTTGCTTATGATCATCCCATTTTGGAGACCAAGAGGGCATGCTGGGACCA 728
QY 732 TGAATCAGTTAAATATGTTTAAAGAAATGCAAGAGGCTCCAGAGTCAGCTACAGTTA 791
Db 729 TGAATCAGTTAAATATGTTTAAAGAAATGCAAGAGGCTCCAGAGTCAGCTACAGTTA 788
QY 792 TATTTTCAGGAGATCAAAATCTAAGGGATCGAGAGGTTTACAGATGTGTGTGTTTACCCA 851
Db 789 TATTTTCAGGAGATCAAAATCTAAGGGATCGAGAGGTTTACAGATGTGTGTGTTTACCCA 848
QY 852 ACAACATTTGTGATGCTGGGAGTTTGGGCAACCTTAACATTTGCCAGTATACATGGG 911
Db 849 ACAACATTTGTGATGCTGGGAGTTTGGGCAACCTTAACATTTGCCAGTATACATGGG 908
QY 912 ATACAAATGAATCTAATCTTGAATTAACCTGCTGTGTAACCTGCTTTTGAATGCA 971
Db 909 ATACAAATGAATCTAATCTTGAATTAACCTGCTGTGTAACCTGCTTTTGAATGCA 968
QY 972 TATTTTTCAGAGCAGCAGAGAGGAGACATTAATTTCCCGAAGTTTGGACCTTCTTG 1031
Db 969 TATTTTTCAGAGCAGCAGAGAGGAGACATTAATTTCCCGAAGTTTGGACCTTCTTG 1028
QY 1032 GATTAGAAAACCTGACGTGTGTAGATTTTCCAGTGTGATCACTGGGCTCTCTGTGCAACT 1091
Db 1029 GATTAGAAAACCTGACGTGTGTAGATTTTCCAGTGTGATCACTGGGCTCTCTGTGCAACT 1088
QY 1092 TAGATATAATATTTGAAAATGCTTTTCAAGTGTGGTTTGGCCCTGATTTGTGCAATAC 1151
Db 1089 TAGATATAATATTTGAAAATGCTTTTCAAGTGTGGTTTGGCCCTGATTTGTGCAATAC 1148
QY 1152 AATTTCCACCTTCTCGAAAGGTAGGTTTGTGTGGAGGAAATAATGTACTAGATCAATGT 1211
Db 1149 AATTTCCACCTTCTCGAAAGGTAGGTTTGTGTGGAGGAAATAATGTACTAGATCAATGT 1208
QY 1212 CACAGAAAACCAACTATGATTTATGTTGTGTTTTCAGATTTCAACATTTAAAGATTAT 1271
Db 1209 CACAGAAAACCAACTATGATTTATGTTGTGTTTTCAGATTTCAACATTTAAAGATTAT 1268
QY 1272 GTTTATTTAAACGACACATCTCCATTTCAAGTGTGAGGCAATTTAATAAAGGGCA 1331
Db 1269 GTTTATTTAAACGACACATCTCCATTTCAAGTGTGAGGCAATTTAATAAAGGGCA 1328
QY 1332 CAAGCCTGTGAGAGTTTCAACGGTGTCTTACAGCTGCCAGTGGATTTCCAAACAGGTAC 1391
Db 1329 CAAGCCTGTGAGAGTTTCAACGGTGTCTTACAGCTGCCAGTGGATTTCCAAACAGGTAC 1388
QY 1392 CCCATGTCTGAGCTAAATGTTTATATTTTCCATTCAGGACCCGAAATGTTAATATT 1451
Db 1389 CCCATGTCTGAGCTAAATGTTTATATTTTCCATTCAGGACCCGAAATGTTAATATT 1448
QY 1452 TAAAAATAGTCTTCAAAAGAAAACATAAGAGATTATTCAGTTCTTGGGACCTGGATCCCTTT 1511
Db 1449 TAAAAATAGTCTTCAAAAGAAAACATAAGAGATTATTCAGTTCTTGGGACCTGGATCCCTTT 1508
QY 1512 ATTTCAATAGTTTCAGATCATCTTAATGAAATGCCATGATTTATTCGAGTTAAAGTAGAT 1571

Db 1509 ATTTTCATAAGTTTCAGATCATCTTAAATGAAATGCCATGATTTATCTGCAGTTAAAGTAGAT 1568
QY 1572 GACAGCTATTCTACATCAGACTTTCATTTTGTGTCAGCTAAATTACATAAATTGCTTAAGNTATA 1631
Db 1569 GACAGCTATTCTACATCAGACTTTCATTTTGTGTCAGCTAAATTACATAAATTGCTTAAGNTATA 1628
QY 1632 ATTTGAAACCTTTATGGCTTAAATTCCTTAACCTCTTTTGAATTCATGTTTGTAGTCATGT 1691
Db 1629 ATTTGAAACCTTTATGGCTTAAATTCCTTAACCTCTTTTGAATTCATGTTTGTAGTCATGT 1688
QY 1692 TGTCAACAGAGGCAAGTTAAGCTTGTGATGTTTAAATCGGTTTGAATACACATGGG 1751
Db 1689 TGTCAACAGAGGCAAGTTAAGCTTGTGATGTTTAAATCGGTTTGAATACACATGGG 1748
QY 1752 ACATTTTAAACAAAATAAATGCATGAGAGACATAGCCCTTTTAGTTTGTCTAAATTGT 1811
Db 1749 ACATTTTAAACAAAATAAATGCATGAGAGACATAGCCCTTTTAGTTTGTCTAAATTGT 1808
QY 1812 GAAATGGAATGCTTTTACAGGAAGTAAATGCAAAATTANTTTTAAAGTGTGCTTTTAAAGAAA 1871
Db 1809 GAAATGGAATGCTTTTACAGGAAGTAAATGCAAAATTACTTTTAAAGTGTGCTTTTAAAGAAA 1868
QY 1872 AATATTTTCCCAACAGAGAAATTTAAATAAGAAATTTTATTTGGTAAA 1920
Db 1869 AATATTTTCCCAACAGAGAAATTTAAATAAGAAATTTTATTTGTTAA 1917

RESULT 10
AAH15146
ID AAH15146 standard; cDNA; 1898 BP.
XX AAH15146;
AC AAH15146;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:13209.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX Homo sapiens.
XX
FN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 2000EP-00116126.
XX
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
PT
PT
XX
PS Claim 8; SEQ ID NO 13209; 2537pp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC	cancer or neurodegenerative diseases and many others listed in the
CC	specification. The present sequence represents a novel human cDNA. Note:
CC	The sequence data for this patent did not form part of the printed
CC	specification but was obtained in electronic format directly from USPTO
CC	at seqdata.uspto.gov/sequence.html?DocID=20030104529.
XX	
SQ	Sequence 1948 BP; 614 A; 335 C; 436 G; 563 T; 0 U; 0 Other;
	Query Match 98.8%; Score 1897.6; DB 9; Length 1948;
	Best Local Similarity 99.7%; Pred. No. 0;
	Matches 1900; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY	15 GGAAGATGAGTTGGGAGTTGCCTGGAGGGCGGAGGAGGGCGGAGGAGGGCG 74
DB	34 GGAAGATGAGTTGGGAGTTGCCTGGAGGGCGGAGGAGGGCGGAGGAGGGCG 93
QY	75 AGCTCAGGTGAAAGCGCGACTTCTGTGTGTGAGTTTGCTCGGTGCGAAGCTGGG 134
DB	94 AGCTCAGGTGAAAGCGCGACTTCTGTGTGTGAGTTTGCTCGGTGCGAAGCTGGG 153
QY	135 ATGCCGAGTGGCTCAGTGTCTTCTGCGCGAGAACGACTGGGAGATGGAAGGGCTCTGA 194
DB	154 ATGCCGAGTGGCTCAGTGTCTTCTGCGCGAGAACGACTGGGAGATGGAAGGGCTCTGA 213
QY	195 ACTCCTACTTCGAGCCTCCGGTGGAGAGAGCGCCTTGGAA CGCCGACCTGAAACCATCT 254
DB	214 ACTCCTACTTCGAGCCTCCGGTGGAGAGAGCGCCTTGGAA CGCCGACCTGAAACCATCT 273
QY	255 CTGAGCCCAAGACTATGTTGACCTAACCAATCAAGAAACAACCTGATTCACCACTCTTA 314
DB	274 CTGAGCCCAAGACTATGTTGACCTAACCAATCAAGAAACAACCTGATTCACCACTCTTA 333
QY	315 AAATCAGCCCATCTGAAGATACTCAGCAAGAAATGGCAGCATGTTCTCTCTCATTAACCT 374
DB	334 AAATCAGCCCATCTGAAGATACTCAGCAAGAAATGGCAGCATGTTCTCTCTCATTAACCT 393
QY	375 GGAATATGTAGATTAGATCTAAACAATCTGTGAGAGGGCTCGAGGGGTGTGTTCT 434
DB	394 GGAATATGTAGATTAGATCTAAACAATCTGTGAGAGGGCTCGAGGGGTGTGTTCT 453
QY	435 ACTTAGCTTTGTACGCCAGATGTGATATTCTCAGGGAAGTTATTCCCCCATATTATA 494
DB	454 ACTTAGCTTTGTACGCCAGATGTGATATTCTCAGGGAAGTTATTCCCCCATATTATA 513
QY	495 GCTACCTAAAGAGAGATCAAGTAATTATGAGATTATTA CAGGTCTATGAAGAGGATTT 554
DB	514 GCTACCTAAAGAGAGATCAAGTAATTATGAGATTATTA CAGGTCTATGAAGAGGATTT 573
QY	555 TCACAGCTATAATGTTGAAGAAATCAAGAGTGAAATTA AAAAGCCAAAGATTTTCCTT 614
DB	574 TCACAGCTATAATGTTGAAGAAATCAAGAGTGAAATTA AAAAGCCAAAGATTTATTCCTT 633
QY	615 TTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAATGTCTCAGGAATG 674
DB	634 TTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAATGTCTCAGGAATG 693
QY	675 AGCTTTGCTTTATGACATCCCATTTGGAGAGCACGAGGGCATGTGCGGAAACGAATGA 734
DB	694 AGCTTTGCTTTATGACATCCCATTTGGAGAGCACGAGGGCATGTGCGGAAACGAATGA 753
QY	735 ATCAGTTTAAAAATGGTTTTTAAAGAAAAATGCAAGAGGCTCCAGAGTCAAGTATATAT 794
DB	754 ATCAGTTTAAAAATGGTTTTTAAAGAAAAATGCAAGAGGCTCCAGAGTCAAGTATATAT 813
QY	795 TTGAGGAGATACAAATCTAAGGATCGAGAGGTTACAGATGTGGTGTATCCCAACA 854
DB	814 TTGAGGAGATACAAATCTAAGGATCGAGAGGTTACAGATGTGGTGTATCCCAACA 873
QY	855 ACATTTGGATGTCTGGAGTTTTTGGGCAAACTTAAACATTTGCCAGTATACATGGGATA 914
DB	874 ACATTTGGATGTCTGGAGTTTTTGGGCAAACTTAAACATTTGCCAGTATACATGGGATA 933
QY	915 CACAAATGAACTTAATCTTGGAAATAA CTGCTGTGTTGTAACCTTCGTTTTGATCGAATAT 974

DB	934 CACAAATGAACTCTAATCTTGGAAATAA CTGCTGTGTTGTAACCTTCGTTTTGATCGAATAT 993
QY	975 TTTTCAGAGCAGCAGCAGAGAGGGACACATATTATCCCGAAGTTTGGACCTTCTTGGAT 1034
DB	994 TTTTCAGAGCAGCAGCAGAGAGGGACACATATTATCCCGAAGTTTGGACCTTCTTGGAT 1053
QY	1035 TAGAAAAA CTGGACTGTGTAGATTTCCTAGTAGATCACTGGGGTCTTCTGTGCAACTTAG 1094
DB	1054 TAGAAAAA CTGGACTGTGTAGATTTCCTAGTAGATCACTGGGGTCTTCTGTGCAACTTAG 1113
QY	1095 ATATAATAATTTGAAATGCTTTTCAAGTGTGGTTTTGCCCCTGATGTTTGC AAAATACAA 1154
DB	1114 ATATAATAATTTGAAATGCTTTTCAAGTGTGGTTTTGCCCCTGATGTTTGC AAAATACAA 1173
QY	1155 TTCCACCTTCTGGAAAAGGTAGGTTTTCTGTGTGAGGAAATAATGTACTAGATCATTTGTAC 1214
DB	1174 TTCCACCTTCTGGAAAAGGTAGGTTTTCTGTGTGAGGAAATAATGTACTAGATCATTTGTAC 1233
QY	1215 AGAAAAA CCAACTATCATTTATGTTGTTTTTCAAGATTCAACATTTAAAGATTAAATGTT 1274
DB	1234 AGAAAAA CCAACTATCATTTATGTTGTTTTTCAAGATTCAACATTTAAAGATTAAATGTT 1293
QY	1275 TATTTAAAACGAACACATCTCTGCATTTCAAGATGTGAGGCCATTTAATAAAAAAGGGACAA 1334
DB	1294 TATTTAAAACGAACACATCTCTGCATTTCAAGATGTGAGGCCATTTAATAAAAAAGGGACAA 1353
QY	1335 AGCTGTGAGATTTTCAACGGTGTTCAGCTGCCAGCTGGATTTCCAAACAGGTACCCC 1394
DB	1354 AGCTGTGAGATTTTCAACGGTGTTCAGCTGCCAGCTGGATTTCCAAACAGGTACCCC 1413
QY	1395 ATTGTCTCTGAGCTAATGTTTATATTTTCCATTTCAGGCACCGCAATAGTAAATATTATA 1454
DB	1414 ATTGTCTCTGAGCTAATGTTTATATTTTCCATTTCAGGCACCGCAATAGTAAATATTATA 1473
QY	1455 AATAAGTCTTTCAAAAGAAAAACATAAGAGATTATTTGAGTTCTTGGGACTGGATCCTTTATT 1514
DB	1474 AATAAGTCTTTCAAAAGAAAAACATAAGAGATTATTTGAGTTCTTGGGACTGGATCCTTTATT 1533
QY	1515 TCATAAGTTTCAGATCATCTTTAAATGAAATGCCATGATTTATCTGCAAGTTAAGTAGATGAC 1574
DB	1534 TCATAAGTTTCAGATCATCTTTAAATGAAATGCCATGATTTATCTGCAAGTTAAGTAGATGAC 1593
QY	1575 AGCTATTTCTACATCAGACTTTGATTTTTTGTGAGCTAATTTACATAATTTGGTAAAGNTATAAT 1634
DB	1594 AGCTATTTCTACATCAGACTTTGATTTTTTGTGAGCTAATTTACATAATTTGGTAAAGNTATAAT 1653
QY	1635 GAAACCTTATGGCTTAAAAATTCCTTAACTCCTTTTGAATTCATGTTTGTAGTCATGTTGT 1694
DB	1654 GAAACCTTATGGCTTAAAAATTCCTTAACTCCTTTTGAATTCATGTTTGTAGTCATGTTGT 1713
QY	1695 CAA CAGAGGCAAAAGTTTAAAGCTTGATGTTTAAATTCGGTTTAAATTCGGTTTGAAGCCATGGGACA 1754
DB	1714 CAA CAGAGGCAAAAGTTTAAAGCTTGATGTTTAAATTCGGTTTAAATTCGGTTTGAAGCCATGGGACA 1773
QY	1755 TTTTTTTTAA CAAAAATAAATGCAATGCAAGACATAGCCTTTTAAAGTGTCTTAAATGTA 1814
DB	1774 TTTTTTTTAA CAAAAATAAATGCAATGCAAGACATAGCCTTTTAAAGTGTCTTAAATGTA 1833
QY	1815 ATGGAATGCTTTTACAGGAAGTAAATGCAAAATTAATTTTAAAGTGTCTTTTAAAGAAAAAT 1874
DB	1834 ATGGAATGCTTTTACAGGAAGTAAATGCAAAATTAATTTTAAAGTGTCTTTTAAAGAAAAAT 1893
QY	1875 ATTTTCCCCACAGGAGAAATTTTAAATAAGAAATTTTATTTTGGTTAA 1920
DB	1894 ATTTTCCCCACAGGAGAAATTTTAAATAAGAAATTTTATTTTGGTTAA 1939

RESULT 8
ADD19013
ID ADD19013 standard; DNA; 1936 BP.
XX
AC ADD19013;

Db 394 GGAATATTGATGGATTAGATCTAAACAATCTGTACAGAGGGCTCGAGGGGTGTGTCTCT 453
Qy 435 ACTTAGCTTTGACAGCCAGATGTGATATTTCTACAGGAAGTATTTCCCCCATATTATA 494
Db 454 ACTTAGCTTTGACAGCCAGATGTGATATTTCTACAGGAAGTATTTCCCCCATATTATA 513
Qy 495 GCTACTTAAGAAGAGATCAAGTAATATGAGATTTATACAGGTCAATGAAGAAGATATT 554
Db 514 GCTACTTAAGAAGAGATCAAGTAATATGAGATTTATACAGGTCAATGAAGAAGATATT 573
Qy 555 TCACAGCTATATGTTGAAGAAATCAAGAGTCAAAATTAAGAGCCCAAGAGATTTATCTCT 614
Db 574 TCACAGCTATATGTTGAAGAAATCAAGAGTCAAAATTAAGAGCCCAAGAGATTTATCTCT 633
Qy 615 TTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCATGTGAATGTGTGTCAGGAAATG 674
Db 634 TTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCATGTGAATGTGTGTCAGGAAATG 693
Qy 675 AGCTTTGCCCTTATGACATCCCATTTTGGAGAGCAACAGAGGGCATGCTGCGGAAACGAATGA 734
Db 694 AGCTTTGCCCTTATGACATCCCATTTTGGAGAGCAACAGAGGGCATGCTGCGGAAACGAATGA 753
Qy 735 ATCAGTTAAATATGTTTAAAGAAATGCAAGAGGCTCCAGAGTCAGCTACAGTTATAT 794
Db 754 ATCAGTTAAATATGTTTAAAGAAATGCAAGAGGCTCCAGAGTCAGCTACAGTTATAT 813
Qy 795 TTGCGAGGATACAAATCTAAGGGATCGAGAGGTTTACCAGATGTGTGTTTACCACAACA 854
Db 814 TTGCGAGGATACAAATCTAAGGGATCGAGAGGTTTACCAGATGTGTGTTTACCACAACA 873
Qy 855 ACATTGTGATGCTCTGGGAGTTTGGGCAAACTTAAACATGTCAGTATACATGGGATA 914
Db 874 ACATTGTGATGCTCTGGGAGTTTGGGCAAACTTAAACATGTCAGTATACATGGGATA 933
Qy 915 CACAAATGAACCTAATCTTGAATAAATCTGCTGTTGTAACCTGTTTGTGATCAATAT 974
Db 934 CACAAATGAACCTAATCTTGAATAAATCTGCTGTTGTAACCTGTTTGTGATCAATAT 993
Qy 975 TTTTCAGAGCAGCAGAGGAGGACACATTTATTTCCCGAAGTTTGGACCTTCTTGGAT 1034
Db 994 TTTTCAGAGCAGCAGAGGAGGACACATTTATTTCCCGAAGTTTGGACCTTCTTGGAT 1053
Qy 1035 TAGAAAAAATGACCTGTGTGATTTCTTGTGATGATCACTGGGGTCTTCTGTGCAACTTAG 1094
Db 1054 TAGAAAAAATGACCTGTGTGATTTCTTGTGATGATCACTGGGGTCTTCTGTGCAACTTAG 1113
Qy 1095 ATATAATATTGTAATAATGCTTTTCAAGTGTGGTGTGCTGCTGATTTGCAAAATACAAAT 1154
Db 1114 ATATAATATTGTAATAATGCTTTTCAAGTGTGGTGTGCTGCTGATTTGCAAAATACAAAT 1173
Qy 1155 TTCCACCTTCTGGAAGGTAGGTTTGTGCTGTGGAGAAATAATGTACTAGATCATTGTGCAC 1214
Db 1174 TTCCACCTTCTGGAAGGTAGGTTTGTGCTGTGGAGAAATAATGTACTAGATCATTGTGCAC 1233
Qy 1215 AGAAAAACAACATGATTTATGTTGTGTTTTCAGAAATCAACATTAAGATTAATGTT 1274
Db 1234 AGAAAAACAACATGATTTATGTTGTGTTTTCAGAAATCAACATTAAGATTAATGTT 1293
Qy 1275 TATTTAAACGACACATTCCTGATTCAGGATGTGAGGCCATTTAATAAAGGCGACAA 1334
Db 1294 TATTTAAACGACACATTCCTGATTCAGGATGTGAGGCCATTTAATAAAGGCGACAA 1353
Qy 1335 AGCCTGTGAGAGTTTCAACGGTGTCTTACAGCTGCAGCTGGATTCCAACAGGTACCCC 1394
Db 1354 AGCCTGTGAGAGTTTCAACGGTGTCTTACAGCTGCAGCTGGATTCCAACAGGTACCCC 1413
Qy 1395 ATTGTCTGTGAGCTAATGTTTATATTTTCCATTCAGGACCGGAATAGTTAATATTTAA 1454
Db 1414 ATTGTCTGTGAGCTAATGTTTATATTTTCCATTCAGGACCGGAATAGTTAATATTTAA 1473
Qy 1455 AATAGTCTTCAAGAAAAACATAAGATATTATGAGTTCTTGGAGCTGGATCTTTTATT 1514

Db 1474 AATAAGTCTTCAAAAGAAAAACATAAGAGATTTATTGAGTCTTGGGACTGGATCCCTTTATT 1533
Qy 1515 TCATAAGTTTCAGATCATCTTAAATGAAAAATGCCATGATTATCTGCAGTTAAGTAGATGAC 1574
Db 1534 TCATAAGTTTCAGATCATCTTAAATGAAAAATGCCATGATTATCTGCAGTTAAGTAGATGAC 1593
Qy 1575 AGCTATTCTACATCAGACTTGTGATTTTGTGTGAGCTAAATTACATAAATTGGTAAGNTATAATT 1634
Db 1594 AGCTATTCTACATCAGACTTGTGATTTTGTGTGAGCTAAATTACATAAATTGGTAAGNTATAATT 1653
Qy 1635 GAAACCTTATGGCTTAAAAATTCCTTAACTCCCTTTTGAATTCATGTTTGTAGTCATGTTGT 1694
Db 1654 GAAACCTTATGGCTTAAAAATTCCTTAACTCCCTTTTGAATTCATGTTTGTAGTCATGTTGT 1713
Qy 1695 CAACAGAGGCAAAAGTTAAGCTTTGATGTTGTTAAATCGGTTTGTATAGCACCATGGGACA 1754
Db 1714 CAACAGAGGCAAAAGTTAAGCTTTGATGTTGTTAAATCGGTTTGTATAGCACCATGGGACA 1773
Qy 1755 TTTTAAACAAAAATTAATGCATGAAGAGACATAGCCCTTTTAGTTTGTCTAAATTGTGAA 1814
Db 1774 TTTTAAACAAAAATTAATGCATGAAGAGACATAGCCCTTTTAGTTTGTCTAAATTGTGAA 1833
Qy 1815 ATGGAATGCTTTACAGGAAGTAAATGCARAATTANTTTTAAAGTGTGCTTTAAAGAAAAAT 1874
Db 1834 ATGGAATGCTTTACAGGAAGTAAATGCARAATTANTTTTAAAGTGTGCTTTAAAGAAAAAT 1893
Qy 1875 ATTTTCCCCACAGGAGAAATTTAAATAAGAAATTTTATTTGGTAAA 1920
Db 1894 ATTTTCCCCACAGGAGAAATTTAAATAAGAAATTTTATTTGTTAAA 1939

RESULT 7

ADB48979
ID ADB48979 standard; cDNA; 1948 BP.
XX
AC ADB48979;
XX
DT 04-DEC-2003 (first entry)
XX
DE Novel human cDNA SEQ ID NO 889.
XX
KW ss; cancer; neurodegenerative disease; human.
XX
OS Homo sapiens.
XX
PN US2003104529-A1.
XX
PD 05-JUN-2003.
XX
PF 04-JAN-2002; 2002US-00037270.
XX
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 19-JUL-2000; 2000US-00620312.

XX
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R T.

XX
PI Zhou P, Tang YT, Liu C, Asundi V, Drmanac RT;
XX
XX WPI; 2003-678194/64.

XX
PT New polynucleotide, useful for treating diseases e.g., cancer or
PT neurodegenerative diseases.

XX
PS Claim 1; SEQ ID NO 889; 99pp; English.

XX
CC The invention relates to a polynucleotide comprising a sequence given in
CC the specification, or its mature protein-coding portion, or its
CC complement. The polynucleotide is useful for treating diseases e.g.,

KW	antidiabetic; GPCR-like protein; ophthalmic disorder;
KW	neurological disorder; immunological disorder; nephritic disorder;
KW	hormonal dysfunction; cancer; atherosclerosis; diabetes;
KW	molecular weight marker; food supplement; human; ss.
XX	
OS	Homo sapiens.
XX	
PN	US6569662-B1.
XX	
PD	27-MAY-2003.
XX	
PF	19-JUL-2000; 2000US-00620312.
XX	
PR	21-JAN-2000; 2000US-00498725.
PR	25-APR-2000; 2000US-00552317.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Zhou P, Drmanac RT;
XX	
DR	WPI; 2001-442255/47.
XX	
XX	New G-protein-coupled receptor-like polypeptides and polynucleotides,
PT	useful for treating diseases of ophthalmic, neurological, immunological,
PT	and nephritic systems and hormonal dysfunction, cancer, atherosclerosis
PT	and diabetes.
PT	
XX	
PS	Example 2; SEQ ID NO 889; 92pp; English.
XX	
CC	The invention describes an isolated polynucleotide (I) comprising a fully
CC	defined (S1) of 749, 3188, 2484, 1169, 2936, 1467, 5773, 5714, 4041,
CC	1372, 3996, 3945, 2735, 1788, 585, 1782, 927, 5714 or 2282 nucleotides as
CC	given in the specification, its translated or protein coding portion, its
CC	extracellular portion or its active domain. The GPCR-like polypeptides
CC	and polynucleotides are useful for the treatment of diseases of
CC	ophthalmic, neurological, immunological and nephritic systems. They may
CC	also be used to treat hormonal dysfunction, cancer, atherosclerosis and
CC	diabetes. The antibodies are useful for detecting or quantitating the
CC	polypeptide in tissue. The polypeptides can also be used as molecular
CC	weight markers and as a food supplement. This sequence represents a human
CC	polynucleotide of the invention.
XX	
SQ	Sequence 1948 BP; 614 A; 335 C; 436 G; 563 T; 0 U; 0 Other;
	Query Match
	Best Local Similarity 98.8%; Score 1897.6; DB 5; Length 1948;
	Matches 1900; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy	15 GGAAGATGGAAGTTGGGAGTTGCTCTGGAGGCGGGAGGAGCGCGGAGGAGAGGGCG 74
Db	34 GGAAGATGGAAGTTGGGAGTTGCTCTGGAGGCGGGAGGAGCGCGGAGGAGAGGGCG 93
Qy	75 AGCTGAGGTGAAAAAGCGCGACTTCTGTGTGTGGAGTTTGCTCGGTGCGAAGCTGCG 134
Db	94 AGCTGAGGTGAAAAAGCGCGACTTCTGTGTGTGGAGTTTGCTCGGTGCGAAGCTGCG 153
Qy	135 ATGCCGAGTGGCTCAGTGCTTCTCTGCGCGAGAACCACTGGGAGATGGAAGGCTCTGA 194
Db	154 ATGCCGAGTGGCTCAGTGCTTCTCTGCGCGAGAACCACTGGGAGATGGAAGGCTCTGA 213
Qy	195 ACTCTTACTTCGAGCTCCGGTGGAGGAGAGCGCTTTGGAACGCCGACCTGGAACCATCT 254
Db	214 ACTCTTACTTCGAGCTCCGGTGGAGGAGAGCGCTTTGGAACGCCGACCTGGAACCATCT 273
Qy	255 CTGAGGCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACCTGATTCACACCTTCTA 314
Db	274 CTGAGGCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACCTGATTCACACCTTCTA 333
Qy	315 AAATCAGCCCATCTGAAGATACTCAGCAAGAAAATGGCAGCATGTTCTCTCATTTACCT 374
Db	334 AAATCAGCCCATCTGAAGATACTCAGCAAGAAAATGGCAGCATGTTCTCTCATTTACCT 393
Qy	375 GGAATATTGATGATTAGATCTAAACAATCTGTACAGAGGGCTCGAGGGGTGTGTTCTCT 434

|||||
1807 TTGCTAAATGTGAAATGGAATGCTTTTACAGGAAGTAAATGCAAAATTAATCTTTTAAGTGTG 1866
QY 1861 CTTTAAAGAAAATATTTTCCCAAGGAGAAATTTAAATAAGAAATTTTATTTGGTAAA 1920
Db 1867 CTTTAAAGAAAATATTTTCCCAAGGAGAAATTTAAATAAGAAATTTTATTTGGTAAA 1926
RESULT 5
AA158997
ID AA158997 standard; cDNA; 1948 BP.
XX
AC AA158997;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 1200.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
OS Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US034263.
XX
XX 23-DEC-1999; 99US-00471275.
XX
XX 21-JAN-2000; 2000US-00488725.
XX
XX 25-APR-2000; 2000US-00552317.
XX
XX 20-JUN-2000; 2000US-00598042.
XX
XX 19-JUL-2000; 2000US-00620312.
XX
XX 03-AUG-2000; 2000US-00653450.
XX
XX 14-SEP-2000; 2000US-00662191.
XX
XX 19-OCT-2000; 2000US-00693036.
XX
XX 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
XX Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
XX
XX P-PSDB; AAM39841.
XX
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
XX as central nervous system injuries.
XX
XX Claim 1; SEQ ID NO 1200; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and the
XX encoded polypeptides (AAM38642-AAM42213) with nootropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: Immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemias and
XX C.N.S disorders. Note: The sequence data for this patent did not form
XX part of the printed specification

Sequence 1948 BP; 614 A; 335 C; 436 G; 563 T; 0 U; 0 Other;
Query Match 98.8%; Score 1897.6; DB 4; Length 1948;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1900; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 15 GGAAGATGGAGTTGGGAGTTGCTTGGAGGCGGAGGAGGCGCGGAGGAGGCGG 74
Db 34 GGAAGATGGAGTTGGGAGTTGCTTGGAGGCGGAGGAGGCGCGGAGGAGGCGG 93
QY 75 AGCCTGAGGTGAAAAGGGGCGACTTCTGTGTGTGGAGTTTGGCTCCGACGCTCGG 134
Db 94 AGCCTGAGGTGAAAAGGGGCGACTTCTGTGTGTGGAGTTTGGCTCCGACGCTCGG 153
QY 135 ATGCGGAGTGGCTCAGTGTCTTCTGCGCCGAGAACGACTGGGAGATGGAAGGGGCTCTGA 194
Db 154 ATGCGGAGTGGCTCAGTGTCTTCTGCGCCGAGAACGACTGGGAGATGGAAGGGGCTCTGA 213
QY 195 ACTCTACTTTCAGCGCTCCGCTGGAGGAGAGCGCTTGGAAACGCGGACCTGAAACCATCT 254
Db 214 ACTCTACTTTCAGCGCTCCGCTGGAGGAGAGCGCTTGGAAACGCGGACCTGAAACCATCT 273
QY 255 CTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACCACTGATTCACCACTTCTTA 314
Db 274 CTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACCACTGATTCACCACTTCTTA 333
QY 315 AAATCAGCCCATCTGAAGATACTCAGCAAGAAAATGGCAGCATGTTCTCTCTCATTAACCT 374
Db 334 AAATCAGCCCATCTGAAGATACTCAGCAAGAAAATGGCAGCATGTTCTCTCTCATTAACCT 393
QY 375 GGAATATTGATGGATTAGATCTAAACAATCTGTCTCAGAGAGGCTCGAGGGGTGTTCCT 434
Db 394 GGAATATTGATGGATTAGATCTAAACAATCTGTCTCAGAGAGGCTCGAGGGGTGTTCCT 453
QY 435 ACTTAGCTTTGTACAGCCGAGATCTGATATTTCTACAGGAAGTTATTTCCCCCATATTATA 494
Db 454 ACTTAGCTTTGTACAGCCGAGATCTGATATTTCTACAGGAAGTTATTTCCCCCATATTATA 513
QY 495 GCTACCTAAAGAGAGATCAAGTAAATATGAGATTATTTACAGGTCATGAAGAAGGATATT 554
Db 514 GCTACCTAAAGAGAGATCAAGTAAATATGAGATTATTTACAGGTCATGAAGAAGGATATT 573
QY 555 TCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAGCCCAAGAGATTATTCCTT 614
Db 574 TCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAGCCCAAGAGATTATTCCTT 633
QY 615 TTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGTCATGTGAATGTGTTCAGGAATG 674
Db 634 TTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGTCATGTGAATGTGTTCAGGAATG 693
QY 675 AGCTTTGCTTTATGACATCCCATTTGGAGAGCACAGAGGCGCATGCTGCGGAAACGAATGA 734
Db 694 AGCTTTGCTTTATGACATCCCATTTGGAGAGCACAGAGGCGCATGCTGCGGAAACGAATGA 753
QY 735 ATCAGTTTAAAAATGGTTTTTAAAGAAAATGCAAGAGGCTCCAGAGTCAGTACAGTTATAT 794
Db 754 ATCAGTTTAAAAATGGTTTTTAAAGAAAATGCAAGAGGCTCCAGAGTCAGTACAGTTATAT 813
QY 795 TTGAGAGAGATCAAAATCTAAGGATCGAGAGTTTACAGATGTGGTGTGTTCACCAACA 854
Db 814 TTGAGAGAGATCAAAATCTAAGGATCGAGAGTTTACAGATGTGGTGTGTTCACCAACA 873
QY 855 ACATTGTGGATGTCTGGAGTTTGGGCAAACTTAAACATTTGCCAGTATACATGGGATA 914
Db 874 ACATTGTGGATGTCTGGAGTTTGGGCAAACTTAAACATTTGCCAGTATACATGGGATA 933
QY 915 CACAAATGAATCTTAATCTTTGGAAATAAATGCTGCTGTGTGTAATCTTGGTTCGTAATAT 974
Db 934 CACAAATGAATCTTAATCTTTGGAAATAAATGCTGCTGTGTGTAATCTTGGTTCGTAATAT 993
QY 975 TTTTCAGAGCAGCAGAGAGAGAGGAGACATTTATTTCCCGAAGTTTGGACCTTCTTGAT 1034
Db 994 TTTTCAGAGCAGCAGAGAGAGGAGACATTTATTTCCCGAAGTTTGGACCTTCTTGAT 1053

whether a mammal will respond or is responding to an anti-cancer agent that modulates cyclin-dependent kinase (cdk) activity. The method comprises measuring the level of one or more biomarkers selected from 2774 biomarkers given in the specification (nucleotide sequence SEQ ID NO:1246 (Genbank EST W28729) is especially preferred). The method of the invention is utilized in a kit for determining or predicting whether patient would be susceptible or resistant to treatment by an agent modulating cdk activity. The invention also describes a method for utilizing individualized genetic profiles for treating diseases and disorders based on patient's response and molecular level, specialized microarrays comprising the biomarkers described, antibodies directed against the biomarkers and a cell culture model to identify biomarkers. The cdk modulator is preferably N-5-[(1,1-Dimethylethyl)-2-oxazolyl]methylthio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-tartaric acid salt. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published pct sequences. This sequence encodes a biomarker used in the method of the invention.			XX		
SQ Sequence 1940 BP; 613 A; 330 C; 439 G; 558 T; 0 U; 0 Other;					
Query Match 99.2%; Score 1905.2; DB 14; Length 1940;					
Best Local Similarity 99.5%; Pred. No. 0;					
Matches 1910; Conservative 0; Mismatches 10; Indels 0; Gaps 0;					
QY	1	GTGCAGAGCGCGCAGGAAGATGAGTTGGGAGTTGCTTGAGGGCGGGAGGGAGCGGC	60		
DB	7	GTGCAGAGCGCGCAGGAAGATGAGTTGGGAGTTGCTTGAGGGCGGGAGGGAGCGGC	66		
QY	61	GGAGGAAGGGCGGAGCCTGAGTGAAGAAAGCGCGACTTCTGTGTGGAGTTGCCTC	120		
DB	67	GGAGGAAGGGCGGAGCCTGAGTGAAGAAAGCGCGACTTCTGTGTGGAGTTGCCTC	126		
QY	121	GGTCCGAAGCTGCGATGCCAGTGGCTCAGTGGCTTCTGCGCGAGAACGACTGGGAGAT	180		
DB	127	GGTCCGAAGCTGCGATGCCAGTGGCTCAGTGGCTTCTGCGCGAGAACGACTGGGAGAT	186		
QY	181	GGAAAGGGCTCTGAATCTCTACTTCGAGCCTCCGGTGGAGGAGCGCCTTGGAAAGCGCG	240		
DB	187	GGAAAGGGCTCTGAATCTCTACTTCGAGCCTCCGGTGGAGGAGCGCCTTGGAAAGCGCG	246		
QY	241	ACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAATGA	300		
DB	247	ACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAATGA	306		
QY	301	TTCCACCACTTCTAAATCAGCCCATCTGAAGTACTCAGCAAGAAATGGCAGCATGTT	360		
DB	307	TTCCACCACTTCTAAATCAGCCCATCTGAAGTACTCAGCAAGAAATGGCAGCATGTT	366		
QY	361	CTCTCTCATTTACCTGGGAATTTGATGGATTAGATCTTAAACAAATCTGTCCAGAGGGCTCG	420		
DB	367	CTCTCTCATTTACCTGGGAATTTGATGGATTAGATCTTAAACAAATCTGTCCAGAGGGCTCG	426		
QY	421	AGGGGTGTGTTCTTACCTTTGTCACGCCAGATGTGATTTCTTACAGGAAGTTAT	480		
DB	427	AGGGGTGTGTTCTTACCTTTGTCACGCCAGATGTGATTTCTTACAGGAAGTTAT	486		
QY	481	TCCCCCATATTTATAGCTTACCTTAAGAGAGATCAAGTAATTTATCAGAGTTATTACAGGTCA	540		
DB	487	TCCCCCATATTTATAGCTTACCTTAAGAGAGATCAAGTAATTTATCAGAGTTATTACAGGTCA	546		
QY	541	TGAAGAGGATATTTTCACAGCTATAATGTTTGAAGAAATCAAGAGTGAATTTAAAGGCCA	600		
DB	547	TGAAGAGGATATTTTCACAGCTATAATGTTTGAAGAAATCAAGAGTGAATTTAAAGGCCA	606		
QY	601	AGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTGAA	660		
DB	607	AGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTGAA	666		
QY	661	TGTCGTAGGAATTCAGCTTTGCTTATGACATCCATTTTGGAGAGCACAGAGGGCATGC	720		
DB	667	CGTGTAGGAATTCAGCTTTGCTTATGACATCCATTTTGGAGAGCACAGAGGGCATGC	726		

QY	721	TGCGGAACGAATGAATCAGTTAAAAATGGTTTTAAAGAAAAATGCAAGAGGCTCCAGAGTC	780
DB	727	TGCGGAACGAATGAATCAGTTAAAAATGGTTTTAAAGAAAAATGCAAGAGGCTCCAGAGTC	786
QY	781	AGCTACAGTTATTTTGCAGGAGATACAAATCTAAGGATCGAGAGTTTACCAGATGTGG	840
DB	787	AGCTACAGTTATTTTGCAGGAGATACAAATCTAAGGATCGAGAGTTTACCAGATGTGG	846
QY	841	TGTTTTACCCACACATTTGTCGAGTCTGGGAGTTTTTGGGCAAACTTAAACATTTGCCA	900
DB	847	TGTTTTACCCACACATTTGTCGAGTCTGGGAGTTTTTGGGCAAACTTAAACATTTGCCA	906
QY	901	GTATACATGGGATACACAAATGAATCTAATCTTGAATAACTGCTGCTTGTAAACTTCG	960
DB	907	GTATACATGGGATACACAAATGAATCTAATCTTGAATAACTGCTGCTTGTAAACTTCG	966
QY	961	TTTTGATCGAAATTTTTTTCAGAGCAGCAGAGAGGGACACATTTATTTCCCGAAGTTT	1020
DB	967	TTTTGATCGAAATTTTTTTCAGAGCAGCAGAGAGGGACACATTTATTTCCCGAAGTTT	1026
QY	1021	GGACCTTCTTGGATTAGAAAACTGGACTGTGTAGATTTCTTAGTGATCCTCTGGGCTCT	1080
DB	1027	GGACCTTCTTGGATTAGAAAACTGGACTGTGTAGATTTCTTAGTGATCCTCTGGGCTCT	1086
QY	1081	TCTGTCAACTTAGATATAATTTGTAATAATGCTTTTCAAGTGTGGGTTTTGCCCCTGATT	1140
DB	1087	TCTGTCAACTTAGATATAATTTGTAATAATGCTTTTCAAGTGTGGGTTTTGCCCCTGATT	1146
QY	1141	GTTTCAAAATACAAATTTTCCACCTTCTGGAAAGGTAGTTTGTGTGGAGGAAATAATGTAC	1200
DB	1147	GTTTCAAAATACAAATTTTCCACCTTCTGGAAAGGTAGTTTGTGTGGAGGAAATAATGTAC	1206
QY	1201	TAGATCATTTGTACAGAAAAACCAACTATGATTTATGTTGTGTTTTTCAGAAATTCACAT	1260
DB	1207	TAGATCATTTGTACAGAAAAACCAACTATGATTTATGTTGTGTTTTTCAGAAATTCACAT	1266
QY	1261	TAAAGATTATGTTTTTAAACGAACATCTCTGCATTCAGATGTGAGGCCATTATA	1320
DB	1267	TAAAGATTATGTTTTTAAACGAACATCTCTGCATTCAGATGTGAGGCCATTATA	1326
QY	1321	TAAAGAGGCGCACAAAGCCTGTACAGAGTTTTCACCGTGTTCACGCTGCCAGCTGATTC	1380
DB	1327	TAAAGAGGCGCACAAAGCCTGTACAGAGTTTTCACCGTGTTCACGCTGCCAGCTGATTC	1386
QY	1381	CAAAAGGTACCCCATTTGCTCTGACTAATGTTTATATTTTCCATTTCAGGCGACCGAAA	1440
DB	1387	CAAAAGGTACCCCATTTGCTCTGACTAATGTTTATATTTTCCATTTCAGGCGACCGAAA	1446
QY	1441	TAGTTAATATTTTAAATAAGTCTTCAAAAGAAAAACATAAGAGATTATTGAGTTCTTGGGA	1500
DB	1447	TAGTTAATATTTTAAATAAGTCTTCAAAAGAAAAACATAAGAGATTATTGAGTTCTTGGGA	1506
QY	1501	CTGGATCCTTTTATTTTCATAGTTTCAGATCATCTTAAATGAAAAATGCCATATCTGCA	1560
DB	1507	CTGGATCCTTTTATTTTCATAGTTTCAGATCATCTTAAATGAAAAATGCCATATCTGCA	1566
QY	1561	GTTAAGTAGATGACAGCTATTTACATCAGACTTGATTTTTTGTTCAGCTAATTCATATTT	1620
DB	1567	GTTAAGTAGATGACAGCTATTTACATCAGACTTGATTTTTTGTTCAGCTAATTCATATTT	1626
QY	1621	GGTAAGNTAATTTGAACCTTATGGCTTAAATTCCTTAACTCCTTTTGTGATTCACTGTT	1680
DB	1627	GGTAAGNTAATTTGAACCTTATGGCTTAAATTCCTTAACTCCTTTTGTGATTCACTGTT	1686
QY	1681	TGTAGTCATGTTGTCAACAGAGGCAAAAGTTTAAAGCTTCATGATGGTTAAAAATCGGTTGAT	1740
DB	1687	TGTAGTCATGTTGTCAACAGAGGCAAAAGTTTAAAGCTTCATGATGGTTAAAAATCGGTTGAT	1746
QY	1741	AGCACCATGGGACATTTTTTTTTTAAACAAATAATGATGATGAGACATAGCCTTTTATGTT	1800
DB	1747	AGCACCATGGGACATTTTTTTTTTAAACAAATAATGATGATGAGACATAGCCTTTTATGTT	1806
QY	1801	TTGCTAATTTGTGAAATGGAATGCTTTTACAGGAAGTAAATGCAAAATTTANTTTTTAAGTGTG	1860

QY 301 TTCCACCCTTCTAAATCAGCCCATCTGAAGATACTCAGCAAGAAATGGCAGCATGTT 360
Db |||||
1533 TTCCACCCTTCTAAATCAGCCCATCTGAAGATACTCAGCAAGAAATGGCAGCATGTT 1592
QY 361 CTCTCTATTACCTGGAATATTGATGGATTAGATCTAAACAATCTGTGAGAGGGCTCG 420
Db |||||
1593 CTCTCTATTACCTGGAATATTGATGGATTAGATCTAAACAATCTGTGAGAGGGCTCG 1652
QY 421 AGGGGTGTCTCTACTTACTAGCTTTGTACAGGCCAGATGTGATTTCTACAGGAAGTTAT 480
Db |||||
1653 AGGGGTGTCTCTACTTACTAGCTTTGTACAGGCCAGATGTGATTTCTACAGGAAGTTAT 1712
QY 481 TCCCCCATATTATAGTACTCTAAGAAGAGATCAAGTAAATTTATGAGATTATTACAGGTCA 540
Db |||||
1713 TCCCCCATATTATAGTACTCTAAGAAGAGATCAAGTAAATTTATGAGATTATTACAGGTCA 1772
QY 541 TGAAGAAGATATTTCACAGCTATTAATGTTGAAGAAATCAAGAGTGAAATTTAAAGGCA 600
Db |||||
1773 TGAAGAAGATATTTCACAGCTATTAATGTTGAAGAAATCAAGAGTGAAATTTAAAGGCA 1832
QY 601 AGAGATTATTCCTTTTCCAAAGTACCAGAAATGATGAGAAACCTTTTATGTGTCATGTGAA 660
Db |||||
1833 AGAGATTATTCCTTTTCCAAAGTACCAGAAATGATGAGAAACCTTTTATGTGTCATGTGAA 1892
QY 661 TGTGTGAGAAATGAGCTTTGCTTTATGACATCCCATTTGGAGAGACACAGAGGGCATGC 720
Db |||||
1893 TGTGTGAGAAATGAGCTTTGCTTTATGACATCCCATTTGGAGAGACACAGAGGGCATGC 1952
QY 721 TCGGAAACGAATGAATCAGTTAAATGTTTAAAGAAATGGAAGAGGCTTCAGAGTC 780
Db |||||
1953 TCGGAAACGAATGAATCAGTTAAATGTTTAAAGAAATGGAAGAGGCTTCAGAGTC 2012
QY 781 AGCTACAGTTATTTTCAGAGGAGATACAAATCTAAGGGATCGAGAGTTTACAGAGTGG 840
Db |||||
2013 AGCTACAGTTATTTTCAGAGGAGATACAAATCTAAGGGATCGAGAGTTTACAGAGTGG 2072
QY 841 TGGTTTACCCAAACATTTGCGAGTCTGCGAGTTTGGGCAAACTTAAACATTTGCCA 900
Db |||||
2073 TGGTTTACCCAAACATTTGCGAGTCTGCGAGTTTGGGCAAACTTAAACATTTGCCA 2132
QY 901 GTATACATGGGATACACAAATGAACTCTAACTCTTGAATACTGCTGTGTTGAACTTCG 960
Db |||||
2133 GTATACATGGGATACACAAATGAACTCTAACTCTTGAATACTGCTGTGTTGAACTTCG 2192
QY 961 TTTTGCATCGAATATTTTTCAGAGCAGCAGCAGAGGAGACATATTCCCCGAGTTT 1020
Db |||||
2193 TTTTGCATCGAATATTTTTCAGAGCAGCAGCAGAGGAGACATATTCCCCGAGTTT 2252
QY 1021 GGACCTTCTTGATTTAGAAAACTGGACTGTGGTAGATTTCTAGTGATCACTGGGGTCT 1080
Db |||||
2253 GGACCTTCTTGATTTAGAAAACTGGACTGTGGTAGATTTCTAGTGATCACTGGGGTCT 2312
QY 1081 TCTGTGCAACTTAGATATAAATTTGTAATAATGCTTTTCAAGTGTGGGTTTGGCCCTGATT 1140
Db |||||
2313 TCTGTGCAACTTAGATATAAATTTGTAATAATGCTTTTCAAGTGTGGGTTTGGCCCTGATT 2372
QY 1141 GTTGCAAATACAAATTTCCACCTTCTGGAAGGTAGGTTTGTGTCGAGGAAATATGTAC 1200
Db |||||
2373 GTTGCAAATACAAATTTCCACCTTCTGGAAGGTAGGTTTGTGTCGAGGAAATATGTAC 2432
QY 1201 TAGATCATTTGTACAGAAAAACCACTATGATTTATGTTGTGTTTTCAGAAATTCACAT 1260
Db |||||
2433 TAGATCATTTGTACAGAAAAACCACTATGATTTATGTTGTGTTTTCAGAAATTCACAT 2492
QY 1261 TAAAGATTAAATTTTAAACGAACACATTCCTGCAATTCAGGATGTGAGGCCATTAA 1320
Db |||||
2493 TAAAGATTAAATTTTAAACGAACACATTCCTGCAATTCAGGATGTGAGGCCATTAA 2552
QY 1321 TAAAAAGGCAAAAGCCTGTGAGAGTTTTCACCGTGTACAGCTGCCAGCTGGATTC 1380
Db |||||
2553 TAAAAAGGCAAAAGCCTGTGAGAGTTTTCACCGTGTCTTATAGCTGCCAGCTGGATTC 2612

QY 1381 CAAACAGGTACCCCATTTGCTCTGAGCTAAATGTTTATATTTTCCATTCCAGCACCGAAA 1440
Db |||||
2613 CAAACAGGTACCCCATTTGCTCTGAGCTAAATGTTTATATTTTCCATTCCAGCACCGAAA 2672
QY 1441 TAGTTAATATTAAATAAGTCTTCAAAAGAAAACATAAGAGATTTATGAGTTCTTGGGA 1500
Db |||||
2673 TAGTTAATATTAAATAAGTCTTCAAAAGAAAACATAAGAGATTTATGAGTTCTTGGGA 2732
QY 1501 CTGAGTCCCTTTATTTTCAATAGTTTCAGATCATCTTAAATGAAAATGCCATGATTTCTGCA 1560
Db |||||
2733 CTGAGTCCCTTTATTTTCAATAGTTTCAGATCATCTTAAATGAAAATGCCATGATTTCTGCA 2792
QY 1561 GTTAAGTAGATGACAGCTATTCTACATCAGACTTTGATTTTTGTGTCAGCTAAATTACATAAT 1620
Db |||||
2793 GTTAAGTAGATGACAGCTATTCTACATCAGACTTTGATTTTTGTGTCAGCTAAATTACATAAT 2852
QY 1621 GGTAAAGTATTAATTTGAAACCTTATGGCTTAAATTCCTTAACTCTTTTGTGATTCATGTT 1680
Db |||||
2853 GGTAAAGTATTAATTTGAAACCTTATGGCTTAAATTCCTTAACTCTTTTGTGATTCATGTT 2912
QY 1681 TGTAGTCAATGTTGTCAACAGAGGCAAAAGTTTAAAGCTTGATGATGTTTAAATCGGTTTCAT 1740
Db |||||
2913 TGTAGTCAATGTTGTCAACAGAGGCAAAAGTTTAAAGCTTGATGATGTTTAAATCGGTTTCAT 2972
QY 1741 AGCACCATGGACATTTTTTTTAAACAAAATAAATGCATGAAGAGACATAGCCTTTTAGTT 1800
Db |||||
2973 AGCACCATGGACATTTTTTTTAAACAAAATAAATGCATGAAGAGACATAGCCTTTTAGTT 3032
QY 1801 TTGCTAATTGTGAATGGAATGCTTTTACAGGAAGTAAATGCAAAATTTTAAAGTGTG 1860
Db |||||
3033 TTGCTAATTGTGAATGGAATGCTTTTACAGGAAGTAAATGCAAAATTTTAAAGTGTG 3092
QY 1861 CTTTAAAGAAAAATATTTTCCCCACAGGAGAAATTTAAATAAAGAAATTTTATTTGGTAA 1919
Db |||||
3093 CTTTAAAGAAAAATATTTTCCCCACAGGAGAAATTTAAATAAAGAAATTTTATTTGTTTA 3151

RESULT 4

ADX06356
ID ADX06356 standard; DNA; 1940 BP.

XX ADX06356;

XX 21-APR-2005 (first entry)

XX Cyclin-dependent kinase modulation biomarker DNA SEQ ID NO 921.

XX cytostatic; cyclin-dependent kinase; cdk; biomarker; gene; ds.

XX Homo sapiens.

XX W02005012875-A2.

XX 10-FEB-2005.

XX 29-JUL-2004; 2004WO-US024424.

XX 29-JUL-2003; 2003US-0490890P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Li M, Rupnow BA, Webster XR, Jackson DG, Wong TW;

XX WPI; 2005-163068/17.

XX P-PSDB; ADX06357.

XX Biomarkers useful for predicting or determining the response of a mammal
to a cancer treatment comprising administration of a modulator of cyclin-
dependent kinase activity.

XX Claim 5; SEQ ID NO 921; 141pp; English.

XX This invention describes a novel method of predicting or determining

Db 812 AGCTACAGTTATATTTGACAGGAGATACAAATCTAAGGATCGAGAGTTTACAGATGCG 871

Qy 841 TGGTTTACCCAAACAATTTGATGTCGAGAGTTTGGGCAACCTAAACATTTGCCA 900

Db 872 TGGTTTACCCAAACAATTTGATGTCGAGAGTTTGGGCAACCTAAACATTTGCCA 931

Qy 901 GTATACATGGGATACACAAATGAATCTTAATCTTGGAAATAAAGTCTGCTTGAACCTTCG 960

Db 932 GTATACATGGGATACACAAATGAATCTTAATCTTGGAAATAAAGTCTGCTTGAACCTTCG 991

Qy 961 TTTTGTGATCGAATATTTTTCAGAGCAGCAGCAGAGAGGACACATTAATTCCTCCGAGTTT 1020

Db 992 TTTTGTGATCGAATATTTTTCAGAGCAGCAGCAGAGAGGACACATTAATTCCTCCGAGTTT 1051

Qy 1021 GGACCTTCTTGGATTAGAAAACTGGACTGTGTGATAGTTTCTTGTAGTATCTTGTGGGTTT 1080

Db 1052 GGNCTTCTTGGATTAGAAAACTGGACTGTGTGATAGTTTCTTGTAGTATCTTGTGGGTTT 1111

Qy 1081 TCTGTGCAATTTAGATATTAATATTTGTAATAATGCTTTTCAAGTGTGGGTTTGGCCTGATT 1140

Db 1112 TCTGTGCAATTTAGATATTAATATTTGTAATAATGCTTTTCAAGTGTGGGTTTGGCCTGATT 1171

Qy 1141 GTTGCAAATACAAATTTCCACCTTCTGAAAGGTAGGTTTGTCTGTGAGGAAATAATGTAC 1200

Db 1172 GTTGCAAATACAAATTTCCACCTTCTGAAAGGTAGGTTTGTCTGTGAGGAAATAATGTAC 1231

Qy 1201 TAGATCAATTTGTACAGAAAAACCAACTATGATTTATGTTTGTGTTTTCAGAAATCAACAT 1260

Db 1232 TAGATCAATTTGTACAGAAAAACCAACTATGATTTATGTTTGTGTTTTCAGAAATCAACAT 1291

Qy 1261 TAAAGATTAATGTTTATTAACAGAACACATCTCTGCAATCAGGATGTAGGCAATTTAA 1320

Db 1292 TAAAGATTAATGTTTATTAACAGAACACATCTCTGCAATCAGGATGTAGGCAATTTAA 1351

Qy 1321 TAAAGGGCACAAAGCCTCTCAGAGTTTCAAGGTGCTTACAGCTGCCAGCTGATTC 1380

Db 1352 TAAAGGGCACAAAGCCTCTCAGAGTTTCAAGGTGCTTACAGCTGCCAGCTGATTC 1411

Qy 1381 CAAACAGGTACCCCATTTCTCTGAGCTAATGTTTATTTATTTTCCATTCAGGCCACCGAA 1440

Db 1412 CAAACAGGTACCCCATTTCTCTGAGCTAATGTTTATTTTCCATTCAGGCCACCGAA 1471

Qy 1441 TAGTTAATTTAAATTAAGTCTTCAAAAGAAACATAAGAGATTAATGAGTTCTTGGGA 1500

Db 1472 TAGTTAATTTAAATTAAGTCTTCAAAAGAAACATAAGAGATTAATGAGTTCTTGGGA 1531

Qy 1501 CTGATCCTTTATTTCAATAGTTTCAAGTATCTTAAATGAATGCCATGATTAATCTGCA 1560

Db 1532 CTGATCCTTTATTTCAATAGTTTCAAGTATCTTAAATGAATGCCATGATTAATCTGCA 1591

Qy 1561 GTTAAGTAGATGACAGCTATTTCTACATCAGACTTGATTTTGTGAGCTAATTAATTAAT 1620

Db 1592 GTTAAGTAGATGACAGCTATTTCTACATCAGACTTGATTTTGTGAGCTAATTAATTAAT 1651

Qy 1621 GGTAAAGTATAATTTGAAACCTTATGCTTAAATTCCTTAACTCTCTTTTGTATTCATGTT 1680

Db 1652 GGTAAAGTATAATTTGAAACCTTATGCTTAAATTCCTTAACTCTCTTTTGTATTCATGTT 1711

Qy 1681 TGTAGTCAATGTTTCAACAGAGGCAAGTTTAAAGCTTCATGATGTTTAAATTCGGTTTGTAT 1740

Db 1712 TGTAGTCAATGTTTCAACAGAGGCAAGTTTAAAGCTTCATGATGTTTAAATTCGGTTTGTAT 1771

Qy 1741 AGCACCATGGGACATTTTAAACAAAATAAATGTCATGAAGAGACATAGCCTTTTATGTT 1800

Db 1772 AGCACCATGGGACATTTTCTAACAAAATAAATGTCATGAAGAGACATAGCCTTTTATGTT 1831

Qy 1801 TTGCTAATTTGTAATGGAATGCTTTTACAGGAAGTAAATGCAAAATTAATTTTAAAGTGTG 1860

Db 1832 TTGCTAATTTGTAATGGAATGCTTTTACAGGAAGTAAATGCAAAATTAATTTTAAAGTGTG 1891

Qy 1861 CTTTAAAGAAAATATTTTCCACAGAGGAAATTTAAATAAGAAATTTTATTTTGGTAAA 1920

Db 1892 CTTTAAAGAAAATATTTTCCACAGAGGAAATTTAAATAAGAAATTTTATTTTGGTAAA 1951

RESULT 3

ADA10970
ID ADA10970 standard; cDNA; 3152 BP.

XX
AC ADA10970;

XX
DT 06-NOV-2003 (first entry)

XX
DE Human cDNA differentially expressed in colon cancer #60.

XX
KW ss; differential expression; colon cancer; cancer; human.

XX
OS Homo sapiens.

XX
PN US2002160382-A1.

XX
PD 31-OCT-2002.

XX
PF 11-OCT-2001; 2001US-00981353.

XX
PR 11-OCT-2000; 2000US-0239841P.

XX
(LASE/) LASEK A W.

PA (JONE/) JONES D A.

XX
Lasek AW, Jones DA;

XX
WPI; 2003-265756/26.

XX
PT New combination comprising cDNAs that are differentially expressed in colon disorder, useful for diagnosing, treating, staging or monitoring treatment for colon cancers.

XX
PS Claim 1; SEQ ID NO 88; 231pp; English.

XX
CC The invention relates to a combination comprising cDNAs that are differentially expressed in colon disorder. The methods and compositions of the present invention are useful for diagnosing, treating, staging or monitoring treatment for colon cancer. They are also useful in high throughput methods for using cDNAs to detect differential expression of nucleic acids in a sample, screening molecules or compounds to identify a ligand which specifically binds a cDNA and using a protein to screen molecules or compounds to identify at least one ligand which specifically binds the protein. The present sequence represents a human cDNA differentially expressed in colon cancer.

XX
SQ Sequence 3152 BP; 875 A; 643 C; 707 G; 926 T; 0 U; 1 Other;

Query Match 99.4%; Score 1909; DB 9; Length 3152;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1912; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GTCCAGAGCGCGCAGGAAGATGAGTTGGGAGTTGCTCGAGGGCGGAGGAGGCGGC 60
Db 1233 GTGCAGAGCGCGCAGGAAGATGAGTTGGGAGTTGCTCGAGGGCGGAGGAGGCGGC 1292

Qy 61 GGAGGAAGAGCGCGAGCCTGAGGTGAAAAAGCGCGACTTCTGTGTGTGAGTTTGCTC 120
Db 1293 GGAGGAAGAGCGCGAGCCTGAGGTGAAAAAGCGCGACTTCTGTGTGTGAGTTTGCTC 1352

Qy 121 GGTGCGAAGCTGCGATGCCCGAGTGGCTCAGTGTCTTCTGCGCGAGAACGACTGGGAGAT 180
Db 1353 GGTGCGAAGCTGCGATGCCCGAGTGGCTCAGTGTCTTCTGCGCGAGAACGACTGGGAGAT 1412

Qy 181 GGAAAGGGCTCTGAATCTTCTACTTTCGAGCTCCGTTGAGAGAGCGCCTTGGAAACGCGC 240
Db 1413 GGAAAGGGCTCTGAATCTTCTACTTTCGAGCTCCGTTGAGAGAGCGCCTTGGAAACGCGC 1472

Qy 241 ACCTGAAACCATCTCTGAGGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACCTGA 300
Db 1473 ACCTGAAACCATCTCTGAGGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACCTGA 1532

385	38.8	2.0	15574	6	ABL70513	Chemical	Ab170513	458	38.2	2.0	8634	6	ABL33056	Human	Ab133056
386	38.8	2.0	15574	7	AD99737	Bisulphite	Ad99737	459	38.2	2.0	9483	6	ABL32377	Human	Ab132377
387	38.8	2.0	15853	6	ABL70465	Chemical	Ab170465	460	38.2	2.0	9483	6	ABL70516	Chemical	Ab170516
388	38.8	2.0	15853	6	AA561456	Human gen	AA561456	461	38.2	2.0	9483	6	AA561092	Human gen	AA561092
389	38.8	2.0	56153	4	AA546793	Tumour su	AA546793	462	38.2	2.0	16579	10	ADB54246	Pretrate	ADB54246
390	38.8	2.0	61020	4	AA546788	Tumour su	AA546788	463	38.2	2.0	16579	10	ADB54246	Pretrate	ADB54246
391	38.6	2.0	281	3	AA546788	Tumour su	AA546788	464	38.2	2.0	16579	10	ADB54246	Pretrate	ADB54246
392	38.6	2.0	1008	6	ABQ90167	Human sec	Ab27551	465	38.2	2.0	16579	13	ADS89548	Human che	Ad89548
393	38.6	2.0	1008	6	ABQ90167	Human sec	Ab27551	466	38.2	2.0	16579	13	ADS89548	Human che	Ad89548
394	38.6	2.0	1290	11	ACL28457	Rice abio	ACL28457	467	38.2	2.0	16579	13	ADS89548	Human che	Ad89548
395	38.6	2.0	1881	5	ADL63283	Human ova	ADL63283	468	38.2	2.0	33292	6	ABL5203	Human imm	Ab132767
396	38.6	2.0	2801	14	ADV97994	Bisulphite	AdV97994	469	38.2	2.0	110000	12	ADQ97138	AmEPV gen	AD156203
397	38.6	2.0	3189	4	AAH54330	S. epider	AAH54330	470	38.2	2.0	110000	12	ADQ97138	AmEPV gen	AD156203
398	38.6	2.0	4020	13	ADT44734	Bacterial	AdT44734	471	38.2	2.0	113515	6	ABL34175	Human imm	Ab134175
399	38.6	2.0	4164	14	ACL68198	Human imm	Ab168198	472	38.2	2.0	517	13	ACN56273	Cotton an	ACN56273
400	38.6	2.0	6050	6	ABL34011	Human imm	Ab134011	473	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
401	38.6	2.0	6291	6	ABL34038	Human imm	Ab134038	474	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
402	38.6	2.0	6291	6	ABL34038	Human imm	Ab134038	475	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
403	38.6	2.0	6292	4	AA546795	Tumour su	AA546795	476	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
404	38.6	2.0	6343	8	AB210193	Human imm	Ab132917	477	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
405	38.6	2.0	6478	6	ABL32498	Human imm	Ab132498	478	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
406	38.6	2.0	7353	6	ABL32073	Human imm	Ab132073	479	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
407	38.6	2.0	7353	6	ABL32073	Human imm	Ab132073	480	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
408	38.6	2.0	10328	6	ABL33544	Human imm	Ab133544	481	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
409	38.6	2.0	13420	6	ABL32917	Human imm	Ab132917	482	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
410	38.6	2.0	19734	6	ABL33933	Human imm	Ab133933	483	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
411	38.6	2.0	29384	14	ACL64766	Human pro	AbV04482	484	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
412	38.6	2.0	110000	2	AA20248_04	Continuation (5 of	Continuation (5 of	485	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
413	38.6	2.0	116277	2	AA20248_04	Continuation (5 of	Continuation (5 of	486	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
414	38.6	2.0	199878	10	ADL13719	AA20249 Borrelia	AA20249 Borrelia	487	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
415	38.4	2.0	528	4	ABA61310	Human foe	Ab61310	488	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
416	38.4	2.0	528	4	ABA61310	Human foe	Ab61310	489	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
417	38.4	2.0	528	4	ABA61310	Human foe	Ab61310	490	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
418	38.4	2.0	528	4	ABA61310	Human foe	Ab61310	491	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
419	38.4	2.0	528	4	ABA61310	Human foe	Ab61310	492	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
420	38.4	2.0	528	4	ABA61310	Human foe	Ab61310	493	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
421	38.4	2.0	528	4	ABA61310	Human foe	Ab61310	494	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
422	38.4	2.0	972	5	ABV04482	Human pro	AbV04482	495	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
423	38.4	2.0	1194	14	ADZ71076	Human chr	AdZ71076	496	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
424	38.4	2.0	1458	10	ADF09332	Swinepox	AdF09332	497	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
425	38.4	2.0	2131	14	ADZ71009	Human chr	AdZ71009	498	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
426	38.4	2.0	2739	6	ABQ67176	Human ang	AbQ67176	499	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
427	38.4	2.0	3552	10	ADF09331	Swinepox	AdF09331	500	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
428	38.4	2.0	5743	6	ABL34068	Human imm	Ab134068	501	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
429	38.4	2.0	6130	4	AA546722	Tumour su	AA546722	502	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
430	38.4	2.0	6130	4	AA546722	Tumour su	AA546722	503	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
431	38.4	2.0	7127	6	ABL58898	Human gen	Ab158898	504	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
432	38.4	2.0	8990	4	AAK77783	Human imm	Ab177783	505	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
433	38.4	2.0	19634	8	AB210162	Human imm	Ab10162	506	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
434	38.4	2.0	19634	13	ADS89672	Human imm	AdS89672	507	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
435	38.4	2.0	50000	6	ABL55644	AmEPV gen	Ab155644	508	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
436	38.4	2.0	96589	9	ADA02708	Human ZFH	AdA02708	509	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
437	38.4	2.0	96589	10	ADB72446	Human ZFH	AdB72446	510	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
438	38.4	2.0	96589	10	ADB72446	Human ZFH	AdB72446	511	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
439	38.4	2.0	110000	6	ABA92787_5	Continuation (6 of	Continuation (6 of	512	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
440	38.2	2.0	374	10	ADA19391	Human ins	AdA19391	513	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
441	38.2	2.0	1372	13	ADX49898	Plant ful	AdX49898	514	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
442	38.2	2.0	2652	11	ADM01671	Human CDN	AdM01671	515	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
443	38.2	2.0	5033	8	ABZ09999	Haematopo	AbZ09999	516	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
444	38.2	2.0	5236	6	ABL32351	Human imm	Ab132351	517	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
445	38.2	2.0	5682	6	ABL32572	Human imm	Ab132572	518	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
446	38.2	2.0	5682	6	ABL34500	Human met	Ab134500	519	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
447	38.2	2.0	5682	7	AD99761	Bisulphite	Ad99761	520	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
448	38.2	2.0	5822	6	ABL33097	Human imm	Ab133097	521	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
449	38.2	2.0	6311	6	ABL33963	Human imm	Ab133963	522	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
450	38.2	2.0	7165	6	ABL32750	Human imm	Ab132750	523	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
451	38.2	2.0	7165	6	ABL31266	Signal tr	Ab131266	524	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
452	38.2	2.0	7631	6	ABL32860	Human imm	Ab132860	525	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
453	38.2	2.0	8033	4	AA546307	Tumour su	AA546307	526	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
454	38.2	2.0	8033	4	AA546307	Tumour su	AA546307	527	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
455	38.2	2.0	8033	6	ABL70169	Chemical	Ab170169	528	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
456	38.2	2.0	8033	6	ABL70169	Chemical	Ab170169	529	38.2	2.0	558	4	ABA61834	Human foe	Ab61834
457	38.2	2.0	8033	6	AA561116	Human gen	AA561116	530	38.2	2.0	558	4	ABA61834	Human foe	Ab61834

ALIGNMENTS

RESULT 1

AAZ47118	AAZ47118 standard; cDNA; 1920 BP.
XX	AAZ47118;
AC	AAZ47118;
XX	15-MAR-2000 (first entry)
DT	Human CD40 receptor associated protein gene.
DE	Human CD40 receptor associated protein gene.
XX	Antiarteriosclerotic; antiarthritic; neuroprotective; dermatological;
KW	immunosuppressive; antinflammatory; immunosuppressive; antiallergic;
KW	human; CD40 receptor associated protein; CRAP; cytoplasmic domain;
KW	tumour necrosis factor; TNF; receptor; superfamily; CD30; homology;
KW	TNF receptor associated factor; TRAF; modulator; signalling pathway;
KW	diagnosis; NF-kappaB; Jun; kinase; atherosclerosis; multiple sclerosis;
KW	arthritis; systemic lupus erythematosus; graft rejection; allergy;
XX	graft versus host disease; autoimmune disease; ds.
OS	Homo sapiens.
XX	WO9955859-A2.
PN	04-NOV-1999.
XX	
PD	
XX	

239	2.1	17897	13	ADS89602	Adg89602 Oligonucl
240	40.8	2.1	1884	3	Aac77846 Human can
241	40.8	2.1	2650	14	Ady84712 Mouse neu
242	40.8	2.1	3730	11	ACN92489
243	40.8	2.1	6182	6	ABL49388 Human pol
244	40.8	2.1	6431	6	Abq67119 Human ang
245	40.8	2.1	6432	4	Aas46557 Tumour su
246	40.8	2.1	6432	10	ADBS4161 Pretreat
247	40.8	2.1	6432	10	ADBS4123 Human lym
248	40.8	2.1	6432	13	ADS89315
249	40.8	2.1	8889	6	ABL32210 Human inm
250	40.8	2.1	16914	6	ABL70315 Chemicall
251	40.8	2.1	16914	6	AS61253 Human gen
252	40.8	2.1	29993	10	ADBS37663 Human che
253	40.8	2.1	110000	13	ADBS32968 ⁶ Continuation (7 of
254	40.8	2.1	113306	10	ADC86554 Human gfc
255	40.8	2.1	235033	2	AAV57926 Hereditar
256	40.6	2.1	4984	3	AAV57926
257	40.6	2.1	6132	6	ABL32862 Human inm
258	40.6	2.1	129021	3	AAF22296 BAC conta
259	40.4	2.1	1428	14	Aah24065 Yeast AOD
260	40.4	2.1	4590	5	AAH24065
261	40.4	2.1	6013	6	ABK31361 Signal tr
262	40.4	2.1	6013	6	AS61255 Human gen
263	40.4	2.1	6270	6	ABL33872 Human inm
264	40.4	2.1	8951	6	ABL32795 Human inm
265	40.4	2.1	9810	6	ABL32426 Human inm
266	40.4	2.1	10957	6	ABL33110 Human inm
267	40.4	2.1	11691	6	ABL34240 Human inm
268	40.4	2.1	19380	6	AS61427 Human gen
269	40.2	2.1	2501	14	ADV98088 Bisulfite
270	40.2	2.1	2880	11	Adm01653 Human cdn
271	40.2	2.1	17293	6	Abk31171 Signal tr
272	40.2	2.1	17293	6	Abi70126 Chemicall
273	40.2	2.1	17293	6	AS61058 Human gen
274	40	2.1	570	5	ADL38113 Human ova
275	40	2.1	570	5	ADI72977 Human ova
276	40	2.1	5324	6	ABL33791 Human inm
277	40	2.1	6210	6	ABK28471 DNA trans
278	40	2.1	6220	6	ABL33300 Human inm
279	40	2.1	7508	6	ABK31207 Signal tr
280	40	2.1	8537	6	ABL92267 Chemicall
281	40	2.1	8537	6	ABL49342 Human pol
282	40	2.1	10329	6	ABL34122 Human inm
283	40	2.1	15951	6	ABL33680 Human inm
284	40	2.1	15951	6	ABL34580 Human met
285	40	2.1	15951	6	ABL70373 Chemicall
286	40	2.1	15951	7	ADS99841 Bisulphit
287	40	2.1	40681	6	Continuation (7 of
288	40	2.1	110000	6	Continuation (6 of
289	39.8	2.1	2529	13	ADX60260 Plant ful
290	39.8	2.1	6327	4	AS45445 Chemicall
291	39.8	2.1	6327	6	ABK28294 DNA trans
292	39.8	2.1	7047	6	ABK28385 Human inm
293	39.8	2.1	9268	6	ABL33600 Chemicall
294	39.8	2.1	34548	6	ABQ67060 Human ang
295	39.8	2.1	34688	6	ABQ67060 Human inm
296	39.8	2.1	35962	8	ABZ09958 Human met
297	39.8	2.1	35962	8	ABZ09958 Chemicall
298	39.8	2.1	37007	12	ADL98341
299	39.6	2.1	1620	10	ADJ99891 Potato sa
300	39.6	2.1	1620	14	ADJ99891 Potato sa
301	39.6	2.1	2987	13	ADS89604 Oligonucl
302	39.6	2.1	5706	6	ABL70598 Chemicall
303	39.6	2.1	5706	6	AS61319 Human gen
304	39.6	2.1	5987	10	ADBS4308 Pretreat
305	39.6	2.1	8334	10	ADF01667 Bacterial
306	39.6	2.1	9157	6	ABL33500 Human inm
307	39.6	2.1	12138	6	ABL33943 Human inm
308	39.6	2.1	12138	6	ABK28336 DNA trans
309	39.6	2.1	17534	6	ABK40025 Human che
310	39.6	2.1	50000	6	ABL5843 AmEPV gen
311	39.6	2.1	78082	12	ADQ97968 Human can

312	39.6	2.1	163382	13	ABD32659
313	39.4	2.1	1452	14	ADZ71095 Human can
314	39.4	2.1	6361	6	ABL33140 Human inm
315	39.4	2.1	6816	12	ADQ24856 Human sof
316	39.4	2.1	9953	4	ABK42449 Genomic s
317	39.4	2.1	9953	9	ADBS60605 Connectiv
318	39.4	2.1	11189	4	ABK42448 Genomic s
319	39.4	2.1	11189	9	ADB60604 Connectiv
320	39.4	2.1	11996	6	ABL34493 Human met
321	39.4	2.1	11996	7	ADS99754 Complemen
322	39.4	2.1	12610	13	ADS89699 Oligonucl
323	39.4	2.1	12610	13	ADS89425 Oligonucl
324	39.4	2.1	12639	6	ABN80107 Human che
325	39.4	2.1	13131	6	ABL92248 Chemicall
326	39.4	2.1	110000	11	ACN43998 ⁵ Continuation (2 of
327	39.4	2.1	110000	13	Continuation (4 of
328	39.4	2.1	110000	13	ADBS32629 ¹ Continuation (2 of
329	39.2	2.0	3716	8	ABZ10212 Haematopo
330	39.2	2.0	5371	6	ABL33186 Human inm
331	39.2	2.0	6432	10	ADB54289 Pretreat
332	39.2	2.0	6432	10	ADBS4199 Human lym
333	39.2	2.0	6432	13	ADS89589 Oligonucl
334	39.2	2.0	6794	6	ABK31264 Signal tr
335	39.2	2.0	6794	6	ABi70219 Chemicall
336	39.2	2.0	6794	6	AS61174 Human gen
337	39.2	2.0	8047	6	AAK66981 Human inm
338	39.2	2.0	13131	6	ABL92249 Chemicall
339	39.2	2.0	16258	6	ABK40038 Human che
340	39.2	2.0	16258	6	ABL70376 Chemicall
341	39.2	2.0	18155	6	ABK38808 CODR4 ORF
342	39.2	2.0	19087	6	ABL32793 Human inm
343	39.2	2.0	91552	6	ABL32793 BAC clone
344	39.2	2.0	151826	3	AAF22291
345	39.2	2.0	681	6	ABQ58837 Human col
346	39	2.0	1444	3	Aaz94422 Plasmodiu
347	39	2.0	5917	6	AAZ94422 Plasmodiu
348	39	2.0	6325	8	ABZ10232 Haematopo
349	39	2.0	7849	6	ABL92278 Chemicall
350	39	2.0	7849	6	ABZ22329 Chemicall
351	39	2.0	8056	8	ABZ10100 Haematopo
352	39	2.0	9204	6	ABL33129 Human inm
353	39	2.0	9204	6	ABK31293 Chemical tr
354	39	2.0	9204	6	ABL70270 Chemicall
355	39	2.0	9204	6	AS61195 Human gen
356	39	2.0	9499	6	ABL32585 Human inm
357	39	2.0	9888	6	ABL33240 Human inm
358	39	2.0	15479	6	ABK39965 Human che
359	39	2.0	17848	4	AS45323 Chemicall
360	39	2.0	17848	6	ABK28164 DNA trans
361	39	2.0	50000	6	ABK28164 AmEPV gen
362	39	2.0	54081	11	ACN44726 Human gen
363	39	2.0	63588	8	ABS57150 Human gen
364	39	2.0	357	4	AAI81967 Human pol
365	39	2.0	357	4	AAI81967 Bovine ES
366	38.8	2.0	333	8	ABX39417 Staphyloc
367	38.8	2.0	1296	13	ADSO4425 Plant ful
368	38.8	2.0	1380	13	ADX11686 Plant ful
369	38.8	2.0	1750	13	ADX114558 Arabidops
370	38.8	2.0	2000	6	ABZ16325 Human inm
371	38.8	2.0	6062	6	ABL34078 Human inm
372	38.8	2.0	6070	6	ABL32241 Human inm
373	38.8	2.0	6070	6	ABL92199 Chemicall
374	38.8	2.0	6070	6	ABL49310 Human pol
375	38.8	2.0	6963	6	ABL32979 Human inm
376	38.8	2.0	7319	6	ABL34044 Human inm
377	38.8	2.0	9832	6	ABL32656 Human inm
378	38.8	2.0	12405	4	AS45331 Chemicall
379	38.8	2.0	12405	4	ABK28170 DNA trans
380	38.8	2.0	12405	6	AAK61144 Human gen
381	38.8	2.0	15500	4	AS46507 Tumour su
382	38.8	2.0	15674	6	ABL32362 Human inm
383	38.8	2.0	15674	6	ABL32362 Human met
384	38.8	2.0	15674	6	ABL34476 Human met

93 46.4 2.4 18154 6 ABL32255 Human imm
94 46.2 2.4 3586 6 AAS63367 Human
95 45.8 2.4 2580 6 ABK33947 Human DNA
96 45.8 2.4 2580 8 ADA20403 Prostate
97 45.8 2.4 2580 8 ADA84210 Human ren
98 45.8 2.4 5376 6 ABL34150 Human imm
99 45.6 2.4 237326 2 AAV57903 Hereditar
100 45.4 2.4 6036 6 ABK31308 Signal tr
101 45.4 2.4 8056 8 ABZ10246 Haematopo
102 45.4 2.4 20486 6 ABL34611 Human met
103 45.4 2.4 20486 7 ADS99872 Complemen
104 45 2.3 858 11 ACN85885 Breast ca
105 45 2.3 2355 14 ADM10541 Colon pro
106 44.8 2.3 1452 14 ADZ71095
107 44.6 2.3 3315 14 ADW71859
108 44.6 2.3 6106 4 AAS46429
109 44.6 2.3 6106 6 ABK40031
110 44.6 2.3 6106 6 ABL33472 Human imm
111 44.4 2.3 26997 4 AAS46748
112 44.2 2.3 5445 4 AAS46595 Tumour su
113 44.2 2.3 6681 6 ABL32155
114 44.2 2.3 6681 6 ABL54304
115 44.2 2.3 7644 6 ABL32531 Human imm
116 43.8 2.3 2000 11 ACL37108
117 43.8 2.3 2486 3 AAR97037
118 43.8 2.3 9483 6 ABL32376
119 43.8 2.3 9483 6 ABL70515
120 43.8 2.3 9483 6 AAS61091 Human gen
121 43.6 2.3 437 8 ABX47670 Bovine ES
122 43.6 2.3 6191 6 ABL33217 Human imm
123 43.6 2.3 6191 6 ABK31307 Signal tr
124 43.6 2.3 6191 6 ABL70282 Chemical
125 43.6 2.3 6191 6 ABN80161 Human che
126 43.6 2.3 12610 13 ADS89700
127 43.6 2.3 12610 13 ADS89426
128 43.6 2.3 18218 6 ABL33949
129 43.4 2.3 5641 6 ABL33397
130 43.4 2.3 6075 6 ABL70595
131 43.4 2.3 6075 6 AAS61316 Human gen
132 43.4 2.3 6123 6 ABL32821
133 43.4 2.3 11812 4 AAS45502
134 43.4 2.3 11812 4 AAS46742 Tumour su
135 43.4 2.3 11812 6 ABL34119 Human imm
136 43.4 2.3 11812 6 ABK28432 DNA trans
137 43.4 2.3 17183 6 ABL32486 Human imm
138 43.2 2.3 7001 6 ABK33920 Human DNA
139 43.2 2.3 7001 8 ADA20395
140 43.2 2.3 7001 8 ADA84202 Human ren
141 43.2 2.3 17538 6 ABL33157 Human imm
142 43.2 2.3 29544 2 AAT12460 Ovine ade
143 43.2 2.3 158001 12 ADL17884
144 43.2 2.3 335913 5 AAL61371 Soybean 2
145 43.2 2.3 335913 5 AAL61372 Soybean 2
146 43 2.2 14752 2 AAX20256 Borrelia
147 42.8 2.2 1062 10 ACC61218 Gene sequ
148 42.8 2.2 1062 10 ADK63203 Disease t
149 42.8 2.2 110000 6 ABA92787 Buchnera
150 42.6 2.2 2745 12 ADI00905 Human muc
151 42.6 2.2 372 14 ADX05735 Cyclin-de
152 42.6 2.2 6092 6 AAS61079 Human gen
153 42.6 2.2 7849 6 ABL92279 Chemical
154 42.6 2.2 7849 6 ADI22330 Chemical
155 42.6 2.2 22773 12 ADI00878
156 42.4 2.2 1174 6 ABZ15348 Arabidops
157 42.4 2.2 6467 6 ABN80168 Human che
158 42.4 2.2 8056 8 ABZ10100 Haematopo
159 42.4 2.2 9110 4 AAS46394 Tumour su
160 42.4 2.2 14041 4 AAH48024 Internal
161 42.4 2.2 29993 10 ADB37661
162 42.4 2.2 38342 4 AAS46746
163 42.4 2.2 38342 6 ABK31507 Signal tr
164 42.2 2.2 543 13 ACN57427 Cotton gy
165 42 2.2 2131 14 ADZ71009 Human chr

166 42 2.2 17234 6 ABQ67018
167 41.8 2.2 2000 11 ACL35363
168 41.8 2.2 2676 5 ABV23194 Human pro
169 41.8 2.2 2676 5 ABV22761 Human pro
170 41.8 2.2 2676 5 ABV28586 Human pro
171 41.8 2.2 2676 5 ABV29031 Human pro
172 41.8 2.2 2950 13 ADV35046 Human CDN
173 41.8 2.2 2950 13 ADV35045 Human CDN
174 41.8 2.2 2970 12 ADQ15135 Human can
175 41.8 2.2 3051 6 ABN95793 Gene #229
176 41.8 2.2 3051 13 ADR25274 Breast ca
177 41.8 2.2 3051 13 ACN39086 Tumour-as
178 41.8 2.2 3051 14 ADX05731 Cyclin-de
179 41.8 2.2 3051 14 ADZ48933 Insulin s
180 41.8 2.2 3100 5 AAS77181 DNA encod
181 41.8 2.2 3100 10 ADC32478 Human nov
182 41.8 2.2 3203 12 ADE77173 Human CDN
183 41.8 2.2 3239 6 ABL339757 Human NS
184 41.8 2.2 5421 6 ABL32133 Human imm
185 41.8 2.2 6350 6 ABK31198 Signal tr
186 41.8 2.2 6350 6 ABL70165 Chemical
187 41.8 2.2 6350 6 AAS61110 Human gen
188 41.8 2.2 6925 6 ABL33388 Human imm
189 41.8 2.2 7304 6 ABL92269 Chemical
190 41.8 2.2 7304 6 ABL49344 Human pol
191 41.8 2.2 8056 8 ABZ10246 Haematopo
192 41.8 2.2 8992 6 ABK31421 Signal tr
193 41.8 2.2 10183 4 AAS46751 Tumour su
194 41.8 2.2 12393 6 ABL33263 Human imm
195 41.8 2.2 12405 4 AAS45330 Chemical
196 41.8 2.2 12405 6 ABK28169 DNA trans
197 41.8 2.2 12405 6 AAS61143 Human gen
198 41.8 2.2 19380 6 AAS61426 Human gen
199 41.8 2.2 50000 6 ABL55644 AmEPV gen
200 41.6 2.2 1524 14 ADZ70897 Human mat
201 41.6 2.2 2000 11 ACL35887 Rice stre
202 41.6 2.2 4660 14 ADZ70902 Human mat
203 41.6 2.2 6158 8 AAS45318 Chemical
204 41.6 2.2 6158 6 ABK28157 DNA trans
205 41.6 2.2 6179 4 AAS46343 Tumour su
206 41.6 2.2 6179 6 ABK31250 Signal tr
207 41.6 2.2 9733 6 ABL32683 Human imm
208 41.6 2.2 11745 6 ABK28332 DNA trans
209 41.6 2.2 15667 6 ABL34146 Human imm
210 41.6 2.2 50000 6 ABL55643 AmEPV gen
211 41.4 2.2 5033 8 ABZ10145 Haematopo
212 41.4 2.2 8423 6 ABL33407 Human imm
213 41.4 2.2 9742 6 ABL70479 Chemical
214 41.4 2.2 15479 6 ABK39964 Human che
215 41.2 2.1 472 5 ADI73113 Human ova
216 41.2 2.1 472 5 ADL38246 Human ova
217 41.2 2.1 644 14 ADZ71032 Human chr
218 41.2 2.1 1551 10 ADC93875 E. faeciu
219 41.2 2.1 1649 8 ADA72310 Rice gene
220 41.2 2.1 1710 12 ADO62844 Transcrip
221 41.2 2.1 6074 6 ABL33064 Human imm
222 41.2 2.1 7348 4 AAS46335 Tumour su
223 41.2 2.1 18683 6 ABL32312 Human imm
224 41.2 2.1 18683 6 ABL54333 Chemical
225 41.2 2.1 50000 6 ABL56202 AmEPV gen
226 41 2.1 937 6 ABQ28420 Oligonucle
227 41 2.1 937 6 ABQ28421 Oligonucle
228 41 2.1 1481 4 AAF57223 A. niger
229 41 2.1 1481 10 ADA48124 Aspergill
230 41 2.1 5518 6 ABK28306 DNA trans
231 41 2.1 5768 6 ABK31192 Signal tr
232 41 2.1 5768 6 ABL70517 Chemical
233 41 2.1 5768 6 AAS61105 Human gen
234 41 2.1 10988 6 ABK31245 Signal tr
235 41 2.1 10988 6 ABL70200 Chemical
236 41 2.1 10988 6 AAS61158 Human gen
237 41 2.1 17137 6 ABL32191 Human imm
238 41 2.1 17897 10 ADB54306 Pretreat

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 06:13:56 ; Search time 1180.27 Seconds
(without alignments)
10841.779 Million cell updates/sec

Title: US-10-757-745-1
Perfect score: 1920
Sequence: 1 gtgcagagcgccaggaaga.....aaagaattttatttggtataa 1920

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :		N_Geneseq_21.*	
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		5: Geneseqn2001bs.*	
		6: Geneseqn2002s.*	
		7: Geneseqn2002bs.*	
		8: Geneseqn2003s.*	
		9: Geneseqn2003bs.*	
		10: Geneseqn2003cs.*	
		11: Geneseqn2003ds.*	
		12: Geneseqn2004s.*	
		13: Geneseqn2004bs.*	
		14: Geneseqn2005s.*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
1	1918	99.9	1920	3	Az47118 Human CD4
2	1910	99.5	1958	4	Aa160783 Human pol
3	1909	99.4	3152	9	Adal0970 Human cDN
4	1905.2	99.2	1940	14	Adx06356 Cyclin-de
5	1897.6	98.8	1948	4	Aa158997 Human pol
6	1897.6	98.8	1948	5	Adq99219 DNA encod
7	1897.6	98.8	1948	9	Adb48979 Novel hum
8	1892.6	98.6	1936	10	Add19013 Human dis
9	1892.6	98.6	1936	13	Adp25361 PRO poly
10	1880	97.9	1898	4	Aa115146 Human cDN
11	1815.4	94.6	2499	2	Aax28153 Topoisome
12	1246.2	64.9	1296	3	Ac98160 Human col
13	1066.4	55.5	1079	2	Aax84209 DNA encod
14	1066.4	55.5	1079	3	Aac79438 cDNA sequ
15	1066.4	55.5	1079	6	Abk28982 Human bre
16	987.2	51.4	1088	5	Aas86254 DNA encod
17	693	36.1	752	4	Aa08073 Human cDN
18	668.2	34.8	1312	3	Aaz47119 Mouse CD4
19	642	33.4	674	11	Adt95548 Colon can

20	642	33.4	674	11	ADX42030	Adx42030 Human cDN
21	611.4	31.8	644	11	ADT95551	Adt95551 Colon can
22	611.4	31.8	644	11	ADX42033	Adx42033 Human cDN
23	606.4	31.6	773	14	ACL60394	Ac160394 Human col
24	600	31.2	633	11	ADT95565	Adt95565 Colon can
25	600	31.2	633	11	ADX42047	Adx42047 Human cDN
26	587	30.6	625	11	ADT95029	Adt95029 Colon can
27	587	30.6	625	11	ADX41511	Adx41511 Human cDN
28	584	30.4	625	11	ADT95512	Adt95512 Colon can
29	584	30.4	625	11	ADX41994	Adx41994 Human cDN
30	513	26.7	579	4	AAH13035	Aa13035 Human cDN
31	512	26.7	553	11	ADT95464	Adt95464 Colon can
32	512	26.7	553	11	ADX41946	Adx41946 Human cDN
33	493	25.7	547	11	ADT96654	Adt96654 Colon can
34	493	25.7	547	11	ADX43136	Adx43136 Human cDN
35	483	25.2	483	2	AAx40590	Aax40590 Human sec
36	445.4	23.2	774	10	ADD34375	Adt34375 Mouse mit
37	410.2	21.4	503	11	ADT94923	Adt94923 Colon can
38	410.2	21.4	503	11	ADX41405	Adx41405 Human cDN
39	405.2	21.1	476	11	ADT94919	Adt94919 Colon can
40	405.2	21.1	476	11	ADX41401	Adx41401 Human cDN
41	404.2	21.1	479	11	ADT95387	Adt95387 Human cDN
42	404.2	21.1	479	11	ADX41869	Adx41869 Human cDN
43	404.2	21.1	483	11	ADT95383	Adt95383 Colon can
44	404.2	21.1	483	11	ADX41865	Adx41865 Human cDN
45	403.2	21.0	425	11	ADT95667	Adt95667 Colon can
46	403.2	21.0	425	11	ADX42149	Adx42149 Human cDN
47	403.2	21.0	482	11	ADT95359	Adt95359 Colon can
48	403.2	21.0	482	11	ADX41841	Adx41841 Human cDN
49	402.8	21.0	408	9	ACH49461	Adt49461 Human leu
50	401.2	20.9	602	10	ADD34376	Adt34376 Mouse mit
51	398.8	20.8	434	11	ADT95036	Adt95036 Colon can
52	398.8	20.8	434	11	ADX41518	Adx41518 Human cDN
53	397	20.7	1227	5	AA86255	DNA encod
54	395.4	20.6	414	13	ADU12462	Adul2462 Solid tum
55	383	19.9	401	11	ADT95844	Adt95844 Colon can
56	383	19.9	401	11	ADX42326	Adx42326 Human cDN
57	295.4	15.4	391	11	ADT95307	Adt95307 Colon can
58	295.4	15.4	391	11	ADX41789	Adx41789 Human cDN
59	268	14.0	268	6	ABT07150	Abt07150 Human ova
60	268	14.0	268	8	ABX73028	Abx73028 Human ova
61	263.6	13.7	275	6	ABL62243	Ab162243 Colon ade
62	263.6	13.7	275	6	ABL68428	Ab168428 Kidney ca
63	263.6	13.7	275	6	ABN94082	Abn94082 Gene #580
64	241.4	12.6	258	2	AAx41008	Aax41008 Human sec
65	189.2	9.9	296	6	ABQ96263	Abq96263 Tumour su
66	177.2	9.2	179	6	ABK36461	Ab136461 Human col
67	176	9.2	176	6	ABV27684	Abv27684 Human pan
68	150.4	7.8	725	6	ABQ34462	Abq34462 Oligonuc1
69	150.4	7.8	725	6	ABQ34463	Abq34463 Oligonuc1
70	99.4	5.2	444	4	AAI15311	Aai15311 Probe #52
71	99.4	5.2	444	4	AAI24484	Aai24484 Probe #14
72	99.4	5.2	691	5	AA869905	DNA encod
73	98	5.1	267	5	AA869905	DNA encod
74	73.6	3.8	725	6	ABQ34465	Abq34465 Oligonuc1
75	73.6	3.8	725	6	ABQ34464	Abq34464 Oligonuc1
76	60	3.1	60	6	ABN41860	Abn41860 Human spl
77	56.8	3.0	17738	6	ABL33539	Ab133539 Human imm
78	56	2.9	2000	11	ACL37108	Ac137108 Rice stre
79	56	2.9	2000	11	ACL35887	Ac135887 Rice stre
80	53.4	2.8	24939	6	ABL70570	Ab170570 Chemical
81	52.2	2.7	2000	11	ACL35363	Ac135363 Rice stre
82	50	2.6	50	6	ABZ00796	Abz00796 Human leu
83	50	2.6	50	6	ABZ03323	Abz03323 Human leu
84	49.6	2.6	6136	6	ABK40042	Abk40042 Tumour su
85	48.8	2.5	7403	4	AA846804	Aa846804 Human che
86	48.8	2.5	7403	6	ABL34217	Ab134217 Human imm
87	48.4	2.5	595	14	AD271053	Adz71053 Human chr
88	48.2	2.5	2000	8	ADA71938	Ada71938 Rice gene
89	47.8	2.5	2000	8	ADA71938	Ada71938 Rice gene
90	47.4	2.5	6092	6	AA861080	Aa861080 Human gen
91	47	2.4	47	3	AAZ68598	Aaz68598 Human map
92	47	2.4	110000	2	AAV21209_06	Continuation (7 of

QY 1459 AGCTCTTCAAGAAACATAGAGATTATTGAGTTCTTGGAGCTGGATCCTTTATTTCAT 1518
Db 534 TCTGAAGTGAGATAAAATAAGTGACCGGGTTTCCCTACCATTTTCATATTTCACCTGGT 593
QY 1519 AAGTTTCAGATCATCTTAAATGAAATGCAATGATTCATCTGCAGTTAAGTAGATGACAGCT 1578
Db 594 AGGAAATCTGATATTATATAGATATTTTATTATTAAATTTTAAAGTAGAAATCACAT 653
QY 1579 ATTCTACATCAGACTTGATTTTGTGACGCTAATTCATCAATTTGGTGAAGTAAATTGAAA 1638
Db 654 AGTTTATTAACTTCTCTTTATTGTTATTAAACAAAAAGTTAAATTCAGTCAATGAAC 713
QY 1639 CCTTAT 1644
Db 714 TTTT 719

RESULT 30
US-10-750-185-33014/c
; Sequence 33014, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERE, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 33014
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Bovine 19866880644168
US-10-750-185-33014

Query Match 1.8%; Score 35.4; DB 6; Length 1464;
Best Local Similarity 54.8%; Pred. No. 7.6;
Matches 69; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
QY 1755 TTTTAAACAAAATAAATGCATGAAGACATAGCCCTTTTAGTTTGTCTAATTGTGAA 1814
Db 619 TTTTCTATTACATCTAAACATCTAGAAGCTTAGCCCTTGACTGAACTAAATTTCAA 560
QY 1815 ATGGAATGCTTTACAGGAAGTAAATGCAATTTTAAAGTGTGCTTTAAAGAAAAAT 1874
Db 559 ACATTAAATAAGAAAAAGCATAAAAGCAAAATGTTTCTTAGTTGCATAATGAAATTAAT 500
QY 1875 ATTTTC 1880
Db 499 ATTTTC 494

Search completed: December 4, 2005, 00:49:25
Job time : 228.436 secs

Db 799 TGTGTTATTTAAGCCACCCAGTCTGTGATATTTTGTGTGGAGCCCTAGCCACTGATA 858
QY 1376 GATTCCTCAACAGAGTACCCCATTTGCTCTGAGCTAATGTTTATATTTTCCATTCAGGCAC 1435
Db 859 CATGACAATCAATATTTTCTATACACGAATAATGTTTCTTATATGAGATTTAAGTAC 918
QY 1436 CGAATAGTTAATATTTTAAATPAAGTCTTCAAAAGAAACATAAGAGATTTAGATTCT 1495
Db 919 CGAGGTATACCAAGCAAAATGTGAAAGTCCCTTTCAAAACTCCTTTCTTGTTCACCTGC 978
QY 1496 TGGACTGATCCTTTATTTTCAATGTTTCAGATCATCTTAAATGAAATGCCATGATTAT 1555
Db 979 TGCTCAGAGGGTACCAATTTCTTACCTTTGCTTCTGCAATAGGCACATTTGTTATATAT 1038
QY 1556 CTGCAGTTAAGTAGATGACAGCTATTTCTACATCAGACTTGAATTTTGTGAGCTAATTACA 1615
Db 1039 GTAATGGCACTGGCCCAAGGATATTTTCTACAGCTTGCAATGTTTCTCATTTCAACAATA 1098
QY 1616 TAATTG 1621
Db 1099 TCATAG 1104

RESULT 27

US-10-750-185-21141
; Sequence 21141, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 21141
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine MMBT13878
US-10-750-185-21141

Query Match 1.8%; Score 35.4; DB 6; Length 600;
Best Local Similarity 54.1%; Pred. No. 4.2;
Matches 72; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 1192 ATAATGCTAGATCATGTGCACAGAAAACCAACTATGATTTATGTTGTGTTTCAGA 1251
Db 457 ATAAAGCATACTATTTCTTTTAAAGAACAAACAAAACCAAAATTCATTTTTCAGTAGC 516
QY 1252 ATTCACATTAAGATTAATGTTTATTTTAAACGACACATTCCTGCAATTCAGGATGTGAG 1311
Db 517 ATTTATCTTAAAGAACTATAGATTACTTAAACAGAAAGCTAGTATACATTTATCTGTGTT 576
QY 1312 GCCATTTAATAAA 1324
Db 577 GACTTTTCAATA 589

RESULT 28

US-10-750-185-42750
; Sequence 42750, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 42750
; LENGTH: 937
; TYPE: DNA
; ORGANISM: Bovine 19866881351349
US-10-750-185-42750

Query Match 1.8%; Score 35.4; DB 6; Length 937;
Best Local Similarity 50.7%; Pred. No. 5.6;
Matches 110; Conservative 0; Mismatches 106; Indels 1; Gaps 1;
QY 489 ATTATAGCTACCTAAAGAGAGATCAAGTAATATGAGATTTATACAGGTCTATGAAGAAG 548
Db 110 ACTATAGATCCTCTCTAGAAAAGAAATCAACATTAAGAGCTATTTCTGGCCATCAAGGCC 169
QY 549 GATATTTTCAAGCTATATAATGTTTGAAGAAATC-AAGAGTGAATTTAAAGCCCAAGAGATT 607
Db 170 TACCTATGCCACAAATACTTGCATATCTCCCATCACAGGTTGAAAAAATATGGACT 229
QY 608 ATTCTTTTCAAGTACCAAAATGATGAGAAACCTTTTATGTCATGTCATGTCATGTCATG 667
Db 230 TATTTTAACTCCCAACATAATGATGATGATGATGATGATGATGATGATGATGATGATG 289
QY 668 GGAATGAGCTTTGCTTATGATCATCCCATTTTGGAGA 704
Db 290 AGTAAATCATTTTCCCTGCAAAAGCTTCTATTTGCATA 326

RESULT 29

US-10-750-185-27468
; Sequence 27468, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 27468
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Bovine 19866881052981
US-10-750-185-27468

Query Match 1.8%; Score 35.4; DB 6; Length 1017;
Best Local Similarity 46.3%; Pred. No. 5.9;
Matches 114; Conservative 0; Mismatches 132; Indels 0; Gaps 0;
QY 1399 TCTCTGAGCTAATGTTTATATTTTCCATTCAGGCACCGAAATAGTTTAAATATTTAAATA 1458
Db 474 TTTATAAGTAATAAATCAATGAAGCATTTAGAAATTTCCCTAGCATAGGAGCTTTATA 533


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; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 43851
; LENGTH: 1671
; TYPE: DNA
; ORGANISM: Bovine 19866880996177
US-10-750-185-43851

Query Match
Best Local Similarity 1.9%; Score 36; DB 6; Length 1671;
Matches 75; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1596 ATTTTGTGTCAGTAATTCATTAATTTGGTAAGNTAATTAATGAACCTTATGGCTTAAATTT 1655
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
955 ATATTATCAGATATTAAATTTCTCTTTGAAAAAATTCCTATTATATACCTTTTAAATTT 896
QY 1656 CCTTAACCTCTTTTGTGATTCATGTTTGTAGTCATGTTGTCACAGAGGCAAGTTAAGCT 1715
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
895 TTTTCTACTTGTGTTTACTTTTAAAAAAGAGATTTATACAAGTGAGGTAGGCAGCCT 836
QY 1716 TGATGATGTTAAATCGGTT 1736
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
835 TTAATAATGGTTCAATGATT 815

RESULT 21
US-10-750-185-33452
; Sequence 33452, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 33452
; LENGTH: 1354
; TYPE: DNA
; ORGANISM: Bovine 19866880704019
US-10-750-185-33452

Query Match
Best Local Similarity 1.9%; Score 35.8; DB 6; Length 1354;
Matches 76; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 1673 TTCATGTTTCTAGTCATGTTGTCAACAGAGGCAAGTTAAGCTTGTATGATGGTTAAATC 1732
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1031 TACTTTTGGAGAAAATGCTCAATGGAGAAAATCAAGGCTGATGTTACCTGAGATG 1090
QY 1733 GGTTTGATACACATGGGACATTTTAAACAAAATAATGATGATGAAGACATAGCC 1792
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1091 GGTATAATAGACCTTTGAAGGCCCTTTTAGATACATAAATCCAGAAATTTATTTTCAGCC 1150
QY 1793 TTTTGTGTTTGTAAATGTGAAA 1815
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1151 ATTTTAATGGTTAATTAATGAA 1173

RESULT 22
US-10-750-185-40622/c
; Sequence 40622, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 40622
; LENGTH: 1763
; TYPE: DNA
; ORGANISM: Bovine 19866881052137
US-10-750-185-40622

Query Match
Best Local Similarity 1.9%; Score 35.8; DB 6; Length 1763;
Matches 91; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 1718 ATGATGGTTAAATCGTTTGTATAGCACCATGGACATTTTAAACAAAATAAATGCA 1777
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
583 ATGATACTAATGATTTAGTAGACCACTTCTGATATTGATTTCTGACAAATCAGAC 524
QY 1778 TGAAGAGACATAGCCTTTTGTAGTTTGTCTAATTTGTAATGGAATGGAATGCTTTACAGGAACTA 1837
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
523 CCACCTATTATTCACATATTATTGTTGTTATTTATTTGATTTATGATGCACTAGAACA 464
QY 1838 AATGCAAAATTANTTTTAACTGTGCTTTTAAAGAAAATAATTTCCCCACAGGAGAAATTTA 1897
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
463 ATGGACATGTACTTTTAAGATGTAATGCAAAAGTAACATGACTCTGCTATGCAAAATTTT 404
QY 1898 AATA 1901
Db |||||
403 AATA 400

RESULT 23
US-10-750-185-36795/c
; Sequence 36795, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 36795
; LENGTH: 1763
; TYPE: DNA
; ORGANISM: Bovine 19866881052137
US-10-750-185-36795

Query Match
Best Local Similarity 1.9%; Score 35.8; DB 6; Length 1763;
Matches 103; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 1601 TGTACGCTAATTACATAATTTGGTAAGNTAATAATTGAAACCTTATGGCTTAAATTCCTTA 1660
```

[illegible]

Query Match	1.9%;	Score 36.8;	DB 6;	Length 2207;
Best Local Similarity	48.6%;	Pred. No. 4.1;		
Matches 101;	Conservative 0;	Mismatches 107;	Indels 0;	Gaps 0;
1394	CAATTGTCCTGAGCTAAATGTTTATATTTTTTCCATTCAGGCACCGAAATAGTTTAATTTA	1453		
938	CAATGCACTGAGAAATGCTGCTATTTTAAATCTATAGATATTAATTTGCATTTAA	997		
1454	AAATAAGTCTTCAAAAGAAAAATAGAGATTATTCAGTTCTTGGGACTGGATCCTTTAT	1513		
998	AAATGTGTTTTTAAACATCACTTGTGTGATATATAAATATTCACAATGTACTTCCTAGAT	1057		
1514	TTTCATAAGTTCAGATCATCTTAAATGCAAAATGCCATGATTATTCGAGTTAAGTAGATGA	1573		
1058	CAAAACAGTAGATATTATATTAATCTTTAAATGATTTCTATATAAATAATATCAAAATA	1117		
1574	CAGCTATTCTACATCAGACTTGATTTTT	1601		
1118	TTAATAGTTAAATGTTAAACAGATTTCT	1145		

```

RESULT 15
US-10-750-185-62503/c
; Sequence 62503, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: Denise, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62503
; LENGTH: 4038
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-62503

```

Query Match	1.9%;	Score 36.8;	DB 6;	Length 4038;
Best Local Similarity	47.9%;	Pred. No. 6.1;		
Matches 134;	Conservative 0;	Mismatches 144;	Indels 2;	Gaps 1;
QY	1604	CAGCTAATTACATAATTGGTAAGNTATAATTGAACCTTATGCTTAAAAATTCCTTAAC	1663	
DB	2671	CTGTGATTTCCTCAACTTCTTAAAAACAATAATGGACAGAATAATTGGAACATGCTCAAGA	2612	
QY	1664	CCCTTTTGATTCATGTTTGTAGTCATGTTCTCAACAGAGGCACAAAGTTAAAGCTTGATCATG	1723	
DB	2611	GTCTCTCAACTTATGTATATATTTAAATTTACTTTAATAGAAACCAAAAGTCTCTGTGTGG	2552	
QY	1724	GTTAAAAATCGGTTTGATAGCACCATGGAGACATTTTTTTTAAACAAAAATAAATGCATGAAGA	1783	
DB	2551	AACACAACCATGCATAGTACCTCGAAATTAATGAAATTAATGATTCAAATCATTTTGTAA	2492	
QY	1784	GACATAGCCTTTTAGTTTTTGCCTAATTTGTGA--AATGGAATGCTTTTACAGGAAGTAAATG	1841	
DB	2491	GGCTATCTCTTTATGTTCCCTAGTGAGAAAGAATGTAAATATTTTGTGTAATCAAGA	2432	
QY	1842	CAAAATTANTTTTAAGTGTGCTTTTAAAGAAAAATAATTTTCC	1891	
DB	2431	TTATTTATATATTACTCTCTGCAGTAGAAAAATTAATCCC	2392	

```

RESULT 16
US-10-750-185-44492/c
; Sequence 44492, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44492
; LENGTH: 1709
; TYPE: DNA
; ORGANISM: Bovine 19865880587477
US-10-750-185-44492
Querv Match 1.9% Score 36.6; DB 6; Length 1709;

```

Query Match	1.9%	Score 36.6	DB 6	Length 1709
Best Local Similarity	45.5%	Pred. No. 3.9		
Matches 202	Conservative 0	Mismatches 240	Indels 2	Gaps 2
QY	1265	GATTAAAGTTTATTAAACGAACACATTCCTGTCGATTCAGGATCTGAGGCCATTAATAAA	1324	
DB	857	GAGTTACAATACCTTTAAATAATCTCATGCTGGCATGCTGGTTGATGGTCACTTGTCCACA	798	
QY	1325	AAGGGCACAAAGCCTGTCAGAGTTTTCACCGTGCCTTACAGCTGCCAGCTGGATTCCAAA	1384	
DB	797	CACGAAATTCACCCCTTCTGGTAAACATGTATACCTTGTTCTCCAAAAAGATACAACA	738	
QY	1385	CAGGTACCCCATGTCTCTGAGCTTAATGTTTATATATTTTCCATTCAGGCCACCGAAATAGT	1444	
DB	737	CAGGAACGACCCCTGACT-TGGTAATATGTAGACCTTGCTTCTTTCACACACCAAAATACC	679	
QY	1445	TAATATTTTAAAAATAGTCTTCCAAAGAAAAACATAAGAGATTATGTAGTTCCTGGGACTGG	1504	
DB	678	AAATGTTTAAAGAGTGAAATGAAATTTGGGAATGAAATTTTCTTTATATCTATTTGCAACA	619	
QY	1505	ATCCTTTATTTTCATAAGTTCAGATCATCTTAAATGAAAAATGCCATGATTATCTGCAGTTA	1564	
DB	618	AAATGTATATATCAATGTGATAGGAATTAAGAAATTCGTGACTGCACCTTTAATATCTGAA	559	
QY	1565	AGTAGATGACAGCTATTCTACATCAGACTTGAATTTTGTCCAGCTAAATTACATAATTGGTA	1624	
DB	558	GTCATTTTACCTGTATTATTATGACACTTCAAGACAGCCAACTCTGAAAAATAT-ATTGGTA	500	
QY	1625	AGNTATAATTGAAACCTTATGGCTTAAAAATTCCTTAATCTCTTTTGTGATTCATGTTTGTGA	1684	
DB	499	ACCAAGAATTCCACTTTAATATTTAAAAAGTCCCTTAAGAAATTTAAGAACCTTATAGGTTCT	440	
QY	1685	GTCATGTTGTCAACAGAGGCCAAAG	1708	
DB	439	TTAGCTTTTATCGAATGTGTTAAAG	416	

RESULT 17
US-10-750-185-57582
; Sequence 57582, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom

[illegible]

Qy 1886 AGGAGAAATTTAAATAA 1903
| | | | |
Db 637 AAGAGAGAGTTGGAAAAA 620
| | | | |
RESULT 5
US-10-793-626-3694/c
; Sequence 3694, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3694
; LENGTH: 3189
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3694
Query Match 2.0%; Score 38.6; DB 6; Length 3189;
Best Local Similarity 45.4%; Pred. No. 1.7;
Matches 134; Conservative 0; Mismatches 161; Indels 0; Gaps 0;
Qy 1618 ATTGTAAGTATTAATCGAAACCTTATGGCTTAAATTCCTTAACCTCTTTTTCATCAT 1677
| | | | |
Db 2154 ATTATATTTTAGAGTGAACCAATGTAATTTAAATGTTTCTCACTCTTTTATTAT 2095
| | | | |
Qy 1678 GTTTGTAGTCATGTTGTCAACAGAGCGCAAGTTAAGCTTGTATGGTTAAATTCGGTTT 1737
| | | | |
Db 2094 TTAGCGCTAATGTTATTATTCATCTTGTAGTCTCAAAATTTTATTATGAGTAAGTT 2035
| | | | |
Qy 1738 GATAGCACCATGGGACATTTTAAACAAATAAATCATGATGAGAGACATAGCCTTTTA 1797
| | | | |
Db 2034 ACTAATAATTTGTCCAAATCTTATAAAAAATATTTTAAAAATAAATAAATATTTAA 1975
| | | | |
Qy 1798 GTTTGTCTAATGTAATGTAATGTAATGCTTTACAGGAAGTAATGCAATTTTAAAT 1857
| | | | |
Db 1974 TATAATGTAAACAGATAGGGTTTATTATTTTAAACATTTAGGCATTTAATACATTTTAT 1915
| | | | |
Qy 1858 GTGCTTTAAAGAAAAATATTTTCCCAACAGAGAAATTTAAATAAGAAATTTTAT 1912
| | | | |
Db 1914 CAGTTATATATATTAATTAATGTAACAGCTGTTTATTAATAAATAAATTTTAT 1860
| | | | |

RESULT 6
US-10-750-185-20526/c
; Sequence 20526, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
US-10-750-185-20526/c
Query Match 2.0%; Score 37.6; DB 6; Length 727;
Best Local Similarity 54.3%; Pred. No. 1.2;
Matches 76; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
Qy 1357 TGCTTACAGTGCAGCTGGATTCCTCAACAGGTAACCCCATTTCTCTGAGCTAATGTTTA 1416
| | | | |
Db 501 TTCTTTGAACCTGCTTCTTTGAATGCTAATTCACACAGTGTCTATCATCATATAAATTTT 442
| | | | |
Qy 1417 TATTTTCCATTCAGGCGACGAAATAGTTAATATTTTAAATAAGTCTTCAAAAGAAAAA 1476
| | | | |
Db 441 TAAATACGTCTGCTGACAAATTCATTAAGTTTCTTAAATAATTTAAAGACGCA 382
| | | | |
Qy 1477 TAAGAGATTATTGAGTTCTT 1496
| | | | |
Db 381 TTGGAATTAATTTGTTT 362
| | | | |
RESULT 8
US-10-750-185-27683/c
; Sequence 27683, Application US/10750185

; SEQ ID NO 20526
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine MMBT09209
US-10-750-185-20526

Query Match 2.0%; Score 38.2; DB 6; Length 600;
Best Local Similarity 49.0%; Pred. No. 0.7;
Matches 97; Conservative 1; Mismatches 100; Indels 0; Gaps 0;
Qy 1706 AAGTTAAGCTTGATGTTTAAATCGTTTGTATAGCACCATGGACATTTTAAACA 1765
| | | | |
Db 544 AATTTTGAATTTTAAAGATTTTATTTTAAATTTTCCAGCTTTCAGATGAAATGGAAA 485
| | | | |
Qy 1766 AAAATAAATGCATGAAGAGACATAGCCTTTTAGTTTGTCTAAATGTGAAATGGAATGCT 1825
| | | | |
Db 484 CAAAGAGGATATAGAGGTATTTAAATTTCTGTTTATGAGATATATATCAAAATAT 425
| | | | |
Qy 1826 TTACAGGAAGTAATGCAAAATTTAATTTTAAAGTGTGCTTTTAAAGAAAAATATTTTCCCCAC 1885
| | | | |
Db 424 TATGTGGAAGCTAAAGAAATGTTTAAAGTAATACAGCAATAAATATAGATATATGCCCCAG 365
| | | | |
Qy 1886 AGGAGAAATTTAAATAA 1903
| | | | |
Db 364 AAGAGAGAGTTGGAARA 347
| | | | |

RESULT 7
US-10-750-185-64457/c
; Sequence 64457, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64457
; LENGTH: 727
; TYPE: DNA
; ORGANISM: Bovine 19866880922318
US-10-750-185-64457

Query Match 2.0%; Score 37.6; DB 6; Length 727;
Best Local Similarity 54.3%; Pred. No. 1.2;
Matches 76; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
Qy 1357 TGCTTACAGTGCAGCTGGATTCCTCAACAGGTAACCCCATTTCTCTGAGCTAATGTTTA 1416
| | | | |
Db 501 TTCTTTGAACCTGCTTCTTTGAATGCTAATTCACACAGTGTCTATCATCATATAAATTTT 442
| | | | |
Qy 1417 TATTTTCCATTCAGGCGACGAAATAGTTAATATTTTAAATAAGTCTTCAAAAGAAAAA 1476
| | | | |
Db 441 TAAATACGTCTGCTGACAAATTCATTAAGTTTCTTAAATAATTTAAAGACGCA 382
| | | | |
Qy 1477 TAAGAGATTATTGAGTTCTT 1496
| | | | |
Db 381 TTGGAATTAATTTGTTT 362
| | | | |
RESULT 8
US-10-750-185-27683/c
; Sequence 27683, Application US/10750185

Qy	525	AGATTATTACAGGT	CATGAAGAAGATATTTC	CAGCTATAATGTTGAAGAAATCAAGAG	584
Db	799	AAATACCTGAGGTCGT	GAAGAAGATATTTC	CAGCTATAATGTTGAAGAAATCAAGAG	740
Qy	585	TGAATTTAAAAACCA	AGAGATTATTCCTTTTCCAAAGT	TCCAAAATGATCAGAAAACTTTT	644
Db	739	TGAGTTTAAAAACCA	AGAAATTATTCCTTTTCCAAATA	CGCAATGATCAGAAAACTTTT	680
Qy	645	TATGTGTCATGTGAAT			661
Db	679	TGTGTGTTCATGTAAGT			663

C 389	30.8	1.6	1690	6	US-10-750-185-51738	Sequence 51738, A	C 462	30.4	1.6	959	6	US-10-750-185-61411	Sequence 61411, A
C 390	30.8	1.6	1692	6	US-10-750-185-45965	Sequence 45965, A	C 463	30.4	1.6	1002	6	US-10-750-185-31634	Sequence 31634, A
C 391	30.8	1.6	1727	6	US-10-750-185-28336	Sequence 28336, A	C 464	30.4	1.6	1026	7	US-11-112-908-93	Sequence 93, Appl
C 392	30.8	1.6	1815	6	US-10-750-185-29236	Sequence 29236, A	C 465	30.4	1.6	1033	6	US-10-750-185-36482	Sequence 36482, A
C 393	30.8	1.6	1832	6	US-10-750-185-42529	Sequence 42529, A	C 466	30.4	1.6	1042	6	US-10-750-185-49649	Sequence 49649, A
C 394	30.8	1.6	1843	6	US-10-750-185-33240	Sequence 33240, A	C 467	30.4	1.6	1074	6	US-10-750-185-28421	Sequence 28421, A
C 395	30.8	1.6	1873	6	US-10-750-185-54481	Sequence 54481, A	C 468	30.4	1.6	1159	6	US-10-750-185-41116	Sequence 41116, A
C 396	30.8	1.6	2101	6	US-10-750-185-62222	Sequence 62222, A	C 469	30.4	1.6	1226	6	US-10-750-185-43541	Sequence 43541, A
C 397	30.8	1.6	2238	6	US-10-793-626-1499	Sequence 1499, Ap	C 470	30.4	1.6	1281	6	US-10-750-185-45841	Sequence 45841, A
C 398	30.8	1.6	2268	6	US-10-750-185-25517	Sequence 25517, A	C 471	30.4	1.6	1283	6	US-10-750-185-38599	Sequence 38599, A
C 399	30.8	1.6	2497	6	US-10-750-185-35100	Sequence 35100, A	C 472	30.4	1.6	1328	6	US-10-750-185-52755	Sequence 52755, A
C 400	30.8	1.6	2520	6	US-10-750-185-52723	Sequence 52723, A	C 473	30.4	1.6	1331	6	US-10-750-185-61714	Sequence 61714, A
C 401	30.8	1.6	2602	6	US-10-750-185-28383	Sequence 28383, A	C 474	30.4	1.6	1332	6	US-10-750-185-38771	Sequence 38771, A
C 402	30.8	1.6	2611	6	US-10-750-185-60784	Sequence 60784, A	C 475	30.4	1.6	1343	6	US-10-750-185-29888	Sequence 29888, A
C 403	30.8	1.6	2671	6	US-10-750-185-42813	Sequence 42813, A	C 476	30.4	1.6	1405	6	US-10-750-185-25572	Sequence 25572, A
C 404	30.8	1.6	2781	6	US-10-750-185-62209	Sequence 62209, A	C 477	30.4	1.6	1470	6	US-10-750-185-58531	Sequence 58531, A
C 405	30.8	1.6	3037	6	US-10-750-185-31775	Sequence 31775, A	C 478	30.4	1.6	1482	6	US-10-750-185-58657	Sequence 58657, A
C 406	30.8	1.6	3219	6	US-10-750-185-26874	Sequence 26874, A	C 479	30.4	1.6	1486	6	US-10-750-185-35504	Sequence 35504, A
C 407	30.8	1.6	3207	6	US-10-750-185-51664	Sequence 51664, A	C 480	30.4	1.6	1580	6	US-10-750-185-42644	Sequence 42644, A
C 408	30.8	1.6	3207	6	US-10-793-626-3413	Sequence 3413, Ap	C 481	30.4	1.6	1583	6	US-10-750-185-58326	Sequence 58326, A
C 409	30.8	1.6	3393	6	US-10-793-626-4085	Sequence 4085, Ap	C 482	30.4	1.6	1623	6	US-10-750-185-43506	Sequence 43506, A
C 410	30.8	1.6	44848	7	US-11-106-672A-42	Sequence 42, Appl	C 483	30.4	1.6	1671	6	US-10-750-185-32076	Sequence 32076, A
C 411	30.8	1.6	171162	7	US-11-112-908-38	Sequence 38, Appl	C 484	30.4	1.6	1702	6	US-10-750-185-63289	Sequence 63289, A
C 412	30.8	1.6	182314	7	US-11-112-908-45	Sequence 45, Appl	C 485	30.4	1.6	1838	6	US-10-750-185-47394	Sequence 47394, A
C 413	30.6	1.6	598	6	US-10-750-185-21977	Sequence 21977, A	C 486	30.4	1.6	1847	6	US-10-750-185-52582	Sequence 52582, A
C 414	30.6	1.6	756	6	US-10-750-185-29766	Sequence 29766, A	C 487	30.4	1.6	1851	6	US-10-750-185-32439	Sequence 32439, A
C 415	30.6	1.6	914	6	US-10-750-185-32423	Sequence 32423, A	C 488	30.4	1.6	1861	6	US-10-750-185-62270	Sequence 62270, A
C 416	30.6	1.6	1005	6	US-10-793-626-229	Sequence 229, App	C 489	30.4	1.6	1940	6	US-10-750-185-58472	Sequence 58472, A
C 417	30.6	1.6	1044	6	US-10-750-185-49766	Sequence 49766, A	C 490	30.4	1.6	2119	6	US-10-793-626-3950	Sequence 3950, Ap
C 418	30.6	1.6	1064	6	US-10-750-185-25903	Sequence 25903, A	C 491	30.4	1.6	2355	6	US-10-821-234-585	Sequence 585, App
C 419	30.6	1.6	1113	6	US-10-750-185-59847	Sequence 59847, A	C 492	30.4	1.6	2515	6	US-10-750-185-62186	Sequence 62186, A
C 420	30.6	1.6	1153	6	US-10-750-185-48864	Sequence 48864, A	C 493	30.4	1.6	2545	6	US-10-750-185-34077	Sequence 34077, A
C 421	30.6	1.6	1230	6	US-10-750-185-24951	Sequence 24951, A	C 494	30.4	1.6	2561	6	US-10-750-185-50532	Sequence 50532, A
C 422	30.6	1.6	1288	6	US-10-750-185-38599	Sequence 38599, A	C 495	30.4	1.6	2591	6	US-10-750-185-64590	Sequence 64590, A
C 423	30.6	1.6	1288	6	US-10-750-185-52185	Sequence 52185, A	C 496	30.4	1.6	3610	6	US-10-750-185-54590	Sequence 54590, A
C 424	30.6	1.6	1354	6	US-10-750-185-62259	Sequence 62259, A	C 497	30.4	1.6	4651	6	US-10-750-185-35641	Sequence 35641, A
C 425	30.6	1.6	1359	6	US-10-750-185-35714	Sequence 35714, A	C 498	30.4	1.6	5110	6	US-10-750-185-59125	Sequence 59125, A
C 426	30.6	1.6	1463	6	US-10-750-185-33292	Sequence 33292, A	C 499	30.4	1.6	125594	6	US-10-658-986-5	Sequence 5, Appl
C 427	30.6	1.6	1531	6	US-10-750-185-36059	Sequence 36059, A	C 500	30.4	1.6	131855	7	US-11-112-908-29	Sequence 29, Appl
C 428	30.6	1.6	1553	6	US-10-750-185-58945	Sequence 58945, A							
C 429	30.6	1.6	1744	9	US-11-040-638-1	Sequence 1, Appl							
C 430	30.6	1.6	1744	6	US-10-750-185-57314	Sequence 57314, A							
C 431	30.6	1.6	1749	6	US-10-750-185-55988	Sequence 55988, A							
C 432	30.6	1.6	1766	6	US-10-750-185-64570	Sequence 64570, A							
C 433	30.6	1.6	1768	6	US-10-750-185-54174	Sequence 54174, A							
C 434	30.6	1.6	1839	6	US-10-750-185-42842	Sequence 42842, A							
C 435	30.6	1.6	1876	6	US-10-750-185-52480	Sequence 52480, A							
C 436	30.6	1.6	1968	6	US-10-750-185-37652	Sequence 37652, A							
C 437	30.6	1.6	2148	6	US-10-750-185-50243	Sequence 50243, A							
C 438	30.6	1.6	2343	6	US-10-750-185-42914	Sequence 42914, A							
C 439	30.6	1.6	2499	6	US-10-512-109-28	Sequence 28, Appl							
C 440	30.6	1.6	2517	6	US-10-750-185-33810	Sequence 33810, A							
C 441	30.6	1.6	2637	6	US-10-750-185-47267	Sequence 47267, A							
C 442	30.6	1.6	2672	6	US-10-750-185-39345	Sequence 39345, A							
C 443	30.6	1.6	3054	6	US-10-750-185-35301	Sequence 35301, A							
C 444	30.6	1.6	3061	6	US-10-793-626-4134	Sequence 4134, Ap							
C 445	30.6	1.6	3446	6	US-10-793-626-3943	Sequence 3943, Ap							
C 446	30.6	1.6	3778	6	US-10-750-185-50674	Sequence 50674, A							
C 447	30.6	1.6	3919	6	US-10-793-626-3814	Sequence 3814, Ap							
C 448	30.6	1.6	4035	6	US-10-750-185-58283	Sequence 58283, A							
C 449	30.6	1.6	4735	7	US-11-066-648A-13	Sequence 13, Appl							
C 450	30.6	1.6	5109	6	US-10-714-781A-56	Sequence 56, Appl							
C 451	30.6	1.6	166111	7	US-11-112-908-47	Sequence 47, Appl							
C 452	30.6	1.6	600	6	US-10-750-185-524	Sequence 524, App							
C 453	30.4	1.6	600	6	US-10-750-185-1308	Sequence 1308, Ap							
C 454	30.4	1.6	600	6	US-10-750-185-3372	Sequence 3372, Ap							
C 455	30.4	1.6	600	6	US-10-750-185-19576	Sequence 19576, A							
C 456	30.4	1.6	600	6	US-10-750-185-20768	Sequence 20768, A							
C 457	30.4	1.6	600	6	US-10-750-185-21595	Sequence 21595, A							
C 458	30.4	1.6	655	7	US-11-112-908-133	Sequence 133, App							
C 459	30.4	1.6	764	6	US-10-750-185-59751	Sequence 59751, A							
C 460	30.4	1.6	802	6	US-10-750-185-43255	Sequence 43255, A							
C 461	30.4	1.6	933	6	US-10-750-185-30261	Sequence 30261, A							

ALIGNMENTS

RESULT 1

US-10-750-185-25698/c

; Sequence 25698, Application US/10750185

; Publication No. US20050260603A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KEHR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: WMI100-2

; CURRENT APPLICATION NUMBER: US/10750,185

; CURRENT FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 25698

; LENGTH: 952

; TYPE: DNA

; ORGANISM: Bovine 19866881510436

US-10-750-185-25698

Query Match 5.7%; Score 109.8; DB 6; Length 952;

Best Local Similarity 87.6%; Pred. No. 1.5e-20;

Matches 120; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

243	31.6	1.6	1191	6	US-10-750-185-54543	Sequence 54543, A	c 316	31.2	1.6	1619	6	US-10-750-185-51406	Sequence 51406, A
c 244	31.6	1.6	1208	6	US-10-750-185-42304	Sequence 42304, A	317	31.2	1.6	1635	6	US-10-750-185-26986	Sequence 26986, A
245	31.6	1.6	1266	6	US-10-793-626-1817	Sequence 1817, Ap	318	31.2	1.6	1644	6	US-10-750-185-27844	Sequence 27844, A
c 246	31.6	1.6	1335	6	US-10-750-185-33037	Sequence 33037, A	c 319	31.2	1.6	1675	6	US-10-750-185-52265	Sequence 52265, A
c 247	31.6	1.6	1401	6	US-10-750-185-49206	Sequence 49206, A	320	31.2	1.6	1680	6	US-10-750-185-51531	Sequence 51531, A
c 248	31.6	1.6	1459	6	US-10-750-185-29613	Sequence 29613, A	321	31.2	1.6	1691	6	US-10-750-185-58132	Sequence 58132, A
c 249	31.6	1.6	1655	6	US-10-750-185-53110	Sequence 53110, A	c 322	31.2	1.6	1709	6	US-10-750-185-44914	Sequence 44914, A
c 250	31.6	1.6	1658	6	US-10-750-185-33931	Sequence 33931, A	323	31.2	1.6	1729	6	US-10-750-185-34558	Sequence 34558, A
c 251	31.6	1.6	1709	6	US-10-750-185-46130	Sequence 46130, A	324	31.2	1.6	1757	6	US-10-750-185-35784	Sequence 35784, A
c 252	31.6	1.6	1793	8	US-11-112-944-12	Sequence 12, Appl	325	31.2	1.6	2013	6	US-10-750-185-47080	Sequence 47080, A
c 253	31.6	1.6	1819	6	US-10-750-185-29496	Sequence 29496, A	c 326	31.2	1.6	2079	6	US-10-750-185-54948	Sequence 54948, A
c 254	31.6	1.6	1877	6	US-10-750-185-64835	Sequence 64835, A	327	31.2	1.6	2191	6	US-10-750-185-47372	Sequence 47372, A
c 255	31.6	1.6	2019	6	US-10-750-185-33697	Sequence 33697, A	328	31.2	1.6	2550	6	US-10-793-626-4343	Sequence 4343, Ap
c 256	31.6	1.6	2064	6	US-10-750-185-26516	Sequence 26516, A	329	31.2	1.6	2703	6	US-10-750-185-46436	Sequence 46436, A
c 257	31.6	1.6	2387	6	US-10-750-185-56815	Sequence 56815, A	c 330	31.2	1.6	3001	7	US-11-145-703-121	Sequence 121, App
c 258	31.6	1.6	2414	6	US-10-750-185-46852	Sequence 46852, A	331	31.2	1.6	3007	7	US-11-145-703-195	Sequence 195, App
c 259	31.6	1.6	2624	6	US-10-750-185-29398	Sequence 29398, A	332	31.2	1.6	3348	6	US-10-793-626-3541	Sequence 3541, Ap
c 260	31.6	1.6	2731	6	US-10-750-185-31955	Sequence 31955, A	c 333	31.2	1.6	3583	6	US-10-750-185-53180	Sequence 53180, A
c 261	31.6	1.6	2909	6	US-10-750-185-63532	Sequence 63532, A	c 334	31.2	1.6	3619	6	US-10-793-626-3335	Sequence 3335, Ap
c 262	31.6	1.6	2926	6	US-10-793-626-3747	Sequence 3747, Ap	335	31.2	1.6	3830	6	US-10-793-626-3934	Sequence 3934, Ap
c 263	31.6	1.6	2958	6	US-10-750-185-31843	Sequence 31843, A	336	31.2	1.6	4019	6	US-10-750-185-34250	Sequence 34250, A
c 264	31.6	1.6	3133	6	US-10-793-626-3431	Sequence 3431, Ap	c 337	31.2	1.6	4557	9	US-11-060-920-3	Sequence 3, Appl
c 265	31.6	1.6	3319	6	US-10-793-626-3835	Sequence 3835, Ap	338	31.2	1.6	5244	6	US-10-750-185-26190	Sequence 26190, A
c 266	31.6	1.6	3859	6	US-10-793-626-3693	Sequence 3693, Ap	c 339	31.2	1.6	6450	7	US-11-091-668-3	Sequence 3, Appl
c 267	31.6	1.6	12482	9	US-11-090-878-25	Sequence 25, Appl	c 340	31.2	1.6	150481	7	US-11-112-908-37	Sequence 37, Appl
c 268	31.6	1.6	319608	7	US-11-145-703-1	Sequence 1, Appl	c 341	31.2	1.6	171162	7	US-11-112-908-38	Sequence 38, Appl
c 269	31.4	1.6	600	6	US-10-750-185-2808	Sequence 2808, Ap	342	31.2	1.6	172781	7	US-11-112-908-25	Sequence 25, Appl
c 270	31.4	1.6	600	6	US-10-750-185-3435	Sequence 3435, Ap	c 343	31	1.6	600	6	US-10-750-185-4347	Sequence 4347, Ap
c 271	31.4	1.6	764	6	US-10-750-185-38845	Sequence 38845, A	c 344	31	1.6	614	6	US-10-793-626-2155	Sequence 2155, Ap
c 272	31.4	1.6	807	6	US-10-392-234A-55	Sequence 55, Appl	c 345	31	1.6	648	6	US-10-793-626-1101	Sequence 1101, Ap
c 273	31.4	1.6	869	6	US-10-750-185-62652	Sequence 62652, A	c 346	31	1.6	748	6	US-10-750-185-60503	Sequence 60503, A
c 274	31.4	1.6	882	6	US-10-750-185-26501	Sequence 26501, A	c 347	31	1.6	900	6	US-10-750-185-60102	Sequence 60102, A
c 275	31.4	1.6	931	6	US-10-750-185-46815	Sequence 46815, A	c 348	31	1.6	1012	6	US-10-750-185-57203	Sequence 57203, A
c 276	31.4	1.6	1007	6	US-10-750-185-57543	Sequence 57543, A	c 349	31	1.6	1053	6	US-10-750-185-38600	Sequence 38600, A
c 277	31.4	1.6	1081	6	US-10-750-185-59899	Sequence 59899, A	c 350	31	1.6	1088	6	US-10-750-185-32734	Sequence 32734, A
c 278	31.4	1.6	1095	6	US-10-750-185-58034	Sequence 58034, A	c 351	31	1.6	1120	6	US-10-750-185-29060	Sequence 29060, A
c 279	31.4	1.6	1197	6	US-10-750-185-62875	Sequence 62875, A	c 352	31	1.6	1165	6	US-10-750-185-56313	Sequence 56313, A
c 280	31.4	1.6	1305	6	US-10-750-185-31565	Sequence 31565, A	c 353	31	1.6	1208	6	US-10-750-185-43206	Sequence 43206, A
c 281	31.4	1.6	1572	6	US-10-750-185-55300	Sequence 55300, A	c 354	31	1.6	1263	6	US-10-986-501-84	Sequence 84, Appl
c 282	31.4	1.6	1577	6	US-10-750-185-45671	Sequence 45671, A	c 355	31	1.6	1314	6	US-10-750-185-26982	Sequence 26982, A
c 283	31.4	1.6	1861	6	US-10-750-185-33082	Sequence 33082, A	c 356	31	1.6	1367	6	US-10-750-185-31646	Sequence 31646, A
c 284	31.4	1.6	1895	6	US-10-750-185-45133	Sequence 45133, A	c 357	31	1.6	1544	6	US-10-750-185-47041	Sequence 47041, A
c 285	31.4	1.6	1898	6	US-10-750-185-34003	Sequence 34003, A	c 358	31	1.6	1897	6	US-10-750-185-51854	Sequence 51854, A
c 286	31.4	1.6	1949	6	US-10-750-185-30235	Sequence 30235, A	c 359	31	1.6	1919	6	US-10-750-185-51938	Sequence 51938, A
c 287	31.4	1.6	1988	6	US-10-750-185-31462	Sequence 31462, A	c 360	31	1.6	1940	6	US-10-750-185-50499	Sequence 50499, A
c 288	31.4	1.6	2045	6	US-10-750-185-40615	Sequence 40615, A	c 361	31	1.6	2022	6	US-10-750-185-49843	Sequence 49843, A
c 289	31.4	1.6	2125	6	US-10-750-185-41395	Sequence 41395, A	c 362	31	1.6	2056	6	US-10-750-185-60042	Sequence 60042, A
c 290	31.4	1.6	2170	6	US-10-750-185-31653	Sequence 31653, A	c 363	31	1.6	2095	6	US-10-750-185-26071	Sequence 26071, A
c 291	31.4	1.6	2481	6	US-10-750-185-36255	Sequence 36255, A	c 364	31	1.6	2218	6	US-10-750-185-52962	Sequence 52962, A
c 292	31.4	1.6	2488	6	US-10-750-185-49176	Sequence 49176, A	c 365	31	1.6	2411	6	US-10-750-185-28579	Sequence 28579, A
c 293	31.4	1.6	2636	6	US-10-750-185-26219	Sequence 26219, A	c 366	31	1.6	2428	6	US-10-485-517-55	Sequence 55, Appl
c 294	31.4	1.6	2707	6	US-10-750-185-26276	Sequence 26276, A	c 367	31	1.6	2563	6	US-10-750-185-39331	Sequence 39331, A
c 295	31.4	1.6	2779	6	US-10-750-185-47665	Sequence 47665, A	c 368	31	1.6	2960	6	US-10-750-185-44604	Sequence 44604, A
c 296	31.4	1.6	3029	6	US-10-750-185-52188	Sequence 52188, A	c 369	31	1.6	3140	6	US-10-750-185-55149	Sequence 55149, A
c 297	31.4	1.6	3316	6	US-10-131-826A-477	Sequence 477, App	c 370	31	1.6	3319	6	US-10-793-626-4370	Sequence 4370, Ap
c 298	31.4	1.6	4075	6	US-10-750-185-57933	Sequence 57933, A	c 371	31	1.6	3333	6	US-10-793-626-4388	Sequence 4388, Ap
c 299	31.4	1.6	4182	6	US-10-750-185-40417	Sequence 40417, A	c 372	31	1.6	3657	6	US-10-793-626-3888	Sequence 3888, Ap
c 300	31.4	1.6	150450	7	US-11-112-908-54	Sequence 54, Appl	c 373	31	1.6	4126	6	US-10-793-626-4154	Sequence 4154, Ap
c 301	31.2	1.6	678	6	US-10-467-657-6037	Sequence 6037, Ap	c 374	31	1.6	125594	6	US-10-658-986-5	Sequence 5, Appl
c 302	31.2	1.6	687	6	US-10-467-657-6237	Sequence 6237, Ap	c 375	31	1.6	191343	7	US-11-112-908-53	Sequence 53, Appl
c 303	31.2	1.6	714	6	US-10-467-657-6247	Sequence 6247, Ap	c 376	30.8	1.6	600	6	US-10-750-185-730	Sequence 730, App
c 304	31.2	1.6	735	6	US-10-750-185-43356	Sequence 43356, A	c 377	30.8	1.6	855	6	US-10-750-185-32467	Sequence 32467, A
c 305	31.2	1.6	880	6	US-10-750-185-63852	Sequence 63852, A	c 378	30.8	1.6	947	9	US-11-033-764-51	Sequence 51, Appl
c 306	31.2	1.6	960	6	US-10-750-185-56709	Sequence 56709, A	c 379	30.8	1.6	1096	6	US-10-750-185-35884	Sequence 35884, A
c 307	31.2	1.6	995	6	US-10-957-569-23	Sequence 23, Appl	c 380	30.8	1.6	1126	6	US-10-750-185-59037	Sequence 59037, A
c 308	31.2	1.6	1123	6	US-10-750-185-57282	Sequence 57282, A	c 381	30.8	1.6	1152	6	US-10-750-185-27788	Sequence 27788, A
c 309	31.2	1.6	1248	6	US-10-750-185-33617	Sequence 33617, A	c 382	30.8	1.6	1200	6	US-10-514-761-33	Sequence 33, Appl
c 310	31.2	1.6	1352	6	US-10-750-185-50963	Sequence 50963, A	c 383	30.8	1.6	1359	6	US-10-750-185-37775	Sequence 37775, A
c 311	31.2	1.6	1367	6	US-10-750-185-46287	Sequence 46287, A	c 384	30.8	1.6	1416	6	US-10-750-185-34972	Sequence 34972, A
c 312	31.2	1.6	1386	6	US-10-750-185-61595	Sequence 61595, A	c 385	30.8	1.6	1439	6	US-10-750-185-27410	Sequence 27410, A
c 313	31.2	1.6	1392	6	US-10-750-185-50757	Sequence 50757, A	c 386	30.8	1.6	1496	6	US-10-750-185-58416	Sequence 58416, A
c 314	31.2	1.6	1494	6	US-10-793-626-4449	Sequence 4449, Ap	c 387	30.8	1.6	1526	6	US-10-750-185-59378	Sequence 59378, A
c 315	31.2	1.6	1578	6	US-10-750-185-40929	Sequence 40929, A	c 388	30.8	1.6	1600	6	US-10-750-185-36992	Sequence 36992, A

C 97	33.4	1.7	1544	6	US-10-750-185-49246	Sequence 49246, A	C 170	32.2	1.7	1277	6	US-10-750-185-48303	Sequence 48303, A
C 98	33.4	1.7	1688	6	US-10-750-185-29497	Sequence 29497, A	C 171	32.2	1.7	1316	7	US-11-089-191-3	Sequence 3, Appl
C 99	33.4	1.7	1824	6	US-10-750-185-32050	Sequence 32050, A	C 172	32.2	1.7	1363	6	US-10-750-185-55452	Sequence 55452, A
C 100	33.4	1.7	2827	6	US-10-750-185-50802	Sequence 50802, A	C 173	32.2	1.7	1424	6	US-10-750-185-60524	Sequence 60524, A
C 101	33.4	1.7	3001	7	US-11-145-703-192	Sequence 192, App	C 174	32.2	1.7	1464	6	US-10-750-185-55268	Sequence 55268, A
C 102	33.2	1.7	595	6	US-10-750-185-59597	Sequence 59597, A	C 175	32.2	1.7	1523	6	US-10-750-185-48367	Sequence 48367, A
C 103	33.2	1.7	875	6	US-10-750-185-44636	Sequence 44636, A	C 176	32.2	1.7	1639	6	US-10-750-185-55599	Sequence 55599, A
C 104	33.2	1.7	1036	6	US-10-750-185-11820	Sequence 31820, A	C 177	32.2	1.7	1686	6	US-10-750-185-24761	Sequence 24761, A
C 105	33.2	1.7	1090	6	US-10-750-185-35077	Sequence 35077, A	C 178	32.2	1.7	1749	6	US-10-750-185-53049	Sequence 53049, A
C 106	33.2	1.7	1757	6	US-10-750-185-54083	Sequence 54083, A	C 179	32.2	1.7	1819	6	US-10-750-185-29571	Sequence 29571, A
C 107	33.2	1.7	1785	6	US-10-750-185-54427	Sequence 54427, A	C 180	32.2	1.7	1947	6	US-10-750-185-53844	Sequence 53844, A
C 108	33.2	1.7	1835	6	US-10-750-185-39749	Sequence 39749, A	C 181	32.2	1.7	2230	6	US-10-750-185-41287	Sequence 41287, A
C 109	33.2	1.7	1842	6	US-10-750-185-26444	Sequence 26444, A	C 182	32.2	1.7	2325	6	US-10-750-185-64566	Sequence 64566, A
C 110	33.2	1.7	1848	6	US-10-750-185-62378	Sequence 62378, A	C 183	32.2	1.7	2633	6	US-10-750-185-39106	Sequence 39106, A
C 111	33.2	1.7	172147	7	US-11-112-908-22	Sequence 22, Appl	C 184	32.2	1.7	3137	6	US-10-793-626-3575	Sequence 3575, Ap
C 112	33.2	1.7	207908	7	US-11-112-908-21	Sequence 21, Appl	C 185	32.2	1.7	3422	6	US-10-750-185-40069	Sequence 40069, A
C 113	33.2	1.7	212805	7	US-11-112-908-19	Sequence 19, Appl	C 186	32.2	1.7	3435	6	US-10-793-626-3648	Sequence 3648, Ap
C 114	33	1.7	860	6	US-10-750-185-56249	Sequence 56249, A	C 187	32.2	1.7	4244	6	US-10-793-626-4256	Sequence 4256, Ap
C 115	33	1.7	952	6	US-10-750-185-26002	Sequence 26002, A	C 188	32.2	1.7	7006	6	US-10-821-234-218	Sequence 218, App
C 116	33	1.7	1141	6	US-10-750-185-56984	Sequence 56984, A	C 189	32.2	1.7	193363	7	US-11-112-908-32	Sequence 32, Appl
C 117	33	1.7	1577	6	US-10-750-185-41998	Sequence 41998, A	C 190	32	1.7	600	6	US-10-750-185-3069	Sequence 3069, Ap
C 118	33	1.7	1840	6	US-10-750-185-37690	Sequence 37690, A	C 191	32	1.7	640	6	US-10-750-185-35702	Sequence 35702, A
C 119	33	1.7	2684	6	US-10-750-185-28545	Sequence 28545, A	C 192	32	1.7	1114	6	US-10-750-185-41570	Sequence 41570, A
C 120	33	1.7	150468	7	US-11-112-908-56	Sequence 56, Appl	C 193	32	1.7	1232	6	US-10-750-185-25367	Sequence 25367, A
C 121	33	1.7	168656	7	US-11-112-908-59	Sequence 59, Appl	C 194	32	1.7	1390	6	US-10-750-185-36836	Sequence 36836, A
C 122	33	1.7	170285	7	US-11-112-908-58	Sequence 58, Appl	C 195	32	1.7	1404	6	US-10-750-185-56117	Sequence 56117, A
C 123	33	1.7	193789	7	US-11-112-908-55	Sequence 55, Appl	C 196	32	1.7	1483	6	US-10-750-185-39052	Sequence 39052, A
C 124	33	1.7	212805	7	US-11-112-908-19	Sequence 19, Appl	C 197	32	1.7	1540	6	US-10-750-185-60438	Sequence 60438, A
C 125	33	1.7	340000	7	US-11-102-978-3	Sequence 3, Appl	C 198	32	1.7	1542	6	US-10-750-185-27838	Sequence 27838, A
C 126	32.8	1.7	996	6	US-10-750-185-54220	Sequence 54220, A	C 199	32	1.7	1564	6	US-10-750-185-44960	Sequence 44960, A
C 127	32.8	1.7	1062	6	US-10-750-185-45534	Sequence 45534, A	C 200	32	1.7	1572	6	US-10-750-185-51907	Sequence 51907, A
C 128	32.8	1.7	1176	6	US-10-750-185-38096	Sequence 38096, A	C 201	32	1.7	1572	6	US-10-750-185-51637	Sequence 51637, A
C 129	32.8	1.7	1329	6	US-10-750-185-43794	Sequence 43794, A	C 202	32	1.7	1577	6	US-10-750-185-57364	Sequence 57364, A
C 130	32.8	1.7	1353	6	US-10-750-185-63040	Sequence 63040, A	C 203	32	1.7	1712	6	US-10-750-185-56826	Sequence 56826, A
C 131	32.8	1.7	1675	6	US-10-750-185-62540	Sequence 62540, A	C 204	32	1.7	1749	6	US-10-750-185-39423	Sequence 39423, A
C 132	32.8	1.7	2008	6	US-10-750-185-52123	Sequence 52123, A	C 205	32	1.7	1755	6	US-10-793-626-1231	Sequence 1231, Ap
C 133	32.8	1.7	2160	6	US-10-750-185-32657	Sequence 32657, A	C 206	32	1.7	1798	6	US-10-750-185-41106	Sequence 41106, A
C 134	32.8	1.7	2398	6	US-10-750-185-33478	Sequence 33478, A	C 207	32	1.7	2136	6	US-10-750-185-35612	Sequence 35612, A
C 135	32.8	1.7	11365	6	US-10-485-517-23	Sequence 23, Appl	C 208	32	1.7	2358	6	US-10-750-185-33755	Sequence 33755, A
C 136	32.8	1.7	340000	7	US-11-102-978-3	Sequence 3, Appl	C 209	32	1.7	2441	6	US-10-750-185-27784	Sequence 27784, A
C 137	32.6	1.7	920	6	US-10-750-185-57097	Sequence 57097, A	C 210	32	1.7	2659	6	US-10-750-185-46973	Sequence 46973, A
C 138	32.6	1.7	1017	6	US-10-750-185-30928	Sequence 30928, A	C 211	32	1.7	3146	6	US-10-793-626-3375	Sequence 3375, Ap
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C 140	32.6	1.7	1317	6	US-10-750-185-43974	Sequence 43974, A	C 213	32	1.7	3569	6	US-10-793-626-4304	Sequence 4304, Ap
C 141	32.6	1.7	1329	6	US-10-750-185-36126	Sequence 36126, A	C 214	32	1.7	4224	6	US-10-750-185-48962	Sequence 48962, A
C 142	32.6	1.7	1463	6	US-10-750-185-51906	Sequence 51906, A	C 215	32	1.7	4675	6	US-10-750-185-28612	Sequence 28612, A
C 143	32.6	1.7	1887	6	US-10-750-185-47817	Sequence 47817, A	C 216	32	1.7	207600	7	US-11-112-908-31	Sequence 31, Appl
C 144	32.6	1.7	2128	6	US-10-750-185-57392	Sequence 57392, A	C 217	31.8	1.7	600	6	US-10-750-185-3634	Sequence 3634, Ap
C 145	32.6	1.7	2547	6	US-10-750-185-53412	Sequence 53412, A	C 218	31.8	1.7	632	6	US-10-750-185-63650	Sequence 63650, A
C 146	32.6	1.7	2945	6	US-10-793-626-3371	Sequence 3371, Ap	C 219	31.8	1.7	806	7	US-11-112-908-398	Sequence 398, Appl
C 147	32.6	1.7	3001	7	US-11-145-703-211	Sequence 211, App	C 220	31.8	1.7	865	6	US-10-986-501-89	Sequence 89, Appl
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GenCore version 5.1.6
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'Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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Consensus quality: 238380 bases at least Q40
Consensus quality: 239660 bases at least Q30
Consensus quality: 240760 bases at least Q20
Estimated insert size: 255581; sum-of-coverage: 7x in Q20 bases; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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VERSION	BC097117.1 GI:66910444
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REFERENCE	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Datchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Scapleton,M., Soares,W.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Usdin,T.B., Tsohyuki,S., Carninci,P., Prange,C., Raha,S., Loquellano,N.A., Peters,G.J.,

CONSTRM TITLE	JOURNAL PUBMED	REFERENCE AUTHORS CONSTRM TITLE	JOURNAL REMARK COMMENT
Abrahamson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J.J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Kryzhanovskiy, M.I., Skalska, U., Smalins, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932 2 (bases 1 to 1455)	NIH MGC Project Direct Submission Submitted (01-JUN-2005) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgabbs@mail.nih.gov Tissue Procurement: Will Talbot cDNA Library Preparation: Dr. Yutaka Suzuki and Dr. Sumio Sugano cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) Center, Stanford University School of Medicine, Stanford, CA 94305 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Web site: http://www.shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.		

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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JOURNAL Patent: WO 02068579-A 12534 06-SEP-2002;
PE Corporation (NY) (US)

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REFERENCE 1 (bases 1 to 1451)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Jordan, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smallos, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Mammalian Gene Collection Program Team

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

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Direct Submission
Submitted (01-OCT-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: John Postlethwait, University of Oregon
cDNA Library Preparation: Dr. Sumio Sugano
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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gene
CDS

ORIGIN

Query Match 21.1%; Score 276.6; DB 5; Length 1451;
Best Local Similarity 60.0%; Pred. No. 9.8e-48;
Matches 481; Conservative 0; Mismatches 314; Indels 6; Gaps 1;

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Qy 487 CACTATTCTTCTTACCTGGAATATTGATGATTAGTATGATGATCAATCTCCCGGAGAG 546


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Qy 653 TACAACATTTATACAGGATTAAGAGAGGATTTTACAGCTATACCTTATTAAGAGAGG 712
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Qy 713 AGAGTGAATTTAAAGTCAGGAGATTTTCTTTTCCAAATACCAAAATGATGAGAAAC 772
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643 AGGTAAAGTTAATAAGCAAGAAATTTGATACATACCCATCCACGGTGATGAGAAAT 702
Qy 773 CTGCTATGCGTAATGAGTTGGTGGGGAATGAATTTTGCCTTATGATCCATCTTG 832
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703 TTGCTTGTAGCAATGTGAATATCTCTGGCAACAGTATATGCTTAATGACTTCTCATCTA 762
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RESULT 26
AL589699 Mouse DNA sequence from clone RP23-92G13 on chromosome 13. Contains
LOCUS the 3' end of the gene for a novel protein similar to KIAA0386,
DEFINITION five novel genes, the Gmn gene for geminin, gene PNAS-27, the
Ttrap gene for Traf and Tnf receptor associated protein, the gene
for a novel protein similar to KIAA0319, the gene for the ortholog
of human and rat aldehyde dehydrogenase 5A1 (succinate-semialdehyde
dehydrogenase) (ALDH5A1) (SSADH), the 5' end of the Gp1d1 gene for
glycosylphosphatidylinositol specific phospholipase D1 and four Cpg
islands, complete sequence.
AL589699
ACCESSION AL589699.4 GI:13810107
VERSION HTG; Aldh5a1; Cpg island; geminin; Gmn; Gp1d1; KIAA0319; KIAA0386;
KEYWORDS phospholipase; SSADH; Ttrap.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 256608)
AUTHORS Pelan,S.
TITLE Direct Submission
JOURNAL Submitted (16-DEC-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
Clonerequests: clonerequest@sanger.ac.uk
On Apr 26, 2001 this sequence version replaced gi:13751568.
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TrEMBL; Wp:, WormPEP; Information on the WormPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep -----

Center: UK Medical Research Council
Center code: UK-MRC
Web site: <http://mrcseq.har.mrc.ac.uk>
Contact: mouse@har.mrc.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

RP23-92G13 is from the RPCI-23 Mouse BAC Library constructed by the group of Pieter de Jong.

For further details see <http://www.choi.org/bacpac/home.htm>

VECTOR: pBACe3.6. Location/Qualifiers

FEATURES

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1. 256608

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Qy 667 AGGTAATGAAGAGGATATTTTCACAGCTATATCTATTGAAGAAAGGAGAGTGAATTTAA 726
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Qy 727 AAGTCAGGAGATATTCCTTTTCCAAATACCAAAATGATGAGAAACCTGCTATGCGTAA 786
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RESULT 29

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LOCUS BC097117
DEFINITION Danio rerio TTRAP protein, mRNA (cdna clone IMAGE:7431816), partial cds.
ACCESSION BC097117
VERSION BC097117.1 GI:66910444
KEYWORDS
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 1455)
Strausberg, R.L., Reingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Siemsen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettunen, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E., Schmech, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Mammalian Gene Collection Program Team

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 1455)

NIH MGC Project

Direct Submission

Submitted (01-JUN-2005) National Institutes of Health, Mammalian

Gene Collection (MGC), Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabs@mail.nih.gov

Tissue procurement: Will Talbot

cdna Library Preparation: Dr. Yutaka Suzuki and Dr. Sumio Sugano

cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www.shgc.stanford.edu>

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,

R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 226 Row: 9 Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 53734140.

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LOCUS AR208051 1079 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 63 from patent US 6379951.
ACCESSION AR208051
VERSION AR208051.1 GI:21507966
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1079)
AUTHORS Reed S.G. and Xu, J.
TITLE Compounds for immunotherapy of breast cancer and methods for their use
JOURNAL Patent: US 6379951-A 63 30-APR-2002;
FEATURES Location/Qualifiers
1. .1079 source

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ORIGIN

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Best Local Similarity 82.8%; Pred. No. 8.4e-93;
Matches 586; Conservative 0; Mismatches 115; Indels 7; Gaps 2;
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QY 1209 TGTGCACCTTGAATGTAGTATTGTGAAAAGCTTCCCACTTGCAGCTTT 1256
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RESULT 22

AX429924/c
LOCUS AX429924 1079 bp DNA linear PAT 21-JUN-2002
DEFINITION Sequence 63 from Patent WO0198339.
ACCESSION AX429924
VERSION AX429924.1 GI:21541088
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
Reed, S.G., Xu, J., Dillon, D.C., Retter, M.W. and Harlocker, S.L.
Compositions and methods for the therapy and diagnosis of breast
cancer

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RESULT 19
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LOCUS
DEFINITION
  Compounds for immunotherapy and diagnosis of breast cancer and
  methods for their use.
ACCESSION
  BD139846
VERSION
  BD139846.1 GI:23234791
KEYWORDS
  JP 2002507387-A/63.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominiidae; Homo.
REFERENCE
  1 (bases 1 to 1079)
  Read, S.G. and Xu, J.
  Compounds for immunotherapy and diagnosis of breast cancer and
  methods for their use
  Patent: JP 2002507387-A 63 12-MAR-2002;
  CORIXA CORP
COMMENT
  OS Homo sapiens (human)
  PN JP 2002507387-A/63
  PD 12-MAR-2002
  PF 22-DEC-1998 JP 200052543
  PR 24-DEC-1997 US 08/998253,24-DEC-1997 US 08/998255 PR
  17-JUL-1998 US 09/118627,17-JUL-1998 US 09/118554 PI STEVEN
  G REED,JIANGCHUN XU
  PC C12N15/09,A61K38/00,A61K39/00,A61K39/39,A61K39/395,A61P35/00,
  PC C07K14/47,
  PC
  C07K16/18,C12N1/19,C12N1/21,C12N5/10,C12P21/08,C12Q1/68,G01N33/ PC
  53,
  PC G01N33/577,C12N15/00,A61K37/02,C12N5/00
  CC Compounds for immunotherapy and diagnosis
  of breast cancer and
  CC methods for
  CC their use
  CC Key Location/Qualifiers
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ORIGIN
  Query Match 37.3%; Score 490; DB 6; Length 1079;
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  Matches 586; Conservative 0; Mismatches 115; Indels 7; Gaps 2;

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LOCUS
DEFINITION
  Sequence 63 from patent US 6365348.
ACCESSION
  AR202950
VERSION
  AR202950.1 GI:21499210
KEYWORDS
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SOURCE
  Unknown.
ORGANISM
  Unknown.
REFERENCE
  1 (bases 1 to 1079)
  Reed,S.G. and Xu,J.
  Compounds for diagnosis of Breast cancer and methods for their use
  Patent: US 6365348-A 63 02-APR-2002;
  JOURNAL Location/Qualifiers
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RESULT 14
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LOCUS BD157138 1898 bp DNA linear PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD157138
VERSION BD157138.1 GI:27862896
KEYWORDS JP 2002191363-A/11981.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1898)
Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 11981 09-JUL-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002191363-A/11981
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
PI SAITO,
PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
PI KEIICHI NAGAI,TETSUJI OTSUKI
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Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
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RESULT 13
AF223469 Locus 1936 bp mRNA linear PRI 17-APR-2000
DEFINITION Homo sapiens AD022 protein (AD022) mRNA, complete cds.
ACCESSION AF223469
VERSION AF223469.1 GI:7578788
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1936)
Song, H., Gao, G., Peng, Y., Ren, S., Chen, Z. and Han, Z.
A novel gene expressed in human adrenal gland
Unpublished
REFERENCE
2 (bases 1 to 1936)
Song, H., Gao, G., Peng, Y., Ren, S., Chen, Z. and Han, Z.

Direct Submission
Submitted (12-JAN-2000) Chinese National Human Genome Center at
Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
Shanghai 201203, China
Location/Qualifiers
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ORIGIN

Query Match 50.8%; Score 666.6; DB 8; Length 1936;
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Matches 842; Conservative 0; Mismatches 244; Indels 9; Gaps 2;
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Db	798	CTCAGCAAGAAATGGCAGCATGTTCTCTCTATTACCTGGAATATTGATGATTAGATC	857
Qy	528	GATCAATCTGCGCCGAGAGGGCTCGAGGGGTGTCTTCTGCTAGCTTTGTATAGTCCAG	587
Db	858	TAAACAATCTGTACAGAGGGCTCGAGGGGTGTCTTCTACTTAGCTTTGTACAGCCAG	917
Qy	588	ATGTGGTATTCTACAGAAAGTTATCCCCCATCTGTGCTGCTACCTAAAGAGAGCAG	647
Db	918	ATGTGATATTCTACAGAAAGTTATCCCCCATATTATAGCTACCTAAAGAGAGATCAA	977
Qy	648	CCAGTTACACAAATTATACAGGTATGAAGAGATATTTACAGCTATCTATTGAAGA	707
Db	978	GTAATTATGAGATTATTACAGGTATGAAGAGATATTTACAGCTATCTATTGAAGA	1037
Qy	708	AAGGAAGAGTGAAATTTAAAGTCAGGAGATTATTCCTTTTCCAAATACCAAAATGATGA	767
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Db	1098	GAACCTTTTATGTGTGATGTAATGTGTGAGGAATGAGCTTTGCTTATGACATCC	1157
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Qy	888	GAAATATGCAAGAGGCTCCAGATTCAACCGGTTATATTGACAGAGATACAAATTTAA	947
Db	1218	AGAAATGCAAGAGGCTCCAGATCAGTACAGTTATATTGACAGAGATACAAATCTAA	1277
Qy	948	GAGATCAAGAGTTATCAAAATGTGGTGTCTGCTGACCACTGTTTGTGCTGCGAAT	1007
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Qy	1008	TTTTAGCAACCTTAAACATGCGAGTATCATGGGATACGAAGCAAAATCAACCTCA	1067
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Db	1458	AGGGACACATTTATCCCGAAGTTTGGACCTTCTTGGATTAGAAAACTGGACTGTGTA	1517
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DEFINITION	Homo sapiens mRNA for TRAF and TNF receptor associated protein (trap gene).		
ACCESSION	AJ269473		
VERSION	AJ269473.1	GI:8247253	
KEYWORDS	TRAF and TNF receptor associated protein; ttrap gene.		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		

AUTHORS	Pype,S., Declercq,W., Ibrahim,A., Michiels,C., Van Rietschooten,J.G., Dewulf,N., de Boer,M., Vandenaabeele,P., Huylebroeck,D. and Remacle,J.E.									
TITLE	TTRAP, a novel protein that associates with CD40, tumor necrosis factor (TNF) receptor-75 and TNF receptor-associated factors (TRAFs), and that inhibits nuclear factor-kappa B activation									
JOURNAL	J. Biol. Chem. 275 (24), 18586-18593 (2000)									
PUBMED	10764746									
REFERENCE	2 (bases 1 to 1921)									
AUTHORS	Pype,S.									
TITLE	Direct Submission									
JOURNAL	Submitted (08-SEP-1999) Pype S., VIB07, Dept. Cell Growth, Differentiation and Development, Flanders Interuniversity Institute for Biotechnology, CELGEN, K.U.Leuven, Gasthuisberg Campus, Herestraat 49, B-3000 Leuven, BELGIUM									
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ORIGIN										
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Best Local Similarity	76.9%; Pred. No. 4.6e-130;									
Matches	842; Conservative 0; Mismatches 244; Indels 9; Gaps 2;									
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Qy	231	GGCTTCAGTGCCTGGGCTTTGCGTTGGTGGGGGATGCGACCCACGATGCTCCACGCG	290							
Db	98	GACTTCTGTGTGGAGTTTGCTCGGTGCAGAGCTGCGATGCGGAGTGCTCAGTGCT	157							
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Qy	351	AGAACACCAAGGTGCGCGCCGACCCCTCCACGCTCTTCAAGTCGGAGCCCTATGTG	410							
Db	218	TGGAGGAGAGCGCTTTGGAAACCGCCGACCTGAAACCATCTCTGAGCCCAAGACCTATGTG	277							
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Db	278	ACCTAACCAATGAGAAACAACTGATTCACCACTTCTAAATACGCCCATCTGAAGATA	337							
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Qy 1242 CCACCTTGCAGCTTT 1256
Db 1116 TTCAAGTGTGGGTTT 1130

RESULT 9

AX011599 1920 bp DNA linear PAT 06-SEP-2000
LOCUS Sequence 1 from Patent WO955859.
DEFINITION AX011599
ACCESSION AX011599
VERSION AX011599.1 GI:9998123

KEYWORDS

Source Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

1 Remacle, J.E., Huylebroeck, D.F. and Pype, S.M.

Cd40-interacting and traf-interacting proteins

Patent: WO 955859-A 1 04-NOV-1999;

REMACLE JACQUES EMILE FERNAND (BE); VLAAMS INTERUNIV INST BIOFTECH

(BE); HUYLEBROECK DANNY FRANCOIS EVE (BE); PIPE STEFAN MARIA

CHRISTIAAN (BE)

Location/Qualifiers

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ORIGIN

Query Match 50.9%; Score 668.2; DB 6; Length 1920;
Best Local Similarity 77.0%; Pred. No. 2.1e-130;
Matches 843; Conservative 0; Mismatches 243; Indels 9; Gaps 2;

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Db 36 GCCTGGAGGCGGAGGCGGCGGAGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGG 95

Qy 231 GGCTTCAGTCTGGGCTTTCGTTGGTGGGGGATCGGACCCACGATGGTCCCGACGC 290
Db 96 GACTTCTGTGTGGAGTTTGGCTTCGTCGCAAGCTCGATGCGGACGCTCAGTGCT 155

Qy 291 TCCTGCGGAGAACGACTGGCAGACGACGAGAGCCCTGAGCGCTACTTCGAGCTGCCAG 350
Db 156 TCCTGCGGAGAACGACTGGGAGATGGAAAGGCTCTGAATCTTCTAGCTCCGCTCCG 215

Qy 351 AGAACACCAAGGGTGCAGCGGCGGACGCTCCACGTCCTTCAAGTCCGAGCGCTATGTTG 410
Db 216 TGGAGGAGAGCGGCTTGGAAACGCGGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTG 275

Qy 411 ATCTAACCAACGAGGATGCAATGATACAAACATTTTAGAGCCAGTCCATCTGGA---A 467
Db 276 ACCTAACCAATGNAGAAAACAATGATTCACCACTTCTAAATCAGCCCATCTGAAGATA 335
Qy 468 CTCCTCTAGAAGATAGCAGACATTTCTTTTCAATACCTGGAAATATGTAGTGAATGATG 527
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Qy 528 GATGCAATCTGCCGAGAGGGCTCGAGGGGTGTGTTCCCTGCTAGCTTGTATAGTCCAG 587
Db 396 TAAACCAATCTGTGAGAGAGGGCTCGAGGGGTGTGTTCCCTAGCTTGTATAGTCCAG 455
Qy 588 ATGTGTTATTTCTACAGGAAGTTATCCCGCCATACCTGCTACCTAAAGAGAGAGCAG 647
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Qy 648 CAGTTACACATTTATACAGGTAATGAAGAGGATATTTTCAGCTATATCTATTTGAAGA 707
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Qy 708 AAGGAAGAGTGAATTTAAAGTTCAGGAGATTTCTTTTCCAAATACCAAAATGATGA 767
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RESULT 10

AR339398

LOCUS

DEFINITION

AR339398

ACCESSION

AR339398

VERSION

AR339398.1

KEYWORDS

GI:33726255

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 1948)

AUTHORS

Tang, Y.T., Zhou, P. and Drmanac, R.T.

AR339398 Sequence 889 from patent US 659662.
PAT 17-AUG-2003

Query Match		50.9%;	Score 668.2;	DB 8;	Length 1261;
Best Local Similarity		77.0%;	Pred. No. 2e-130;		
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QY	171	GGCGGGCGCGTCCGCCGCCGAGCAGACAGCGGAGGAGGACCGGGTGAAGAGCGGC	230		
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QY	231	GGCTTCAGTCCTGGGCTTTCGGTGTGGTGGGGGATCGGACCCACGATGTCCTCCAGCG	290		
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QY	351	AGAACGACCAAGGGTGGCGCGCGCAGCTCCACGCTCTTCAAGTCGAGGCTATGTTG	410		
DB	222	TGAGGAGAGCGCCTTGGAAACGCCGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTG	281		
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QY	468	CTCTCTAGAAGATAGCAGCACTATTTCCTTCAATTAACCTGGAATATTGATGGATTAGATG	527		
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QY	588	ATGTGTTATTTCTACAGGAAGTTATCCCCCATACTGTGCTACCTTAAAGAGAGAGCAG	647		
DB	462	ATGTGATATTTCTACAGGAAGTTATTCCTCCCATATTATAGTACTACCTTAAAGAGAGATCAA	521		
QY	648	CCAGTTACACAATTTATACAGTAAATGAAGAAGATATTTTACAGCTATATCTATTGAAGA	707		
DB	522	GTAATTTATGAGATTTATACAGTCAATGAAGAAGATATTTTACAGCTATATATGTTTGAAGA	581		
QY	708	AAGGAAGTGAATTTTAAAGTCAGGAGATTTATCTTTTCCAAATACCAAAATGATGA	767		
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DB	642	GAAACCTTTTATGTGTCATGTGAATGTGTGAGGAATGAGCTTTGCTTTATGACATCCC	701		
QY	828	ATTTGGAGAGCACAGAGAACATTTCTCGGAAACGAATTAAGACAAATTAATAAATCTGTTTG	887		
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QY	888	GAAAAATGCAAGAGGCTCCAGATTCAACACGGTTTATTTTGGAGGATACAAATTTAA	947		
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QY	948	GAGATCAAGAGTTATCAAAATGTGGTGTTCCTGACACGTTTGTGATGCTCGGAAAT	1007		
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LOCUS					
DEFINITION		CD40-Interacting and TRAF-interacting protein.			
ACCESSION		BD205490			
VERSION		BD205490.1 GI:33015260			
KEYWORDS		JP 2002512796-A/1.			
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ORGANISM		Homo sapiens			
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE		1 (bases 1 to 1920)			
AUTHORS		Pype,S.M.C., Ghislain,J.B.F.J., Remacle and Huylebroeck,D.F.E.			
TITLE		CD40-Interacting and TRAF-interacting protein			
JOURNAL		Patent: JP 2002512796-A 1 08-MAY-2002;			
		VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE VZW			
COMMENT		OS Homo sapiens (human)			
		PN JP 2002512796-A/1			
		PD 08-MAY-2002			
		PF 28-APR-1999 JP 2000546003			
		PR 29-APR-1998 EP 98201392.2			
		PI STEFAN MARIA CHRISTIAAN PYPE,			
		PI JACQUES EMILE FERNAND JOSIANE GHISLAIN REMACLE, PI DANNY			
		FRANCOIS EVELINE HUYLEBROECK			
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QY	171	GGCGGGCGCGTCCGCCGCCGAGCAGACAGCGGAGGAGGACCGGGTGAAGAGCGGC	230		
DB	36	GCCTGGAGGCGGAGGAGGCGCGGAGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGG	95		
QY	231	GGCTTCAGTCCCTGGGCTTTCGGTGTGGTGGGGGATCGGACCCACGATGTCCTCCAGCG	290		
DB	96	GACTTCTGTGTGGAGTTTGCCTCGTCCGATGTCGATGTCGAGTGGCTCAGTGCT	155		
QY	291	TCCTGCGGAGAACGACTCGGACAGCAGAGAGCCCTGAGCGCTACTTCGAGCTGCCAG	350		
DB	156	TCCTGCCCGAGAACGACTCGGAGATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCCG	215		
QY	351	AGAACGACCAAGGGTGGCGCGCAGCTCCACAGCTCCCAAGCTCTTCAAGTCCGAGGCTATGTTG	410		
DB	216	TGGAGGAGAGCGCTTGGAAACGCCGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTG	275		
QY	411	ATCTAACCAACGAGGATGCAATGATACAAACATTTTAGNAGCCATCTCCATCTGGA---A	467		
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ORIGIN

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Qy 114 GACTTCTGTGTGGAGTTGGCTCGGTGCGAAGCTGCGATGCGCGCAGTGCTCAGTGCT 173
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Qy 174 TCCTCGGGGAGACGACTGGGAGATGGAAGGGCTCTGAACCTCTACTTCGAGGCTCCG 233
Db      |||
Qy 351 AGAAGCAAGGCTGGCGCGCCGAGCTCCCGAGCTCTCAAGTCCGAGGCTATGTG 410
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Db      |||
Qy 354 CTCAGCAAGAAATGGCAGCATGTCTCTCTCATCTACCTGGAATATTGATGATAGATC 413
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Qy 708 AAGGAAGAGTGAATTTTAAAGTCAGGAGATTAATTCCTTTTCCAAATACCAAAATGATGA 767
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RESULT 6
AF201687      1261 bp mRNA linear PRI 16-MAY-2003
LOCUS      Homo sapiens ETS1-associated protein 2 (EAP2) mRNA, complete cds.
DEFINITION
ACCESSION      AF201687
VERSION      AF201687.1 GI:11493668
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
REFERENCE      1 (bases 1 to 1261)
AUTHORS      Pei,H., Yordy,J.S., Leng,Q., Zhao,Q., Watson,D.K. and Li,R.
TITLE      EAP11 interacts with ETS1 and modulates its transcriptional
              function
JOURNAL      Oncogene 22 (18), 2699-2709 (2003)
PUBMED      12743594
REFERENCE      2 (bases 1 to 1261)
AUTHORS      Li,R., Pei,H. and Papas,T.S.
TITLE      Direct Submission
JOURNAL      Submitted (03-NOV-1999) Center for Molecular and Structural
              Biology, Department of Medicine, and Hollings Cancer Center,
              Medical University of South Carolina, 86 Jonathan Lucas St.,
              Charleston, SC 29425, USA

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gene
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ORIGIN
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Qy	555	GGGTGTGTTCCCTGCCTAGCTTTGTATAGTCCAGATGTGGTATTTCTACAGGAAGTTATCC	614
Db	481	GGGTGTGTTCCCTGCCTAGCTTTGTATAGTCCAGATGTGGTATTTCTACAGGAAGTTATCC	540
Qy	615	CCCATACTGCTGCTACTTAAGAGAGAGCAGCCAGTTACACAAATTTATTACAGGTAATG	674
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Qy	675	AAGAAGGATATTTACAGCTTATCTATTGAAGAAAGGAGAGGTGAATTTTAAAGTCAGG	734
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Qy	735	AGATTATTCCTTTCCAAATACCAAAATGATGAAACCTGCTATGCGTAAATGTGAGTT	794
Db	661	AGATTATTCCTTTCCAAATACCAAAATGATGAAACCTGCTATGCGTAAATGTGAGTT	720
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Qy	1275	GTCTGTAATTTGTAGGTCCTCAACCTTTCCAGGACATC	1312
Db	1201	GTCTGTAATTTGTAGGTCCTCAACCTTTCCAGGACATC	1238
RESULT 5	BC017553		
LOCUS			
DEFINITION	BC017553 1952 bp mRNA linear PRI 29-JUN-2004 Homo sapiens TRAF and TNF receptor associated protein, mRNA (CDNA clone MGC:9099 IMAGE:3920790), complete cds.		
ACCESSION	BC017553		
VERSION	BC017553.2 GI:34782842		
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		

REFERENCE
AUTHORS

1. (bases 1 to 1952)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouford, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Kravinsky, M.I., Skalska, U., Smalls, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932

REFERENCE

2. (bases 1 to 1952)

AUTHORS

Strausberg, R.

TITLE

Direct Submission
Submitted (19-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT

On Sep 16, 2003 this sequence version replaced gi:17028464.

Contact: MGC help desk

Email: cgabs-r@mail.nih.gov

Tissue Procurement: ATCC/DC/DTP

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Frahbu, Parvaneh Saeedi, JR Santos, Angeliue Schnerch, Ursula Skalska, Duane Smalius, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 15 Row: m Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23510347.

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RESULT 4
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LOCUS Mus musculus mRNA for putative TRAF and TNF receptor associated
DEFINITION protein (ttrap gene).
ACCESSION AJ251328
VERSION AJ251328.1 GI:8247282
KEYWORDS ttrap gene.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Pye S., Declercq W., Ibrahim A., Michiels C., Van
Rietshoven J.G., Dewulf N., de Boer M., Vandenabeele P.,
Huybreck D. and Remacle J.E.
TITLE TTRAP, a novel protein that associates with CD40, tumor necrosis
factor (TNF) receptor-75 and TNF receptor-associated factors
(TRAFs), and that inhibits nuclear factor-kappa B activation
J. Biol. Chem. 275 (24), 18586-18593 (2000) X
10764746
JOURNAL 2 (bases 1 to 1943)
PUBMED
REFERENCE 2
AUTHORS Pye S.M.C.
TITLE Direct Submission
JOURNAL Submitted (25-NOV-1999) Pye S.M.C., VIB07, Department Cell Growth,
Differentiation and Developme, Planders Interuniversity Institute
for Biotechnology, K.U.Leuven, Campus Gasthuisberg, Herestraat 49,
3000 Leuven, BELGIUM
COMMENT Related sequence: AJ269473.
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RESULT 3
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DEFINITION Sequence 3 from Patent WO9955859.
ACCESSION AX011601
VERSION AX011601.1 GI:9998125
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Euarhontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
1 Remacle,J.E., Huylebroeck,D.,~~P.~~and Pype,S.M.
Cd40-interacting and ~~praf~~-interacting proteins
Patent: WO 9955859-A 3 04-NOV-1999;
JOURNAL REMACLE JACOURS EMILIS-PERNAND (BE); VLAAMS INTERUNIV INST BIOTECH
(BE); HUYLEBROECK DANNY FRANCOIS EVE (BE); PYPE STEFAN MARIA
CHRISTIAAN (BE)

FEATURES
Location/Qualifiers
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1312)
AUTHORS Pye, S.M.C., Renacle, J.B.F. and Huylebroeck, D.F.E.
TITLE CD40-interacting and TRAF-interacting proteins
JOURNAL Patent: US 6812203-A 3 02-NOV-2004;
Vlaams Interuniversitair Instituut voor Biotechnologie VZW;
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138	56.8	4.3	655	6	AX525726	Sequence	211	55.8	4.3	676	6	AX525795	Sequence
139	56.8	4.3	665	6	AX525496	Sequence	212	55.8	4.3	684	6	AX525543	Sequence
140	56.8	4.3	688	6	AX525527	Sequence	213	55.8	4.3	684	6	AX525702	Sequence
141	56.8	4.3	688	6	AX525732	Sequence	214	55.8	4.3	684	6	AX525720	Sequence
142	56.8	4.3	689	6	AX525518	Sequence	215	55.8	4.3	686	6	AX525655	Sequence
143	56.8	4.3	690	6	AX525539	Sequence	216	55.8	4.3	686	6	AX525748	Sequence
144	56.8	4.3	692	6	AX525673	Sequence	217	55.8	4.3	689	6	AX525634	Sequence
145	56.8	4.3	693	6	AX525672	Sequence	218	55.8	4.3	689	6	AX525830	Sequence
146	56.8	4.3	694	6	AX525617	Sequence	219	55.8	4.3	691	6	AX525785	Sequence
147	56.8	4.3	695	6	AX525479	Sequence	220	55.8	4.3	692	6	AX525792	Sequence
148	56.8	4.3	699	6	AX525763	Sequence	221	55.8	4.3	693	6	AX525605	Sequence
149	56.8	4.3	701	6	AX525689	Sequence	222	55.8	4.3	693	6	AX525618	Sequence
150	56.8	4.3	705	6	AX525596	Sequence	223	55.8	4.3	693	6	AX525676	Sequence
151	56.8	4.3	709	6	AX525523	Sequence	224	55.8	4.3	694	6	AX525586	Sequence
152	56.8	4.3	710	6	AX525659	Sequence	225	55.8	4.3	694	6	AX525677	Sequence
153	56.8	4.3	713	6	AX525711	Sequence	226	55.8	4.3	694	6	AX525722	Sequence
154	56.8	4.3	717	6	AX525647	Sequence	227	55.8	4.3	694	6	AX525735	Sequence
155	56.8	4.3	721	6	AX525768	Sequence	228	55.8	4.3	695	6	AX525616	Sequence
156	56.6	4.3	631	6	AX525553	Sequence	229	55.8	4.3	697	6	AX525750	Sequence
157	56.6	4.3	659	6	AX525800	Sequence	230	55.8	4.3	700	6	AX525571	Sequence
158	56.6	4.3	678	6	AX525668	Sequence	231	55.8	4.3	701	6	AX525697	Sequence
159	56.6	4.3	682	6	AX525671	Sequence	232	55.8	4.3	703	6	AX525813	Sequence
160	56.6	4.3	684	6	AX525642	Sequence	233	55.8	4.3	703	6	AX525822	Sequence
161	56.6	4.3	689	6	AX525835	Sequence	234	55.8	4.3	703	6	AX525847	Sequence
162	56.6	4.3	698	6	AX525490	Sequence	235	55.8	4.3	704	6	AX525615	Sequence
163	56.6	4.3	703	6	AX525568	Sequence	236	55.8	4.3	704	6	AX525632	Sequence
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 09:15:11 ; Search time 6684.65 Seconds
(without alignments)
11156.694 Million cell updates/sec

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Perfect score: 1312
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

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- 1: gb_ba.*
- 2: gb_in.*
- 3: gb_env.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_sts.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_vl.*
- 14: gb_htg.*
- 15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1312	100.0	1312	6	BD205491
2	1312	100.0	1312	6	AR594295
3	1312	100.0	1312	6	AX011601
4	1238	94.4	1943	9	MMU251328
5	668.6	51.0	1952	8	BC017553
6	668.2	50.9	1261	8	AF201687
7	668.2	50.9	1920	6	BD205490
8	668.2	50.9	1920	6	AR594294
9	668.2	50.9	1920	6	AX011599
10	668.2	50.9	1948	6	AR339398
11	668.2	50.9	2499	6	E23195
12	666.6	50.8	1921	8	BSA269473
13	666.6	50.8	1936	8	AF223469
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15	665	50.7	1898	6	AX878304
16	665	50.7	1898	6	AX002168
17	648.2	49.4	150344	14	AC152027
18	585.2	44.6	2151	8	HA420495

Db 522 TGCCAGTATACATGGGATACACAAATGAA 550

Search completed: December 3, 2005, 11:01:01
Job time : 820.517 secs

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Qy 608 GTTATCCCCCATACTGTGCTTACCTTAAGAGAGAGAGCAGCTTACACAAATTATTACA 667
Db 86 GTTATCCCCCATATTATAGTCTACTTAAGAGAGATCAAGTAATTATGAGATTATTACA 145
Qy 668 -GGTAATGAAGAAGGATATTTTACAGCTATATCTATTGAAGAAAGAGAGTGAATTTAA 726
Db 146 GGGTCATCAAGAAGGATATTTTACAGCTATATCTATTGAAGAAATCAAGAGTGAATTTAA 205
Qy 727 AAGTCAGAGATATTTCTTTTCCAAATACCAAAATGATGAAACCTGCTATGCGTTAA 786
Db 206 AAGCCAAGAGATATTTCTTTTCCAAATGATGAAACCTTTTATGTTGCA 265
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Db 266 TGTGAATGTGTCAAGAAATGAGCTTTGCTTATGATCCCATTTGGAGAGCACCAGAGG 325
Qy 847 ACATTCTCGGGAACGAATAAGACAAATTTAAATCTGTTTGGAAAAATGCAAGAGGCTCC 906
Db 326 GCATCTCGGGAACGAATGAATCACTTAAATGTTTAAAGAAATGCAAGAGGCTCC 385
Qy 907 AGATTCAACCAAGGTTATTTTGGAGAGATACAAATTTAGAGATCAAGAGTTATCAA 966
Db 386 AGAGTCAGCTACAGTTATTTTGCAGGAGATACAAATCTAAGGGATCGAGAGGTTACCAG 445
Qy 967 ATGTGTTGTTTACCTGCAACAGTTTGTGCTGCGGAATTTTGGAAAAATGCAAGAGGCTCC 1026
Db 446 ATGTGTTGTTTACCAACAAATTTGTGATGCTGCGGAGTTTGGGCAACCTTAACA 505
Qy 1027 TTGCCAGTATACATGGGATACGAAAGCAAAATCAACCTCAGGATCCCTGCTGCTTATAA 1086
Db 506 TTGCCAGTATACATGGGATACGAAATGAATCTTAATCTTGAATAACTGCTGCTGTAA 565
Qy 1087 GCATCGTTTGTATCAATTTTTCAGAGCAGAAG 1121
Db 566 ACTTCGTTTGTATCAATTTTTCAGAGCAGAG 600
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RESULT 30

ADT95464

ID ADT95464 standard; cDNA; 553 BP.

XX AC

XX ADT95464;

XX DT

XX 16-DEC-2004 (first entry)

XX DE

XX Colon cancer associated human cDNA sequence #983.

XX KW

KW Colon cancer; T cell; tumour protein; C634S; C635S; C637S; C640S; C636S;

KW humoral immune response; cellular immune response; cytostatic;

KW immunostimulant; human; ss.

XX OS

OS Homo sapiens.

XX PN

PN US2003087818-A1.

XX PD

PD 08-MAY-2003.

XX PF

PF 01-FEB-2002; 2002US-00066543.

XX PR

PR 02-FEB-2001; 2001US-0267400P.

XX PR

PR 07-FEB-2001; 2001US-0267382P.

XX PR

PR 11-MAY-2001; 2001US-0290322P.

XX PR

PR 12-JUL-2001; 2001US-030526SP.

XX PR

PR 16-AUG-2001; 2001US-0313077P.

XX PA

PA (CORI-) CORIXA CORP.

XX PI

PI Jiang Y, Chenault RA, Xu J, Indirias CY, Lodes MJ, Secretist H;

PI Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;

XX

WPI; 2003-040540/03.

New isolated nucleic acids and polypeptides capable of eliciting a humoral and/or cellular immune response, useful for diagnosing, preventing or treating cancer, particularly colon cancer.

Claim 1; SEQ ID NO 983; 87pp; English.

The invention relates to polynucleotide and polypeptide sequences associated with cancer, particularly colon cancer. Also disclosed are (i) an expression vector comprising the polynucleotide, (ii) a host cell transformed or transfected with the expression vector, (iii) an isolated antibody, or its antigen-binding fragment, which specifically binds to the polypeptide, (iv) a method of detecting or determining the presence of cancer in a patient, (v) a fusion protein comprising at least one of the polypeptides, (vi) an oligonucleotide that hybridises to the polynucleotide sequence under highly stringent conditions, and (vii) a method of stimulating and/or expanding T cells specific for a tumour protein. The polypeptide specifically comprises the amino acid sequence of C634S, C635S, C637S, C640S, C636S or one of the potential open reading frames (ORFs) of C636S. These polypeptides are encoded by the polynucleotide sequences, where both are capable of eliciting a humoral and/or cellular immune response. The polynucleotides, polypeptides, and antibodies are useful for diagnosing, preventing or treating cancer, particularly colon cancer. The polynucleotide and polypeptide sequences are also useful in DNA strand invasion, antisense inhibition, mutational analysis, nucleic acid purification, isolation of transcriptionally active genes, blocking or transcription factor binding, genome cleavage or in situ hybridisation, and as enhancers of transcription or biomarkers. This sequence represents a human colon cancer associated cDNA. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov

Sequence 553 BP; 181 A; 94 C; 125 G; 151 T; 0 U; 2 Other;

Query Match 29.4%; Score 385.8; DB 11; Length 553;

Best Local Similarity 84.9%; Pred. No. 2.4e-96;

Matches 432; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

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Qy 548 GCTCAGGGGTGTGTTCTCGCTAGCTTTGTATAGTCCAGATGTGTTTCTACAGAA 607
Db 42 GCTCGAGGGGTGTGTTCTCTACTTAGCTTTGTACAGCCAGATGTATTTCTACAGAA 101
Qy 608 GTTATCCCCCATACTGTGCTTACCTTAAGAGAGAGCAGCTTACACAAATTATTACA 667
Db 102 GTTATTTCCCTCATTTATATAGTCTACCTTAAGAGAGATCAAGTAATTATGAGATTATTACA 161
Qy 668 GGTAAATGAAGAAGGATATTTTCCAGCTATATCTATTGAAGAAAGAGTGAATTTAAA 727
Db 162 GGTATGAAGAAGGATATTTTCCAGCTATATCTATTGAAGAAATCAAGAGTGAATTTAAA 221
Qy 728 AGTCAGGAGATTTATTTCTTTTCCAAATACCAAAATGATGAGAAACCTGCTATGCTTAAT 787
Db 222 AGCCAAGAGATTTATTTCTTTTCCAAATGATGAGAAACCTTTTATGTGTCAT 281
Qy 788 GTGAGTTGGGTGGAATGAATTTTGCCTTATGACATCCCATTTGGAGAGCACCAGAGAA 847
Db 282 GTGAATGTGTGAGGAATGAGCTTTGCTTATGACATCCCATTTGGAGAGCACCAGAGGG 341
Qy 848 CATTTCTGCGGAACGAATAAGACAAATTTAAAACTGTTCTTGGAAAAATGCAAGAGGCTCA 907
Db 342 CATGCTCGGAACGAATGAATCAGTTAAATGTTTAAAGAAATGCAAGAGGCTCA 401
Qy 908 GATTCAACCAACGTTTATATTTTGCAGGAGATACAAATTTTAAGAGATCAAGAGTTATCAA 967
Db 402 GAGTCAGCTACAGTTATATTTTGCAGGAGATACAAATCTAAGGATCGAGAGGTTACCAGA 461
Qy 968 TGTGTTGTTTACCTGACAAAGTTTTCATGCTGCGGAATTTTTCAGGCAACCTAACAT 1027
Db 462 TGTGTTGTTTACCCCAACCAATTTGATGCTGCGGAGTTTTCGGGCAACCTAACAT 521
Qy 1028 TGCCAGTATACATGGGATACGAAAGCAAA 1056
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PR 12-JUL-2001; 2001US-0305265P.
XX 16-AUG-2001; 2001US-0313077P.
PA (CORI-) CORIXA CORP.
PI Jiang Y, Chenault RA, Xu J, Indirias CY, Lodes MJ, Secretist H;
PI Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;
XX WPI; 2003-040540/03.
XX New isolated nucleic acids and polypeptides capable of eliciting a
PT humoral and/or cellular immune response, useful for diagnosing,
PT preventing or treating cancer, particularly colon cancer.
XX Claim 1; SEQ ID NO 548; 87pp; English.
XX The invention relates to polynucleotide and polypeptide sequences
CC associated with cancer, particularly colon cancer. Also disclosed are (i)
CC an expression vector comprising the polynucleotide, (ii) a host cell
CC transformed or transfected with the expression vector, (iii) an isolated
CC antibody, or its antigen-binding fragment, which specifically binds to
CC the polypeptide, (iv) a method of detecting or determining the presence
CC of cancer in a patient, (v) a fusion protein comprising at least one of
CC the polypeptides, (vi) an oligonucleotide that hybridizes to the
CC polynucleotide sequence under highly stringent conditions, and (vii) a
CC method of stimulating and/or expanding T cells specific for a tumour
CC protein. The polypeptide specifically comprises the amino acid sequence
CC of C634S, C635S, C637S, C640S, C636S or one of the potential open reading
CC frames (ORFs) of C636S. These polypeptides are encoded by the
CC polynucleotide sequences, where both are capable of eliciting a humoral
CC and/or cellular immune response. The polynucleotides, polypeptides, and
CC antibodies are useful for diagnosing, preventing or treating cancer,
CC particularly colon cancer. The polynucleotide and polypeptide sequences
CC are also useful in DNA strand invasion, antisense inhibition, mutational
CC analysis, nucleic acid purification, isolation of transcriptionally
CC active genes, blocking or transcription factor binding, genome cleavage
CC or in situ hybridization, and as enhancers of transcription or
CC biomarkers. This sequence represents a human colon cancer associated
CC cDNA. Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at seqdata.uspto.gov
XX
SQ Sequence 625 BP; 200 A; 107 C; 144 G; 172 T; 0 U; 2 Other;
Query Match 31.9%; Score 418; DB 11; Length 625;
Best Local Similarity 84.0%; Pred. No. 2.9e-105;
Matches 483; Conservative 0; Mismatches 91; Indels 1; Gaps 1;
QY 548 GCTCGAGGGGTGTCTCTGCTAGCTTTGTATAGTCCAGATGTGGTATTCTACAGGAA 607
DB 26 GCTCGAGGGGTGTCTCTACTTACTTGTGTACAGCCAGATGTGNTATTCTACAGGAA 85
QY 608 GTTATCCCCCCTACTGTGCTACTCTAAAGAGAGAGACGCCAGTTACAAATTATTACA 667
DB 86 GTTATCCCCCCTATTATAGTACTCTAAAGAGAGATCAAGTAAATTATGAGATTATTACA 145
QY 668 -GGTAATGAGAGAGATTTTACAGCTATCTATTGAAGAGAGAGAGTGAATTTAA 726
DB 146 GGGTCATGAGAGAGATTTTACAGCTATCTATTGAAGAGAGATCAAGAGTGAATTTAA 205
QY 727 AAGTCAGAGAGATTTCTCTTTCCAAATACCAAAATGATGAGAACTGCTATGCGTAAA 786
DB 206 AAGCAAGAGATTTATCTTTTCCAGTACCAAAATGATGAGAACTTTTATGTGTGCA 265
QY 787 TGTGAGTTTGGGTGGAATGAATTTTGCCTTATGACATCCATTTGGAGAGCACAGAGA 846
DB 266 TGTGAATGTGTCAGAGAAATGAGTTTGCCTTATGACATCCATTTGGAGAGCACAGAG 325
QY 847 ACATTCTCGGAACGAATAGACAAATTTAAACCTGTTCTGGAATAATGCAAGGGCTCC 906
DB 326 GCATGCTGCGGAACGAATAGATCAAGTATGATTTTAAAGAAATGCAAGAGGCTCC 385
QY 907 AGATTTCACCAACGGTTATTTTTCAGGAGATACAAATTTTAAAGATCATCAAGAGTTTCAA 966

386 AGAGTCAGCTACAGTTATATTTTCAGGAGATACAAATCTTAAGGATCGAGAGGTTACCAG 445
967 ATGTGTGTGTTTACCTGACACAGCTTTTGTGCTGCTGGATTTTGTAGGCAACCTAAACA 1026
446 ATGTGTGTGTTTACCTGACACAGCTTTTGTGCTGCTGGATTTTGTAGGCAACCTAAACA 505
1027 TTGCCAGTATACATGGATACGAAAGCAAAATACAACTCAGGATCCCTGCTGCTTATAA 1086
506 TTGCCAGTATACATGGATACGAAAGCAAAATACAACTCAGGATCCCTGCTGCTTATAA 565
1087 GCATCGTTTGTGATCGAATATTTTTCAGAGCAGAG 1121
566 ACTTCGTTTGTGATCGAATATTTTTCAGAGCAGAG 600

RESULT 29
ADX41511
ID ADX41511 standard; cDNA; 625 BP.
XX AC ADX41511;
XX AC ADX41511;
DT 21-APR-2005 (first entry)
DE Human cDNA encoding colon cancer protein SEQ ID NO 548.
XX Cytostatic; Immunostimulant; therapy; diagnosis; colon cancer; neoplasm;
XX ss; gene.
XX Homo sapiens.
XX WC200274156-A2.
PD 26-SEP-2002.
XX 01-FEB-2002; 2002WO-US002870.
XX 02-FEB-2001; 2001US-0267400P.
PR 07-FEB-2001; 2001US-0267382P.
PR 11-MAY-2001; 2001US-0290322P.
PR 12-JUL-2001; 2001US-0305265P.
PR 16-AUG-2001; 2001US-0313077P.
XX (CORI-) CORIXA CORP.
XX Jiang Y, Chenault RA, Xu J, Indirias CY, Lodes MJ, Secretist H;
PI Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;
XX WPI; 2003-040540/03.
XX New isolated nucleic acids and polypeptides capable of eliciting a
PT humoral and/or cellular immune response, useful for diagnosing,
PT preventing or treating cancer, particularly colon cancer.
XX Claim 1; SEQ ID NO 548; 244pp; English.
XX The invention relates to a new isolated nucleic acid. The nucleic acids,
CC polypeptides, antibodies are useful for diagnosing, preventing or
CC treating cancer, particularly colon cancer. The nucleic acid and
CC polypeptides are also useful in DNA strand invasion, antisense
CC inhibition, mutational analysis, nucleic acid purification, isolation of
CC transcriptionally active genes, blocking or transcription factor binding,
CC genome cleavage or in situ hybridization, and as enhancers of
CC transcription or biomarkers. The kits are useful for detecting antibody
CC binding. The present sequence represents a human cDNA encoding a colon
CC cancer protein.
SQ Sequence 625 BP; 200 A; 107 C; 144 G; 172 T; 0 U; 2 Other;
Query Match 31.9%; Score 418; DB 11; Length 625;
Best Local Similarity 84.0%; Pred. No. 2.9e-105;
Matches 483; Conservative 0; Mismatches 91; Indels 1; Gaps 1;
QY 548 GCTCGAGGGGTGTCTCTGCTAGCTTTGTATAGTCCAGATGTGGTATTCTACAGGAA 607

Db 274 GTGAATGTGTCAGGAATGAGCTTTGCTTATGATCCCATTTGGAGAGCAGAGGG 333
Qy 848 CATTCTCGGAAACGAATAAGACAATTAATAAATCTTCTTGGAATAATGCAAGAGCTCCA 907
Db 334 CATCTCTCGGAAACGAATGATCACTTAATAATGCTTTTAAAGAAATGCAAGAGCTCCA 393
Qy 908 GATTCAACCAACGGTTATATTTGAGGAGATACAAATTTTAAGAGATCAAGAAGTTTATCAA 967
Db 394 GAGTCAGCTACAGTTATATTTGAGGAGATACAAATCTAAGGGATCGAGAGGTTTACCAGA 453
Qy 968 TGTGGTGTGTACCTGACACGTTTTTGTGCTGCTGGGAATTTTATAGCAACCTTAAACAT 1027
Db 454 TGTGGTGTGTACCTGACACCAACATTTGATGATGCTTGGGAGTTTTTGGGCAACCTTAAACAT 513
Qy 1028 TGCCAGTATACATGGGATACGAAAGCAAAATTAACAACCTCAGGATCCCTGCTGCTTTATAAG 1087
Db 514 TGCCAGTATACATGGGATACCAAAATGAACCTTAATCTTGAATAAATGCTGCTTTGATAA 573
Qy 1088 CATCGTTTGTGATCGAAATATTTTTCAGAGCAGAG 1121
Db 574 CTTCGTTTGTGATCGAATATTTTTCAGAGCAGCAG 607

RESULT 27

ID ADX42047
XX ADX42047 standard; cDNA; 633 BP.

AC ADX42047;

DT 21-APR-2005 (first entry)

DE Human cDNA encoding colon cancer protein SEQ ID NO 1084.

DE Cytostatic; Immunostimulant; therapy; diagnosis; colon cancer; neoplasm;
KW ss; gene.

OS Homo sapiens.

XX WO200274156-A2.

XX 26-SEP-2002.

XX 01-FEB-2002; 2002WO-US002870.

XX 02-FEB-2001; 2001US-0267400P.

XX 07-FEB-2001; 2001US-0267382P.

XX 11-MAY-2001; 2001US-0290322P.

XX 12-JUL-2001; 2001US-0305265P.

XX 16-AUG-2001; 2001US-0313077P.

XX (CORI-) CORIXA CORP.

XX Jiang Y, Chenault RA, Xu J, Indirias CY, Lodes MJ, Secrist H;

XX Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;

XX WPI; 2003-040540/03.

XX New isolated nucleic acids and polypeptides capable of eliciting a

XX humoral and/or cellular immune response, useful for diagnosing,

XX preventing or treating cancer, particularly colon cancer.

XX Claim 1; SEQ ID NO 1084; 244pp; English.

XX The invention relates to a new isolated nucleic acid. The nucleic acid,

XX polypeptides, antibodies are useful for diagnosing, preventing or

XX treating cancer, particularly colon cancer. The nucleic acid and

XX polypeptides are also useful in DNA strand invasion, antisense

XX inhibition, mutational analysis, nucleic acid purification, isolation of

XX SQ Sequence 633 BP; 205 A; 108 C; 144 G; 175 T; 0 U; 1 Other;

Query Match 32.7%; Score 428.4; DB 11; Length 633;

Best Local Similarity 84.1%; Pred. No. 3.8e-108;

Matches 483; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Qy 548 GCTCGAGGGGTGTGTTCTCTACTTAGCTTTGTACAGCCAGATGTGATTTCTACAGAA 607

Db 34 GCTCGAGGGGTGTGTTCTCTACTTAGCTTTGTACAGCCAGATGTGATTTCTACAGAA 93

Qy 608 GTTATCCCCCATCTGCTTACCTAAAGAAGAGAGCAGCCAGTTACACAAATTTATACA 667

Db 94 GTTATCCCCCATCTGCTTACCTAAAGAAGAGATCAAGTAATTTATGAGATTTATACA 153

Qy 668 GGTAATGAAGAAGATATTTTACAGCTATCTACTTGAAGAAAGAGAGTGAATTTTAAA 727

Db 154 GGTCAATGAAGAAGATATTTTACAGCTATCTACTTGAAGAAATCAAGAGTGAATTTAAA 213

Qy 728 AGTCAGGAGATTTTCTTTTCCAAATACCAAAATGATGAAACCTGCTATGCGTAAT 787

Db 214 AGCCAGAGATTTTCTTTTCCAAATGATGAAACCTGCTATGCGTAAT 273

Qy 788 GTGAGTTTGGGTGGAATGAATTTTGCCTTATGATCCCATTTGGAGAGCACCAGAGAA 847

Db 274 GTGAATGTGTCAGGAATGAGCTTTGCTTATGATCCCATTTGGAGAGCACCAGAGGG 333

Qy 848 CATTCTCGGAAACGAATAAGACAAATTAATAAATCTGTTCTTGGAAAAATGCAAGAGCTCCA 907

Db 334 CATCTCGGAAACGAATGAATCACTTAAATAATGTTTTTAAAGAAATGCAAGAGCTCCA 393

Qy 908 GATTCAACCAACGGTTATATTTGAGGAGATACAAATTTTAAGAGATCAAGAAGTTTATCAA 967

Db 394 GAGTCAGCTACAGTTATATTTGAGGAGATACAAATCTAAGGGATCGAGAGGTTTACCAGA 453

Qy 968 TGTGGTGTGTACCTGACAAAGTTTTTGTGCTGCTGGGAATTTTATAGCAACCTTAAACAT 1027

Db 454 TGTGGTGTGTACCTGACAAACATTTGTGATGCTCTGGGAGTTTTTGGCAACCTTAAACAT 513

Qy 1028 TGCCAGTATACATGGGATACGAAAGCAAAATTAACAACCTCAGGATCCCTGCTGCTTATAAG 1087

Db 514 TGCCAGTATACATGGGATACCAAAATGAACCTTAATCTTGAATAAATGCTGCTTTGATAA 573

Qy 1088 CATCGTTTGTGATCGAATATTTTTCAGAGCAGAG 1121

Db 574 CTTCGTTTGTGATCGAATATTTTTCAGAGCAGCAG 607

RESULT 28

ID ADT95029
XX ADT95029 standard; cDNA; 625 BP.

AC ADT95029;

DT 16-DEC-2004 (first entry)

DE Colon cancer associated human cDNA sequence #548.

DE Colon cancer; T cell; tumour protein; C634S; C635S; C637S; C640S; C636S;

DE humoral immune response; cellular immune response; cytostatic;

DE immunostimulant; human; ss.

OS Homo sapiens.

XX US2003087818-A1.

XX 08-MAY-2003.

XX 01-FEB-2002; 2002US-00066543.

XX 02-FEB-2001; 2001US-0267400P.

XX 07-FEB-2001; 2001US-0267382P.

XX 11-MAY-2001; 2001US-0290322P.

CC	treating cancer, particularly colon cancer. The nucleic acid and
CC	polypeptides are also useful in DNA strand invasion, antisense
CC	inhibition, mutational analysis, nucleic acid purification, isolation of
CC	transcriptionally active genes, blocking or transcription factor binding,
CC	genome cleavage or in situ hybridization, and as enhancers of
CC	transcription or biomarkers. The kits are useful for detecting antibody
CC	binding. The present sequence represents a human cDNA encoding a colon
CC	cancer protein.
XX	
SQ	Sequence 625 BP; 202 A; 104 C; 144 G; 174 T; 0 U; 1 Other;
	Query Match 32.7%; Score 428.4; DB 11; Length 625;
	Best Local Similarity 84.1%; Pred. No. 3.7e-108;
	Matches 483; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
QY	548 GCTCGAGGGGTGTTTCCTGCCTAGCTTGTATAGTCACAGATGGETATTCTTACAGGAA 607
DB	42 GCTCGAGGGGTGTTTCCTACTTAGCTTGTGTACGCCCAGATGATATTTTCTACAGAA 101
QY	608 GTTATCCCCCAVACTGTGCTACTCTCTAAGAAGAGAGCAGCCAGTCTACA CAATATTATACA 667
DB	102 GTTATCCCCCATATATAGCTACTCTAAGNAGAGATCNAGTANTTATGAGATTATTACA 161
QY	668 GGTAATGAAGAAGGATATTTCCACAGCTATACTATTGGAAGAAGGAGAGTGAAATTTAAA 727
DB	162 GGT CATGAAGAAGGATATTTCCACAGCTATAATGTTGAAGAAATCAAGAGTGAAATTTAAA 221
QY	728 AGTCAGAGATATTTCCTTTTCCAAATACCNAATGATGAAACCTGCTATGCGTAAT 787
DB	222 AGCCAAGAGATTA TTCTTTTTCCAAATACCAAATGATGAAACCTTTTATGTGTCAT 281
QY	788 GTGAGTTTGGGTGGAATGAAATTTTGCTTTATGACATCCCATTTGGAGAGCACACAGAGAA 847
DB	282 GTGAATGTGTGAGAAATGAGCTTTGGCTTATGATCATCCCATTTGGHAGACACAGAGGG 341
QY	848 CATTTCTCGGAAACGAATAAGACAAATAAAAA CTGTTCTTGAAAAATTCGAAGAGGCTCCA 907
DB	342 CATGCTCGGAAACGAATGAAATCAGTTTAAATAATGTTTTAAAGAAAAATGCAAGAGGCTCCA 401
QY	908 GATTCAACACGAGTTATATTTCGAGGAGATACAAATTTAAGAGATCAAGAAGTTATCAAA 967
DB	402 GAGTCAGCTACAGTTATATTTCGAGGAGATACAAATCTAAGGGGATCGAGAGGTTACCAGA 461
QY	968 TGTGGTGGTTTACCTGACACAGTTTTTGTGCTCTGGGAAATTTTTTAGGCAACCTAAACAT 1027
DB	462 TGTGGTGGTTTACCCAACAACATTTGTGATGCTGTGGGAGTTTTTGGGCAAACCTTAACAT 521
QY	1028 TGCCAGGTATACATGGGATACGAAAGCAAAATAACCACTTCAGGATCCCTGTGCTTTATAAG 1087
DB	522 TGCCAGGTATACATGGGATACACAATGACTCTAATCTTGGAAATACTGCTGCTTGTATAA 581
QY	1088 CATCGTTTTGATCGAATATTTTTTCAGAGCAGAAG 1121
DB	582 CTTCTGTTTTGATCGAATATTTTTTCAGAGCAGCAG 615

RESULT 26

ADT95565

ID ADT95565 standard; cDNA; 633 BP.

XX

AC ADT

XX

DT 16-

XX

DE COL

XX

KW
CO-KW
hurKW
imr

08-MAY-2003 .
01-FEB-2002; 2002US-0006543 .
02-FEB-2001; 2001US-0267400P .
02-FEB-2001; 2001US-0267382P .
11-MAY-2001; 2001US-0290322P .
12-JUL-2001; 2001US-0305265P .
16-AUG-2001; 2001US-0313077P .
(CORI-) CORIXA CORP .
Jiang Y, Chenault RA, Xu J, Indirias CY, Lodes MJ, Serist H;
Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;
WPI; 2003-040540/03 .
New isolated nucleic acids and polypeptides capable of eliciting a
humoral and/or cellular immune response, useful for diagnosing,
preventing or treating cancer, particularly colon cancer .
Claim 1; SEQ ID NO 1084; 87pp; English .
The invention relates to polynucleotide and polypeptide sequences
associated with cancer, particularly colon cancer. Also disclosed are (i)
an expression vector comprising the polynucleotide, (ii) a host cell
transformed or transfected with the expression vector, (iii) an isolated
antibody, or its antigen-binding fragment, which specifically binds to
the polypeptide, (iv) a method of detecting or determining the presence
of cancer in a patient, (v) a fusion protein comprising at least one of
the polypeptides, (vi) an oligonucleotide that hybridizes to the
polynucleotide sequence under highly stringent conditions, and (vii) a
method of stimulating and/or expanding T cells specific for a tumour
protein. The polypeptide specifically comprises the amino acid sequence
of C634S, C635S, C637S, C640S, C636S or one of the potential open reading
frames (ORFs) of C636S. These polypeptides are encoded by the
polynucleotide sequences, where both are capable of eliciting a humoral
and/or cellular immune response. The polynucleotides, polypeptides, and
antibodies are useful for diagnosing, preventing or treating cancer,
particularly colon cancer. The polynucleotide and polypeptide sequences
are also useful in DNA strand invasion, antisense inhibition, mutational
analysis, nucleic acid purification, isolation of transcriptionally
active genes, blocking or transcription factor binding, genome cleavage
or in situ hybridisation, and as enhancers of transcription or
biomarkers. This sequence represents a human colon cancer associated
cDNA. Note: The sequence data for this patent was obtained in electronic
format directly from the USPTO web site at seqdata.uspto.gov
Sequence 633 BP: 205 A: 108 C: 144 G: 175 T: 0 U: 1 Other:

PN US2003087818-A1.


```
XX Colon cancer; T cell; tumour protein; C634S; C635S; C637S; C640S; C636S;
KW humoral immune response; cellular immune response; cytostatic;
KW immunostimulant; human; ss.
XX Homo sapiens.
XX US2003087818-A1.
XX 08-MAY-2003.
XX 01-FEB-2002; 2002US-00066543.
XX 02-FEB-2001; 2001US-0267400P.
PR 07-FEB-2001; 2001US-0267382P.
PR 11-MAY-2001; 2001US-0290322P.
PR 12-JUL-2001; 2001US-030526SP.
PR 16-AUG-2001; 2001US-0313077P.
XX (CORI-) CORIXA CORP.
XX Jiang Y, Chenault RA, Xu J, Indirias CY, Lodes MJ, Secretist H;
PI Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;
XX WPI; 2003-040540/03.
XX New isolated nucleic acids and polypeptides capable of eliciting a
PT humoral and/or cellular immune response, useful for diagnosing,
PT preventing or treating cancer, particularly colon cancer.
XX Claim 1; SEQ ID NO 1067; 87bp; English.
XX The invention relates to polynucleotide and polypeptide sequences
CC associated with cancer, particularly colon cancer. Also disclosed are (i)
CC an expression vector comprising the polynucleotide, (ii) a host cell
CC transformed or transfected with the expression vector, (iii) an isolated
CC antibody, or its antigen-binding fragment, which specifically binds to
CC the polypeptide, (iv) a method of detecting or determining the presence
CC of cancer in a patient, (v) a fusion protein comprising at least one of
CC the polypeptides, (vi) an oligonucleotide that hybridises to the
CC polynucleotide sequence under highly stringent conditions, and (vii) a
CC method of stimulating and/or expanding T cells specific for a tumour
CC protein. The polypeptide specifically comprises the amino acid sequence
CC of C634S, C635S, C637S, C640S, C636S or one of the potential open reading
CC frames (ORFs) of C636S. These polypeptides are encoded by the
CC polynucleotide sequences, where both are capable of eliciting a humoral
CC and/or cellular immune response. The polynucleotides, polypeptides, and
CC antibodies are useful for diagnosing, preventing or treating cancer,
CC particularly colon cancer. The polynucleotide and polypeptide sequences
CC are also useful in DNA strand invasion, antisense inhibition, mutational
CC analysis, nucleic acid purification, isolation of transcriptionally
CC active genes, blocking or transcription factor binding, genome cleavage
CC or in situ hybridisation, and as enhancers of transcription or
CC biomarkers. This sequence represents a human colon cancer associated
CC cDNA. Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at seqdata.uspto.gov
XX Sequence 674 BP; 213 A; 114 C; 152 G; 191 T; 0 U; 4 Other;
SQ Query Match 35.2%; Score 461.6; DB 11; Length 674;
Best Local Similarity 83.4%; Pred. No. 2.3e-117;
Matches 548; Conservative 0; Mismatches 102; Indels 7; Gaps 2;
QY 548 GCTCGAGGGGTGTCTCTGCTACCTAAAGAGAGAGACGCCAGTTACACAATTTATACA 607
DB 18 GCTCGAGGGGTGTCTCTGCTACCTAAAGAGAGAGATCAAGTAATTTATGAGATTATACA 77
QY 608 GTTATCCCCCATCTGTGCTTACCTAAAGAGAGAGACGCCAGTTACACAATTTATACA 667
DB 78 GTTATCCCCCATCTGTGCTTACCTAAAGAGAGAGATCAAGTAATTTATGAGATTATACA 137
QY 668 GGTAATGAAGAAGGATATTTTACAGCTATCTATTGAAGAAAGGAGAGTGAATTTAAA 727
DB 138 GGTATGAAGAAGGATATTTTACAGCTATCTATTGAAGAAATCAAGAGTGAATTTAAA 197
QY 728 AGTCAGGAGATTTATCTCTTTTCCAAATACCAAAATGATGAGAAACCTGCTATGCGTAAAT 767
DB 198 AGCCAAGAGATTTATCTCTTTTCCAAATGATGAGAAACCTTTTATGTGTGCAT 257
QY 788 GTGAGTTTGGGTGGAAATGAATTTTTCCTTTATGACATCCCATTTTGAGAGCACCAGAGAA 847
DB 258 GTGAATGTCTCAGGAAATGAGCTTTTGCCTTATGACATCCCATTTTGAGAGCACCAGAGGG 317
QY 848 CATTCGCGGAACGAATAGACAAATTAATAAACTGTTCTTGGAAAAATGCAAGAGGTCCA 907
DB 318 CATGCTGCGGAACGAATGAATCAGTTTAAATAATGGTTTTTAAAGAAAAATGCAAGAGGTCCN 377
QY 908 -GATTCAACCAACGCTTATATTTTGCAGGAGATACAAATTTTAAAGAGATCAAGAAGTTCATCA 966
DB 378 TGAGTCAGCTACAGTTATATTTTGCAGGAGATACAAATCTTAAAGAGATCGAGAGGTACCAG 437
QY 967 ATGTGTGTGTTTACCTGACACAGCTTTTTCGCTGGGAATTTTATAGGCACCAACCTTAAACA 1026
DB 438 ATGTGTGTGTTTACCTGACACAGCTTTTTCGCTGGGAATTTTATAGGCACCAACCTTAAACA 497
QY 1027 TTGCCAGTATACATGGGATACGAACCAATTAACAACCTCAGGATCCCTGCTGCTTATAA 1086
DB 498 TTGCCAGTATACATGGGATACGAACCAATTAACAACCTCAGGATCCCTGCTGCTTATAA 557
QY 1087 GCATCGTTTGTGATCGAATATTTTTCAG-----AGCAGAAAGAGGGGCACCTTATCTCTCA 1140
DB 558 ACTTCGTTTGTGATCGAATATTTTTCAGAGCAGCAGCAGAGAGAGGAGACATATTTCCCG 617
QY 1141 AAGTTTACAGCTTGTGGTGTGGAAACTGGAATTTTATAGGAGTGTGATTTCCGAGTGATCA 1197
DB 618 AAGTTTACAGCTTGTGGTGTGGAAACTGGAATTTTATAGGAGTGTGATTTCCGAGTGATCA 674
RESULT 21
AD42030
ID ADX42030 standard; cDNA; 674 BP.
XX AC ADX42030;
XX DT 21-APR-2005 (first entry)
XX DE Human cDNA encoding colon cancer protein SEQ ID NO 1067.
XX KW Cytostatic; Immunostimulant; therapy; diagnosis; colon cancer; neoplasm;
XX ss; gene.
XX OS Homo sapiens.
XX PN WO200274156-A2.
XX PD 26-SEP-2002.
XX PF 01-FEB-2002; 2002WO-US002870.
XX PR 02-FEB-2001; 2001US-0267400P.
PR 07-FEB-2001; 2001US-0267382P.
PR 11-MAY-2001; 2001US-0290322P.
PR 12-JUL-2001; 2001US-030526SP.
PR 16-AUG-2001; 2001US-0313077P.
XX (CORI-) CORIXA CORP.
XX Jiang Y, Chenault RA, Xu J, Indirias CY, Lodes MJ, Secretist H;
PI Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;
XX WPI; 2003-040540/03.
XX New isolated nucleic acids and polypeptides capable of eliciting a
PT humoral and/or cellular immune response, useful for diagnosing,
PT preventing or treating cancer, particularly colon cancer.
XX Claim 1; SEQ ID NO 1067; 87bp; English.
XX The invention relates to polynucleotide and polypeptide sequences
CC associated with cancer, particularly colon cancer. Also disclosed are (i)
CC an expression vector comprising the polynucleotide, (ii) a host cell
CC transformed or transfected with the expression vector, (iii) an isolated
CC antibody, or its antigen-binding fragment, which specifically binds to
CC the polypeptide, (iv) a method of detecting or determining the presence
CC of cancer in a patient, (v) a fusion protein comprising at least one of
CC the polypeptides, (vi) an oligonucleotide that hybridises to the
CC polynucleotide sequence under highly stringent conditions, and (vii) a
CC method of stimulating and/or expanding T cells specific for a tumour
CC protein. The polypeptide specifically comprises the amino acid sequence
CC of C634S, C635S, C637S, C640S, C636S or one of the potential open reading
CC frames (ORFs) of C636S. These polypeptides are encoded by the
CC polynucleotide sequences, where both are capable of eliciting a humoral
CC and/or cellular immune response. The polynucleotides, polypeptides, and
CC antibodies are useful for diagnosing, preventing or treating cancer,
CC particularly colon cancer. The polynucleotide and polypeptide sequences
CC are also useful in DNA strand invasion, antisense inhibition, mutational
CC analysis, nucleic acid purification, isolation of transcriptionally
CC active genes, blocking or transcription factor binding, genome cleavage
CC or in situ hybridisation, and as enhancers of transcription or
CC biomarkers. This sequence represents a human colon cancer associated
CC cDNA. Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at seqdata.uspto.gov
XX Sequence 674 BP; 213 A; 114 C; 152 G; 191 T; 0 U; 4 Other;
SQ Query Match 35.2%; Score 461.6; DB 11; Length 674;
Best Local Similarity 83.4%; Pred. No. 2.3e-117;
Matches 548; Conservative 0; Mismatches 102; Indels 7; Gaps 2;
```

Db 839 TGTGAGAAATGAGCTTTGCTTATGACATCCATTTGGAGAGCACCAGAGGGCATGCTG 780
Qy 855 CGGAACGAATAAGACAAATTAATAAATCTTCTTGGAATAATGCAAGAGGCTCCAGATTCAA 914
Db 779 CGGACGAATGAATCAGTTTAAATGCTTTTAAAGAAATGCAAGAGGCTCCAGAGTCAG 720
Qy 915 CCACGGTTATATTGTCAGGAGATACAAATTTAAGAGATCAAGAAGTTTATCAATATGGTG 974
Db 719 CTACAGTTATATTGTCAGGAGATACAAATCTAAGGGATCGAGAGGTTTACCAGATGTGGTG 660
Qy 975 GTTTACTGACAAAGTTTTTGATGCTGGGAAATTTTAGGCAACCTTAAACATTTGCCAGT 1034
Db 659 GTTTACCACAAACATTTGTGGATGCTGGGAGTTTTTTGGGCAACCTTAAACATTTGCCAGT 600
Qy 1035 ATACATGGGATACGAAGCAAAATAACAACTTCAGATCCCTGCTGTCTTATAAGCATCGTT 1094
Db 599 ATACATGGGATACGAAGCAAAATACTTAATCTTGAATAAATCTGCTGTGTAACTTGGTT 540
Qy 1095 TTGATCGAATATTTTTCAG-----AGCAGAAGAGGGGACCTTTATCTCTCAAAGTTTAG 1148
Db 539 TTGATCGAATATTTTTCAGAGCAGCAGAGAGAGGACACATTTATCCCGAAGTTT-G 481
Qy 1149 ACCTTGTGGTTGGAAAACTGACCTGTGTAGATTTCCGAGTATCACTGGGGCTCT 1208
Db 480 ACCTTCTTGGATTAGAAAACTGGACTGTGTAGATTTTCCCTAGTATCACTGGGGCTCT 421
Qy 1209 TGTGCACCTTGAATGTAGTATTGTGAAAAAGCTTCCCACTTGCAGCTTT 1256
Db 420 TGTGCAACTTAGATATATATTGTAAATGCTTTTCAAGTGTGGGTTT 373

RESULT 19
ABK28982/c
ID ABK28982 standard; cDNA; 1079 BP.
XX AC ABK28982;
XX AC
DT 23-APR-2002 (first entry)
XX DE Human breast tumour polypeptide cDNA clone #11.
XX KW Human; breast tumour polypeptide; gene; ss; breast cancer; cytostatic;
XX KW immunostimulant.
XX OS Homo sapiens.
XX PN WO200198339-A2.
XX PD 27-DEC-2001.
XX PF 12-JUN-2001; 2001WO-US019032.
XX PR 22-JUN-2000; 2000US-00602877.
XX PR 12-OCT-2000; 2000US-00687507.
XX PR 06-FEB-2001; 2001US-00778381.
XX PA (CORI-) CORIYA CORP.
XX PI Reed SG, Xu J, Dillon DC, Retter MW, Harlocker SL;
XX WPI; 2002-147792/19.
XX PT Polynucleotides encoding breast tumor polypeptides, useful for treating
XX PS breast cancer or stimulating an immune response.
XX PS Claim 1; Page 131; 150pp; English.
XX CC The invention relates to polynucleotides encoding breast tumour
XX CC polypeptides. The sequences are useful for treating cancer, preferably
XX CC breast cancer, in a patient or for stimulating an immune response. The
XX CC polynucleotides and polypeptides are also useful in the diagnosis and
XX CC monitoring of breast cancer. A method for detecting the presence of a

CC cancer in a patient, comprises obtaining a biological sample from the
CC patient, contacting the biological sample with a binding agent that binds
CC to a breast tumour polypeptide, detecting in the sample an amount of
CC polypeptide that binds to the binding agent, and comparing the amount of
CC polypeptide to a predetermined cut-off value, therefore determining the
CC presence of a cancer in the patient. Sequences ABK28920-ABK29025
CC represent cDNA clones encoding human breast tumour polypeptides of the
CC invention
XX
SQ Sequence 1079 BP; 327 A; 229 C; 177 G; 346 T; 0 U; 0 Other;
Query Match 37.3%; Score 490; DB 6; Length 1079;
Best Local Similarity 82.8%; Pred. No. 3.9e-125;
Matches 58; Conservative 0; Mismatches 115; Indels 7; Gaps 2;
Qy 555 GGGTGTGTTCTCCTGCTAGCTTTGTATAGTCCAGATGGTATTTCTACAGAAATTTATCC 614
Db 1079 GGGTGTGTTCTCCTGCTAGCTTTGTATAGTCCAGATGGTATTTCTACAGAAATTTATCC 1020
Qy 615 CCCATGCTGCTGCTTACCTAAAGAGAGAGCCAGTTACACAAATTTATACAGTAAATG 674
Db 1019 CCCATGCTGCTTACCTTAAAGAGAGATCAAGTAATTTATGAGATTTATACAGGTCATG 960
Qy 675 AAGAAGGATATTTTACAGCTTATCTATTGAAGAAAGGAAGAGTGAATTTTAAAAAGTCAGG 734
Db 959 AAGAAGGATATTTTACAGCTTATCTATTGAAGAAATCAAGAGTGAATTTTAAAAAGCCAG 900
Qy 735 AGATTTATCTTTTCCAAATACCAAAATGATGAAACCTGCTATGCGTAAATGTGAGTT 794
Db 899 AGATTTATCTTTTCCAAATGATGAAACCTTTTATGTGTGTCATGTAATG 840
Qy 795 TGGTGGAAATGAATTTTGCCTTATGATCCCATTTGGAGAGCACCAGAGAAATTTCTG 854
Db 839 TGTGAGGAAATGAGCTTTGCTTATGATCCCATTTGGAGAGCACCAGAGGGCATGCTG 780
Qy 855 CGGAACGAATAAGACAAATTTAAATACTGTTCTGAAAAATCAAGAGAGCTCCAGATTCAA 914
Db 779 CGGAACGAATGAATCAGTTTAAATAATGTTTAAAGAAATGCAAGAGGCTCCAGAGTCAG 720
Qy 915 CCACGGTTATATTGTCAGGAGATACAAATTTAAGAGATCAAGAAGTTTATCAAAATGTGCTG 974
Db 719 CTACAGTTATATTGTCAGGAGATACAAATCTAAGGGATCGAGAGGTTTACCAGATGTGGTG 660
Qy 975 GTTTACTGACAAAGTTTTTGATGCTGGGAAATTTTAGGCAACCTTAAACATTTGCCAGT 1034
Db 659 GTTTACCACAAACATTTGTGGATGCTGGGAGTTTTTTGGGCAACCTTAAACATTTGCCAGT 600
Qy 1035 ATACATGGGATACGAAGCAAAATAACAACTTCAGATCCCTGCTGTCTTATAAGCATCGTT 1094
Db 599 ATACATGGGATACGAAGCAAAATACTTAATCTTGAATAAATCTGCTGTGTAACTTGGTT 540
Qy 1095 TTGATCGAATATTTTTCAG-----AGCAGAAGAGGGGACCTTTATCTCTCAAAGTTTAG 1148
Db 539 TTGATCGAATATTTTTCAGAGCAGCAGAGAGAGGACACATTTATCCCGAAGTTT-G 481
Qy 1149 ACCTTGTGGTTGGAAAACTGACCTGTGTAGATTTCCGAGTATCACTGGGGCTCT 1208
Db 480 ACCTTCTTGGATTAGAAAACTGGACTGTGTAGATTTTCCCTAGTATCACTGGGGCTCT 421
Qy 1209 TGTGCACCTTGAATGTAGTATTGTGAAAAAGCTTCCCACTTGCAGCTTT 1256
Db 420 TGTGCAACTTAGATATATATTGTAAATGCTTTTCAAGTGTGGGTTT 373

RESULT 20
ADT95548
ID ADT95548 standard; cDNA; 674 BP.
XX AC ADT95548;
XX AC
DT 16-DEC-2004 (first entry)
XX XX
DE Colon cancer associated human cDNA sequence #1067.


```
Db 601 AA 602
RESULT 16
AAS86254
ID AAS86254 standard; cDNA; 1088 BP.
XX AAS86254;
AC
XX
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #22058.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX PR P-PSDB; ABG22067.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 1; SEQ ID NO 22058; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1088 BP; 345 A; 182 C; 236 G; 325 T; 0 U; 0 Other;
XX
XX Query Match 37.6%; Score 493.2; DB 5; Length 1088;
XX Best Local Similarity 82.9%; Pred. No. 5.1e-126;
XX Matches 577; Conservative 0; Mismatches 113; Indels 6; Gaps 1;
XX
XX 548 GCTCGAGGGGTGTCTCGCTAGCTTTGTATAGTCCAGATGTGTGTTTCTACAGGAA 607
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 1 GCTCGAGGGGTGTGTCTTACTTACTTGTACAGCCAGATGTGTATTTCTACAGGA 60
XX
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Db 753 AGAAATGCAAGAGCTCCAGAGTCAGTACAGTATATTTGACGAGATACAAATCTAA 812
Qy 948 GAGATCAAGAGTATCAAAATGTGGTGTGTACCTGCAACGTTTTTGTGCTGGGAAT 1007
Db 813 GGGATCGAGAGTTTACAGATGTGTGTGTACCAACAACATTTGTGATGCTGGGAGT 872
Qy 1008 TTTTAGGCAACCTAAACATTCGAGTATACATGGGATACGAAGCAAAATACAACTCA 1067
Db 873 TTTTGGGCAACCTAAACATTCGAGTATACATGGGATACGAAGCAAAATACAACTCA 932
Qy 1068 GGATCCCTGCTGTATAAGCATGTTTGTATGATCAATATTTTTCAG-----AGCAAG 1121
Db 933 GAATACTGCTGCTGTATAAGCATGTTTGTATGATCAATATTTTTCAGAGCAGCAGCAAG 992
Qy 1122 AGGGCCACCTATTTCCTCAAGATTTAGACCTTTGTGGGTTGGAAAACTGGACTGTGGTA 1181
Db 993 AGGACACATTTATCCCGAAGTTTGGACCTTTCTTGGATTAGAAAACTGGACTGTGGTA 1052
Qy 1182 GATTTCGAGTATCATCTGGGGGCTCTTTGGCACCCTTGAATGTAGTATTGTGAAAACTTT 1241
Db 1053 GATTTCCTAGTATCATCTGGGGGCTCTTCTGTCAACTTAGATATAATTTGTAAAACTCTT 1112
Qy 1242 CCACCTTGCAGCTTT 1256
Db 1113 TTCAAGTGTGGGTTT 1127

RESULT 12

ID ADP25361 standard; cDNA; 1936 BP.

XX AC ADP25361;

XX XX 18-NOV-2004 (first entry)
XX XX

DE PRO polypeptide encoding cDNA SEQ ID NO:475.

XX ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
XX immunosuppressive; osteopathic; antidiabetic; dermatological;
KW antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
KW gene therapy; immune system.

XX Unidentified.

XX WO2004041170-A2.

XX XX 21-MAY-2004.

XX 30-OCT-2003; 2003WO-US034312.

XX 01-NOV-2002; 2002US-0423394P.

XX (GETH) GENENTECH INC.

XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;

XX WPI; 2004-419628/39.

DR P-FSDB; ADP25362.

XX New PRO polypeptides and polynucleotides, useful for treating e.g.
XX erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.

XX Claim 1; SEQ ID NO 475; 2940pp; English.

XX The invention relates to a novel isolated nucleic acid and the PRO

CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antirheumatic, antidiabetic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide

CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence encodes a PRO protein of
CC the invention.

XX SQ Sequence 1936 BP; 617 A; 330 C; 431 G; 558 T; 0 U; 0 Other;

Query Match 50.8%; Score 666.6; DB 13; Length 1936;

Best Local Similarity 76.9%; Pred. No. 4.8e-174;

Matches 842; Conservative 0; Mismatches 244; Indels 9; Gaps 2;

Qy 171 GCGGGCGGCTGCGGCCCGAGAGCAGCACAGCGGAGGAGGACCGGTGAAGAGCGGC 230
Db 33 GCCTGGAGGGCGGAGGAGGCGCGGAGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGG 92
Qy 231 GGGTTTCAAGTGCCTGGGCTTTGCGTTGGTGGGGGATGCGACCCACGATGTCCTCCAGCG 290
Db 93 GACTTCTGTGTGTGAGGTTTGCCTCGGTGCGAGTGGATGCGGAGTGGTCAAGTGT 152
Qy 291 TCCTGCGGAGAACGACTGGCAGACGCGAGAAAGCCCTGAGGCGCTACTTTCAGTGCAG 350
Db 153 TCCTGCGGAGAACGACTGGGAGATGGAAGGGCTCTGAACTCTCTACTTCAGGCTCCGG 212
Qy 351 AGACGACCAAGGCTGCGCGCGGAGGCTCCAGCTCTTCAAGTCGAGGCGCTATGTTG 410
Db 213 TGGAGGAGAGCGCTTGGAAAGCGGACCTGAACCATCTCTGAGCCCAAGACCTATGTTG 272
Qy 411 ATCTAACCAACGAGGATGCAAAATGATACAAACCAATTTTAGAAGCCAGTCCATCTCGA 467
Db 273 ACCTAACCAATGAAGAAACCAACTGATTCACCACTTCTTAAATCAGGCCATCTGAAGATA 332
Qy 468 CTCTCTAGAAGATAGCAGCACTATTTCTTTCATTACCTGGAAATTTGATGGATTAGATG 527
Db 333 CTCAGCAAGAAATGCGCAGCATGTTCTCTCTCATTACCTGGAAATTTGATGGATTAGATC 392
Qy 528 GATCAATCTGCCGAGAGGCTCGAGGGGTGTCTCTCTGCTAGCTTTGATAGTCCAG 587
Db 393 TAAACAACTCTCAGAGAGGCTCGAGGGGTGTCTCTCTTACTTACCTTTGTACGCCAG 452
Qy 588 ATGTGTTATTTCTACAGGAAGTTATCCCCCATACTGTGCCCTACCTAAAGAGAGAGCAG 647
Db 453 ATGTGATATTTCTACAGGAAGTTATCCCCCATATATATAGCTACCTAAAGAGAGATCAA 512
Qy 648 CCAGTTTACAAATTTTACAGGTAATGAAGAGATATTTTCAGACTATATCTATTGAAGA 707
Db 513 GTAAATTTGATATTTTACAGGTCATGAAGAGATATTTTCACAGCTATATATTTGTTGAAGA 572
Qy 708 AAGCAAGAGTCAAAATTTAAAGTCAGAGATATTTCTCTTTTCCAAATACCAAAATGATGA 767
Db 573 AATCAAGAGTCAAAATTTAAAGCCAGAGATATTTCTCTTTTCCAAAGTACCAAAATGATGA 632
Qy 768 GAAACCTGCTATGCGTAAATTTGAGTTTGGGTGGAATGAATTTTGCCTTATGATATCCC 827
Db 633 GAAACCTTTTATGTGTCATGTGAACGCTGTGAGGAATGAGCTTTGCTCTTATGATATCCC 692

Db 798 CTCAGCAAGAAAATGGCAGCATGTTCTCTCTCATTACCTGGAATATTGATGGATTAGATC 857
Qy 528 GATGCAATCTGCCGAGAGGCTCGAGGGTGTTCCTGCTAGCTTTGTATAGTCCAG 587
Db 858 TAAACAAATCTGTCCAGAGAGGCTCGAGGGTGTTCCTACTTAGCTTTGTACAGCCAG 917
Qy 588 ATGTGGTATTCTACAGGAAGTTATCCCCCATATCTGTGCTTACCTTAAAGAGAGAGCAG 647
Db 918 ATGTGATATTCTACAGGAAGTTATCCCCCATATATTAGTACCTTAAAGAGAGATCAA 977
Qy 648 CCAGTTACAAATATTACAGGTAATGAAGAAGATATTTCACAGCTATATTGATGAAGA 707
Db 978 GTAATATTGATGATATTACAGGTCATGAAGAAGATATTTCACAGCTATATTGATGAAGA 1037
Qy 708 AAGCAAGAGTGAATTTAAAGTCAGGAGATATTCTCTTCCAAATACCAAAATGATGA 767
Db 1038 ATCAAGAGTGAATTTAAAGCCAGAGATATTCTCTTCCAGTACCAAAATGATGA 1097
Qy 768 GAAACCTGCTATGCGTAAATGTGAGTTTGGGTGGAATGAATTTTGCCTTATGACATCCC 827
Db 1098 GAAACCTTTTATGTGTCATGTGAATGTGTGAGGAATGAGCTTTCCTTATGACATCCC 1157
Qy 828 ATTTGAGAGCACAGAGAACATTTCTGCGGAACGAATGAAGCAATTTAAAACTGTTCTTG 887
Db 1158 ATTTGAGAGCACAGAGGCGATGCTGCGGACGAATGAATCAATGATTTAAATGTTTTAA 1217
Qy 888 GAAATATGCAAGAGGCTCCAGATTTCAACACGTTATATTGTCAGGAGATACAAATTTAA 947
Db 1218 AGAAATGCAAGAGGCTCCAGATTCAGTACGTTATATTGTCAGGAGATACAAATCTTA 1277
Qy 948 GAGATCAAGAAGTTATCAAAATGTGTTGTTTACCTGACAACTGTTTGTGCTGCGGAAT 1007
Db 1278 GGGATCGAGAGGTTACAGATGTGTTGTTTACCCCAACAACTGTTGATGTTGCGGAGT 1337
Qy 1008 TTTTAGCAACCTAAACATTCGAGTATACATGGGATACGAAGCAATTAACAACTCA 1067
Db 1338 TTTTGGCAACCTAAACATTCGAGTATACATGGGATACGAATTAACAACTCAATCTTG 1397
Qy 1068 GGATCCTGCTGTTTAAAGCATGCTTTTTCATCGAATATTTTTCAG-----AGCAGAAG 1121
Db 1398 GAATACTGCTGTTGTAACCTTCTGTTTGAATGATATTTTTCAGAGCAGCAGAGAG 1457
Qy 1122 AGGGGACACCTTATTCCTCAAAAGTTTACACCTTGTGTTGGTTTGGAAAACTGAGCTGGTA 1181
Db 1458 AGGACACATTAATCCCGAGTTTGGACCTCTTGGATTAGAAAACTGAGCTGGTA 1517
Qy 1182 GATTTCGAGTATCACTGGGGCTCTTGTGCACTTGAATGTAGTATTGTTGAAAACTTT 1241
Db 1518 GATTTCTAGTATCACTGGGGTCTTCTGTGCACTTAGATATAATATTGTAATATGCTT 1577
Qy 1242 CCACCTGCACTTT 1256
Db 1578 TTCAAGTGGGTTT 1592

RESULT 9
ADA10970
ID ADA10970 standard; cDNA; 3152 BP.

XX
AC
XX
XX
DT
XX
DE
XX
KW
XX
OS
XX
PN
XX
XX
PD
XX
31-OCT-2002.

ADA10970;
06-NOV-2003 (first entry)
Human cDNA differentially expressed in colon cancer #60.
ss; differential expression; colon cancer; cancer; human.
Homo sapiens.
US2002160382-A1.

PF 11-OCT-2001; 2001US-00981353.
XX
PR 11-OCT-2000; 2000US-0239841P.
XX
PA (LASE/) LASEK A W.
PA (JONE/) JONES D A.
XX
PI Lasek AW, Jones DA;
XX
XX WPI; 2003-265756/26.
DR
XX
XX New combination comprising cDNAs that are differentially expressed in
PT colon disorder, useful for diagnosing, treating, staging or monitoring
PT treatment for colon cancers.
XX
PS Claim 1; SEQ ID NO 88; 231pp; English.
XX
CC The invention relates to a combination comprising cDNAs that are
CC differentially expressed in colon disorder. The methods and compositions
CC of the present invention are useful for diagnosing, treating, staging or
CC monitoring treatment for colon cancer. They are also useful in high
CC throughput methods for using cDNAs to detect differential expression of
CC nucleic acids in a sample, screening molecules or compounds to identify a
CC ligand which specifically binds a cDNA and using a protein to screen
CC molecules or compounds to identify at least one ligand which specifically
CC binds the protein. The present sequence represents a human cDNA
CC differentially expressed in colon cancer.
XX
SQ Sequence 3152 BP; 875 A; 643 C; 707 G; 926 T; 0 U; 1 Other;
Query Match 50.9%; Score 668.2; DB 9; Length 3152;
Best Local Similarity 77.0%; Pred. No. 2.2e-174;
Matches 843; Conservative 0; Mismatches 243; Indels 9; Gaps 2;
Qy 171 GSGGGGCGGCTCGGCGCCGGAAGCAGACAGCGGAGGAGGACCGGTGAAGAGCGGC 230
Db 1268 GCGTGGAGGCGGGAGGCGGCGGAGAGAGGCGGAGGCTGAGGTGAAAAGCGGC 1327
Qy 231 GCGTTCAGTGCCTGGGCTTTGGTGTGGGGGGATGCGACCCCGAGTGTGCCAGCG 290
Db 1328 GACTTCTGTGTGGAGTTTGCTCGTGCAGCTGCCATGCCGAGTGGCTCAGTGCT 1387
Qy 291 TCGTGGGAGAAACGACTGGCAGACGCAAGAGCCCTGAGCGCCTACTTCGAGCTGCCAG 350
Db 1388 TCCTGCCGAGAAACGACTGGGAGATGGAAGGCGCTCTGAACCTCTACTTCGAGCCTCCG 1447
Qy 351 AGAACACCAAGGTGGCGCCGCGCAGCTCCACGCTCTCAAGTCGAGGCGCTATGTTG 410
Db 1448 TGGAGGAGAGCGCCTTGGAAACGCGGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTG 1507
Qy 411 ATCTAACCAACAGAGGATGCAAAATGATACAAACATTTTAGAGCGAGTCCATCTGGA---A 467
Db 1508 ACCTAACCAATGAGAAACAACTGATTCACCACTTCTAAATCAGCCCATCTGAAGATA 1567
Qy 468 CTCCTCTAGAAGATAGCAGCACTATTTCTTTTCACTACCTGGAATATTGATGATAGATG 527
Db 1568 CTCAGCAAGAAAATGGCAGCATGTTCTCTCTCATTAACCTGGAATATTGATGATAGATC 1627
Qy 528 GATGCAATCTGCCGAGAGGCTCGAGGGTGTGTTCTGCTAGCTTGTATAGTCCAG 587
Db 1628 TAAACAAATCTGTACAGAGGGCTCGAGGGGTGTGTTCTTACTTAGCTTTGTAGAGCCAG 1687
Qy 588 ATGTGTTATTTCTACAGGAAGTTATCCCCCATATCTGTGCTACCTTAAAGAGAGAGCAG 647
Db 1688 ATGTGATATTTCTACAGGAAGTTATTTCCCCCATATTTATAGCTACCTAAGAGAGATCAA 1747
Qy 648 CCAGTTTACAAATATTATACAGTAAATGAAGAAGGATATTTCACAGCTATATTGATGAAGA 707
Db 1748 GTAATTTAGATATTATTAAGGTCATGAAGAAGGATATTTCACAGCTATAATGTTGAAGA 1807
Qy 708 AAGGAAGAGTGAATTTAAAGTCAGGAGATTTTCTCTTCCAAATACCAAAATGATGA 767
Db 1808 AATCAAGAGTGAATTTAAAGCCAGAGATTTATCTTTTCCAAAGTACCAGAAATGATGA 1867

Query Match		50.9%; Score 668.2; DB 4; Length 1958;
Best Local Similarity		77.0%; Pred. No. 1.7e-174;
Matches		843; Conservative 0; Mismatches 243; Indels 9; Gaps 2;
Qy	171	GGCGGGCGGCGTCCGCCCGAAGCAGCAGCAGCGGAGGAGGACCGGGTGAAGAGCGGC 230
Db	67	GCCTGGAGGGCGGAGGAGGCGCGGAGAGGAGGCGGAGCTGAGGTGAAGAAGCGGC 126
Qy	231	GGCTTCAGTGCCTGGGCTTTGCGTGTGGTGGGGGATCGACCCCGACGATGTCCTCCAGCG 290
Db	127	GACTTCGTGTGTGAGTTTGCTCGGTGCGTCAAGCTGCGATGCGCAGTGGCTCAGTGCT 186
Qy	291	TCCTGCGGGAGAACGACTGGCAGACGCGAAGAGCCCTGAGGCGCTACTTCGAGCTGCAG 350
Db	187	TCCTGGCGGAGAACGACTGGGAGATGGAAGGGGCTCTGAACCTCTACTTCGAGCCTCGG 246
Qy	351	AGAACGACCAAGGCTGGCGGCGCAGCTCCACGTCCTTCAAGTCCGAGGCTTATGTTG 410
Db	247	TGGAGGAGAGCGCTTGGAACGCCGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTG 306
Qy	411	ATCTAACCAACGAGGATGCAATGATACCAACATTTTAGAGCCAGTCCATCTGGA---A 467
Db	307	ACCTAACCAATGAAGAACAACACTGATTCACCACTCTTAATAATCAGCCCATCTGAAGATA 366
Qy	468	CTCCTCTAGAAGATAGCAGCACTATTTCTTTTCTTACCTACCTGGAATATTGATGATTAGTG 527
Db	367	CTCAGCAAGAAATGGCAGCATGTTCTCTCTCTTCTTACCTGGAATATTGATGATTAGATC 426
Qy	528	GATCAATCTGCCGAGAGGCTCGAGGGGTGCTCTGCTAGCTTGTATAGTCCAG 587
Db	427	TAAACAACTCTCAGAGAGGCTCGAGGGGTGTGTTCTTACTTAGCTTTGTACAGCCGAG 486
Qy	588	ATGTGGTATTTCTACAGGAAGTATCCGCCCATACTGTGCTTACTTAAAGAGAGAGCAG 647
Db	487	ATGTGATATTTCTACAGGAAGTATTTCCCATATATATAGCTACTTAAAGAGAGATCAA 546
Qy	648	CCAGTTACAAATATTATACAGTAATGAAGAGATATTTACAGCTATATCTATGAAGA 707
Db	547	GTAATATTAGATTTATACAGGTATGAAGAGATATTTTACAGCTATATATGTTGAAGA 606
Qy	708	AAGNAGGTCAAAATTTAAAGTCAGGAGATATTTCTTTTCCAAATACCAAAATGATGA 767
Db	607	AATCAAGAGTGAAATTTAAAGACCAAGAGATATTTCTCTTTTCCAAAGTACCAAAATGATGA 666
Qy	768	GAACCTCTATGCTTAATGTGAGTTTGGGTGGAATGAATTTTGCCTTATGACATCCC 827
Db	667	GAACCTTTTATGTGCAATGTGATGTGTGAGGAATGAGCTTTGCTTATGACATCCC 726
Qy	828	ATTTGGAGAGCACCAGAGAACATTTCTGGGAACGAATAAGACAATTTAAAACTGTCTTTG 887
Db	727	ATTTGGAGAGCACCAGAGGCGATGCTGGGAACGAATGAATCAGTTAAATAATGTTTAA 786
Qy	888	GAAAAATCAGAGGCTCCAGATTCACCAACGTTTATATTTTGCAGGAGATACAAATTTAA 947
Db	787	AGAAAAATCAGAGGCTCCAGAGTCAGCTACAGTTATATTTTGCAGGAGATACAAATTTAA 846
Qy	948	GAGATCAAGAGTTATCAAAATGTGTGTTTACCTTGACAAAGTTTTTCATGCTGGGAAT 1007
Db	847	GGATTCGAGAGGTTACAGATGTGTGTTTATCCCAACAAATTTGTGATGTCTGGGAGT 906
Qy	1008	TTTTAGGCAAACTAAACATTTGCCAGTATACATGGGATACGAAAGCAAAATACCACTCA 1067
Db	907	TTTTGGGCAAACTAAACATTTGCCAGTATACATGGGATACCAAAATGAATCTTAACTTTG 966
Qy	1068	GGATCCCTGCTGCTTATGAAGATCGTTTGTGATCGAATATTTTTCAG-----AGCAGAAG 1121
Db	967	GAATAACTGCTGCTTGTAACTTCGTTTGTGATCGAATATTTTTCAGAGCAGCAGAGAAG 1026
Qy	1122	AGGSGACCTTATTCCTCAAGTTTATAGACCTTGTGGGTGGAAAACTGGACTGTGGTA 1181
Db	1027	AGGGACATATTTATCCCGAAGTTTGGACCTTCTTGGATTAGAAAACTGGACTGTGGTA 1086
Qy	1182	GATTTCCGAGTGCATCTACTGGGGCTCTTGTGCACTTGAATAGTAGTATTGTGAAAAGCTT 1241
Db	1087	GATTTCCGAGTGCATCTACTGGGGCTCTTGTGCACTTGAATAGTAGTATTGTGAAAAGCTT 1146
Qy	1242	CCACATTTGCAGCTTTT 1256
Db	1147	TTCAAGTGTGGTTT 1161
RESULT 8		
AAAX28153		
ID	AAAX28153	standard; DNA; 2499 BP.
XX	XX	
AC	AAAX28153;	
XX	XX	
DT	16-JUN-1999	(first entry)
XX	XX	
DE	Topoisomerase II binding protein 1 coding sequence.	
XX	XX	
KW	Topoisomerase II binding protein; TopBP; anticancer agent; ds.	
OS	Homo sapiens.	
XX	XX	
PN	JPI11075856-A.	
XX	XX	
PD	23-MAR-1999.	
XX	XX	
PF	17-SEP-1997; 97JP-00251544.	
XX	XX	
PR	17-SEP-1997; 97JP-00251544.	
XX	XX	
FA	(TSURU) TSURUO T.	
PA	(CHUS) CHUGAI PHARM CO LTD.	
XX	XX	
DR	WPI; 1999-257704/22.	
XX	XX	
PT	P-PSDB; AAY03182.	
XX	XX	
PS	New Topoisomerase II- binding protein - useful as an anticancer agent.	
CC	Disclosure; Page 18-19; 28pp; Japanese.	
CC	This sequence encodes the topoisomerase II binding protein (TopBP) of the	
CC	invention. The TopBP protein is useful as an anticancer agent. TopBP can	
CC	be used as the target molecule for anticancer agent	
XX	XX	
SQ	Sequence 2499 BP; 720 A; 505 C; 587 G; 687 T; 0 U; 0 Other;	
Query Match		50.9%; Score 668.2; DB 2; Length 2499;
Best Local Similarity		77.0%; Pred. No. 2e-174;
Matches		843; Conservative 0; Mismatches 243; Indels 9; Gaps 2;
Qy	171	GGCGGGCGGCGTCCGCCCGAAGCAGCAGCAGCGGAGGAGGACCGGGTGAAGAGCGGC 230
Db	498	GCCTGGAGGGCGGAGGAGGCGCGGAGGAGGCGGCTGAGGTGAAGAAGCGGC 557
Qy	231	GGCTTCAGTGCCTGGGCTTTGCGTGTGGTGGGATCGACCCCGACGATGTCCTCCAGCG 290
Db	558	GACTTCTGTGTGGAGTTTGCCTCGGTGCGAAGCTGCGATGCGCGAGTGGCTCAGTGCT 617
Qy	291	TCCTGCGGGAGAACGACTGGCAGACGCGAAGAGCCCTGAGCGCTTCTCGAGCTGCCAG 350
Db	618	TCCTGCGGGAGAACGACTGGGAGATGGAAGGGCTCTGAACTCTTACTTTCGAGCCTCGG 677
Qy	351	AGAACGACCAAGGTTGGCGGCGCAGCTCCACGTCCTTCAAGTCCGAGGCTTATGTTG 410
Db	678	TGGAGGAGGCGCTTGGAACGCCGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTG 737
Qy	411	ATCTAACCAACGAGATGCAATGATACCAACATTTTAGAGCCAGTCCATCTGGA---A 467
Db	738	ACCTAACCAATGAAGAAACAACTGATTCACCACTTCTTAAATCAGCCCATCTTGAAGATA 797
Qy	468	CTCCTCTAGAAGATAGCAGCACTATTTCTTTTCTTACCTGGAATATTGATGATTAGATG 527

PT diseases and for improvement of anti-tumor treatments.

XX Claim 9; Page 37-39; 48pp; English.

XX This sequence represents the gene encoding human CD40 receptor associated
 CC protein (CRAP). CRAP is a functional protein capable of interacting with
 CC the cytoplasmic domain of CD40 and/or other receptors of the tumour
 CC necrosis factor (TNF) receptor superfamily such as CD30 and TNF receptor
 CC I, where the protein has no homology to TNF receptor associated factor
 CC (TRAF)-proteins. The CD40 binding proteins can be used as modulators of
 CC the CD40 signalling pathway, especially to diagnose and treat TRAP-
 CC related, CD40-related, NF-kappaB related and/or Jun (kinase)-related
 CC diseases, and for the improvement of anti-tumour diseases. Diseases which
 CC may be treated include atherosclerosis, arthritis, multiple sclerosis,
 CC systemic lupus erythematosus, graft rejection, graft versus host disease,
 CC allergy, and autoimmune disease. The proteins can be used to sensitize
 CC tumour cells to anti-tumour treatments and to screen for compounds which
 CC interfere with the interaction of the proteins with other protein
 CC components of the TRAF, CD40 or NF-kappaB related pathway

XX SQ Sequence 1920 BP; 599 A; 327 C; 435 G; 557 T; 0 U; 2 Other;

Query Match 50.9%; Score 668.2; DB 3; Length 1920;

Best Local Similarity 77.0%; Pred. No. 1.7e-174;

Matches 843; Conservative 0; Mismatches 243; Indels 9; Gaps 2;

Qy	171	GGCGGGCGGCTCGCGCGCGGAGCAGCAGCGGCGGAGGACCGGGTGAAGAGGGCG	230
Db	36	GCCTGGAGGGCGGAGGAGCGGCGGAGGAGGAGGCGGAGCTGAGGTGAAGAAGCGGC	95
Qy	231	GGCTTCAGTGCTGGGCTTCGGTGTGGTGGGGGATGCGACCCACGATGTCGCCAGCG	290
Db	96	GACTTCTGTGTGGAGTTTCCCTCGGTGCGCAAGCTGCGATGCGCGAGTGGCTCAGTGCT	155
Qy	291	TCCTGGGGAGAACGACTGGCAGCGCAGAGAGCCCTGAGGCGCTACTTCAGCTGCCAG	350
Db	156	TCCTGGCGGAGAACGACTGGGAGATGGAAGAGGGCTCTGAACCTCTTTCAGGCTCCGG	215
Qy	351	AGAACGCAAGGTGGCGCGCGCAGCTCCACGCTCTTCAAGTCCGAGGCTTATGTTG	410
Db	216	TGGAGGAGAGCGCTTGGAGCGCGACCTGAACCACTCTGAGCCCAAGACCTATGTTG	275
Qy	411	ATCTAACCAACGAGGATGCAATGATACCAACATTTTGAAGCCAGTCCATCTGGA---A	467
Db	276	ACCTAACCAATGAAGAAACAACTGATTCACCACTTCTAAAATCAGCCCATCTGAAGATA	335
Qy	468	CTCCTCTAGAGATAGCAGCACTATTTCTTTCATTTACCTGGAATATTGATGGATTAGTG	527
Db	336	CTCAGCAAGAAATGGCAGCATGTTCTCTCTCATTTACCTGGAATATTGATGGATTAGATC	395
Qy	528	GATGCAATCTGCCGAGAGGGCTCGAGGGGTGTCTCTGCTAGCTTGTATAGTCCAG	587
Db	396	TAAACAACTGTCTAGAGAGGGCTCGAGGGGTGTCTCTCTACTTAGCTTGTACAGCCAG	455
Qy	588	ATGTGGTATTTCTACAGGAAGTTATCCCCCACTACTGTCCCTACCTAAAGAGAGAGCAG	647
Db	456	ATGTGATATTTCTACAGGAAGTTATTTCCCATATTTATAGCTACCTAAAGAGAGATCAA	515
Qy	648	CCAGTTACACAAATTTACAGTAATGAAGAGGATTTTTCACAGCTATATCTATTGAAGA	707
Db	516	GTAATTATGAGATTATTCAGGTCTATGAAGAGGATATTTTCACAGCTATATGTTGAAGA	575
Qy	708	AAGGAAGAGTGAATTTAAAGTCCAGGAGATTATTCCTTTTCCAAATACCAAAATGATGA	767
Db	576	AATCAAGAGTGAATTTAAAGCCCAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGA	635
Qy	768	GAACCTGCTATGCGTAATGTGAGTTTGGGTGGAATGAATTTTGCCTTATGACATCCC	827
Db	636	GAACCTTTTATGTGTCATGTGAATGTGTGTCAGGAAATGAGCTTTTGCCTTATGACATCCC	695
Qy	828	ATTTGGAGAGCCAGAGAACATTTCTGGGAAACGAAATGAAGCAATTAAGAACTGTTCTTG	887
Db	696	ATTTGGAGAGCCAGAGGGCATGCTGCGGAACGAATGAATCAGTTAAATATGGTTTTAA	755

Qy	888	GAAAAATGCAAGAGGCTCCAGATTCAACCAACGGTTATATTTTGCAGGAGATACAAATTTAA	947
Db	756	AGAAAAATGCAAGAGGCTCCAGAGTCAAGTATATTTTGCAGGAGATACAAATCTAA	815
Qy	948	GAGATCAAGAGATTATCAAAATGTTGGTGTACTCTGACAACTGTTTGTATGATCCCTGGGAAT	1007
Db	816	GGGATCGAGAGGTTTACAGATGTTGGTGTATTTTACCAACAATTTTGTGATGTCTGGGAGT	875
Qy	1008	TTTGTAGCAAACTTAAACATTTGCCAGTATACATGGGATACGAAAGCAAAATAACAACCTCA	1067
Db	876	TTTTGGCAAACTTAAACATTTGCCAGTATACATGGGATACGAAATGAATCTTAATCTTG	935
Qy	1068	GGATCCCTGCTGCTTATAAAGATCGTTTTCATCGAATATTTTTCAG-----AGCAGAAG	1121
Db	936	GAATAACTGCTGCTGTGTAACCTTCGTTTTCATCGAATATTTTTCAGAGCAGCAGCAAG	995
Qy	1122	AGGGGACCTTATTCCTCAAGTTTACAGCTTGTGGTGTGGAAAACTGAGCTGTGCTA	1181
Db	996	AGGAGACATTTATTTCCCGGAGTTTGGACCTTCTTGGATTAGAAAAAACTGGACTGTGCTA	1055
Qy	1182	GATTTCCGAGTGCATCTGGGGGCTCTTGTGCACCTTTGAATGTAGTATTGTGAAAAAGCTT	1241
Db	1056	GATTTCCCTAGTGCATCTGGGGTCTTCTGTGCACTTAGATATAATATTGTAAAAATGCTT	1115
Qy	1242	CCCACTTGCAGCTTTT 1256	
Db	1116	TTCAAGTGTGGGTTT 1130	

RESULT 4

AAI58997
 ID AAI58997 standard; cDNA; 1948 BP.
 XX AAI58997;
 XX 22-OCT-2001 (first entry)
 XX Human polynucleotide SEQ ID NO 1200.

Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;
 peripheral nervous system; neuropathy; central nervous system; CNS;
 Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 leukaemia; BS.

OS Homo sapiens.
 XX WO200153312-A1.
 XX 26-JUL-2001.
 XX 26-DEC-2000; 2000WO-US034263.
 XX 23-DEC-1999; 99US-00471275.
 XX 21-JAN-2000; 2000US-00488725.
 XX 25-APR-2000; 2000US-00552317.
 XX 20-JUN-2000; 2000US-00598042.
 XX 19-JUL-2000; 2000US-00620312.
 XX 03-AUG-2000; 2000US-00653450.
 XX 14-SEP-2000; 2000US-00662191.
 XX 19-OCT-2000; 2000US-00693036.
 XX 29-NOV-2000; 2000US-00727344.

(HYSE-) HYSEQ INC.

XX Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX WPI; 2001-442253/47.
 DR P-PSDB; AAW39841.

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XX 30-AUG-2002; 2002WO-US027886.
PF
XX
PR 30-AUG-2001; 2001US-0316323P.
PR 31-AUG-2001; 2001CA-02356540.
XX
XX (UYEM-) UNIV EMORY.
XX
XX Wallace DC, Levy S, Kerstann K, Procaccio V;
XX WPI; 2003-300821/29.
DR
XX
XX Array containing probes for genes involved in mitochondrial biology,
PT useful for determining mitochondrial biology gene expression profiles for
PT use in diagnosing pathologies and identifying biochemical pathways.
XX
XX Claim 2; SEQ ID NO 2153; 201pp; English.
XX
XX The invention relates to a novel array comprising at least two isolated
CC nucleotide molecules, each molecule having a sequence capable of uniquely
CC hybridising to a nucleic acid molecule which is an expression product of
CC a gene involved in mitochondrial biology. The array comprises two or more
CC isolated nucleic acid molecules or spots, each molecule having a sequence
CC chosen from sequence of 994 human probes and 2046 mouse probes. An array
CC of the invention is useful for determining an expression profile of a
CC mouse or human sample containing nucleic acid, by contacting the array
CC with the sample under conditions allowing selective hybridisation, and
CC measuring hybridisation of nucleic acid in the sample to the array to
CC produce an expression profile. The array is also useful for determining
CC an expression profile of a first labelled sample containing nucleic acid
CC relative to a second, differently labelled sample containing nucleic
CC acid. The second sample is a reference or a standard. An array is useful
CC for determining an expression profile diagnostic of an energy-metabolism-
CC related physiological condition. An array of the invention is useful for
CC determining mitochondrial biology gene expression profiles of organisms,
CC such as human, mice and closely related species, tissue and organs of
CC such organisms, which are useful for determining expression profiles
CC diagnostic of energy metabolism-related physiological conditions.
CC Diagnosing such physiological conditions, identifying biochemical
CC pathways, genes, and mutations involved in such physiological conditions,
CC identifying therapeutic agents useful for preventing and/or treating such
CC physiological conditions, evaluating and/or monitoring the efficacy of
CC such therapies, and creating and identifying animal models of human
CC energy metabolism-related physiological conditions. An array is also
CC useful for defining expression signatures or profiles for mitochondrial
CC diseases, as well as distinguishing clinical disorders that result from
CC oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress,
CC apoptosis and aging. An array of the invention contains probes of genes
CC not previously recognised to participate in mitochondrial biology. The
CC sequences shown in ADD33224-ADD35260 represent murine mitochondrial DNA
CC clones used to make the probes of the invention. Some sequences are not
CC present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905,
CC 1906, 2408 and 2643.
XX
SQ Sequence 774 BP; 218 A; 169 C; 135 G; 252 T; 0 U; 0 Other;
Query Match 52.08; Score 682.8; DB 10; Length 774;
Best Local Similarity 99.48; Pred. No. 9.4e-179;
Matches 706; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
QY 593 GTATTTCTACAGGAAGTTATCCCCCATCTACTGTGCTTACCTAAAGAGAGAGAGCAGCAGT 652
DB 768 GTATTTCTACAGGAAG-TATCCCCCATCTACTGTGCTTACCTAAAGAGAGAGAGCAGCAG- 711
QY 653 TACAAATATTACAGGTAAAGAGAGGATATTTTCACAGCTATATCTATTGAAAGGA 712
DB 710 TACAAATATTACAGGTAAAGAGAGGATATTTTCACAGCTATATCTATTGAAAGGA 651
QY 713 AGAGTGAATTTAAAGCTCAGGAGATTATTCCTTTTCCAAATACCAAAATGATGAGAAC 772
DB 650 AGAGTGAATTTAAAGCTCAGGAGATTATTCCTTTTCCAAATACCAAAATGATGAGAAC 591
QY 773 CTGCTATGCGTAAATGTGAGTTGGGTGGAAATGAATTTTGGCCTTATGACATCCCATTTG 832
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Db 590 CTGCTATGCGTAAATGTGAGTTGGGTGGAAATGAATTTTGGCCTTATGACATCCCATTTG 531
QY 833 GAGAGACACAGAGAACATTTCTGGGNAACGAATAAGACAAATTAATAACTGTTCTTGGAAAA 892
Db 530 GAGAGACACAGAGAACATTTCTGGGNAACGAATAAGACAAATTAATAACTGTTCTTGGAAAA 471
QY 893 ATGCAAGAGGCTCCAGATTAACACCGGTTATATTTGCAAGGAGATACAAATTTTAAGAGAT 952
Db 470 ATGCAAGAGGCTCCAGATTAACACCGGTTATATTTGCAAGGAGATACAAATTTTAAGAGAT 411
QY 953 CAAGAAGTTATCAAAATGTGGTGTACCTGCAACAGTTTGTGATCCCTGGGAAATTTTA 1012
Db 410 CAAGAAGTTATCAAAATGTGGTGTACCTGCAACAGTTTGTGATCCCTGGGAAATTTTA 351
QY 1013 GGCNAACCTTAAACATTTGCCAGTATACATGGGATACGAAAGCAAAATTAACACCTCAGATC 1072
Db 350 GGCNAACCTTAAACATTTGCCAGTATACATGGGATACGAAAGCAAAATTAACACCTCAGATC 291
QY 1073 CTGCTGCTTTATAAGCATCGTTTTCATCGAATATTTTTCAGAGCAGAAGGGGCACCTT 1132
Db 290 CTGCTGCTTTATAAGCATCGTTTTCATCGAATATTTTTCAGAGCAGAAGGGGCACCTT 231
QY 1133 ATTCTCAAAAGTTAGACCTTGTGGTGGGTTGGAATACTGGACTGTGGTAGATTTCCGAGT 1192
Db 230 ATTCTCAAAAGTTAGACCTTGTGGTGGGTTGGAATACTGGACTGTGGTAGATTTCCGAGT 171
QY 1193 GATCCTGGGGCTCTTGGCACTTGAATGTAGTATTTGTAAGAGCTTCCACATTTGCAG 1252
Db 170 GATCCTGGGGCTCTTGGCACTTGAATGTAGTATTTGTAAGAGCTTCCACATTTGCAG 111
QY 1253 CTTTACACGTTTGTAGCACTAGTTCTGAATTTGTGTAGTCTCAACCTT 1302
Db 110 CTTTACACGTTTGTAGCACTAGTTCTGAATTTGTGTAGTCTCAACCTT 61
RESULT 3
AAZ47118
ID AAZ47118 standard; cDNA; 1920 BP.
XX
AC AAZ47118;
XX
DT 15-MAR-2000 (first entry)
DE Human CD40 receptor associated protein gene.
XX
KW Antiarteriosclerotic; antiarthritic; neuroprotective; dermatological;
KW immunosuppressive; antiinflammatory; immunosuppressive; antiallergic;
KW human; CD40 receptor associated protein; CRAP; cytoplasmic domain;
KW tumour necrosis factor; TNF; receptor; superfamily; CD30; homology;
KW TNF receptor associated factor; TRAF; modulator; signalling pathway;
KW diagnosis; NF-kappaB; Jun; kinase; atherosclerosis; multiple sclerosis;
KW arthritis; systemic lupus erythematosus; graft rejection; allergy;
KW graft versus host disease; autoimmune disease; ds.
XX
OS Homo sapiens.
XX
PN WO955859-A2.
XX
PD 04-NOV-1999.
XX
PF 28-APR-1999; 99WO-BP003025.
XX
PR 29-APR-1998; 98EP-00201392.
XX
PA (VLA-- ) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI Pype SMC, Remacle JEFJG, Huylebroeck DFE;
XX
XX WPI; 2000-062029/05.
DR P-PSDB; AAY56019.
XX
PT Novel proteins used to treat inflammatory diseases, NF-kappaB related
```

PF 28-APR-1999; 99WO-EP003025.
XX
PR 29-APR-1998; 98EP-00201392.
XX
XX (VLAA-) VLAMS INTERUNIVERSITAIR INST BIOTECHNOG.
PA
XX Pype SMC, Remacle JEFUG, Huylebroeck DFE;
XX P-PSDB; AAY56020.
XX
DR WPI; 2000-062029/05.
XX
DR Novel proteins used to treat inflammatory diseases, NF-kappaB related
XX diseases and for improvement of anti-tumor treatments.
XX
XX Claim 10; Page 41-43; 48pp; English.
XX
CC This sequence represents the gene encoding mouse CD40 receptor associated
CC protein (CRAP). CRAP is a functional protein capable of interacting with
CC the cytoplasmic domain of CD40 and/or other receptors of the tumour
CC necrosis factor (TNF) receptor superfamily such as CD30 and TNF receptor
CC I, where the protein has no homology to TNF receptor associated factor
CC (TRAF)-proteins. The CD40 binding proteins can be used as modulators of
CC the CD40 signalling pathway, especially to diagnose and treat TRAF-
CC related, CD40-related, NF-kappaB related and/or Jun (kinase)-related
CC diseases, and for the improvement of anti-tumour diseases. Diseases which
CC may be treated include atherosclerosis, arthritis, multiple sclerosis,
CC systemic lupus erythematosus, graft rejection, graft versus host disease,
CC allergy, and autoimmune disease. The proteins can be used to sensitize
CC tumour cells to anti-tumour treatments and to screen for compounds which
CC interfere with the interaction of the proteins with other protein
CC components of the TRAF, CD40 or NF-kappaB related pathway
XX
SQ Sequence 1312 BP; 359 A; 279 C; 352 G; 322 T; 0 U; 0 Other;

Query Match 100.0%; Score 1312; DB 3; Length 1312;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTATTATGATTCGAATTTATAGACTACTATAGGAAATTTGGCCCTCGAGGCCAAG 60
DB 1 AGCTATTATGATTCGAATTTATAGACTACTATAGGAAATTTGGCCCTCGAGGCCAAG 60
QY 61 AATTCGGCAGAGCGCGGAGAGCGGTGAAGAGCGGTGTTTGAAGGGACCTTCGCGGC 120
DB 61 AATTCGGCAGAGCGCGGAGAGCGGTGAAGAGCGGTGTTTGAAGGGACCTTCGCGGC 120
QY 121 GATGCGTCTGCAGCAGTTCGATGCGCGAGCGCCGAGCGCGCGGCGGCGGC 180
DB 121 GATGCGTCTGCAGCAGTTCGATGCGCGAGCGCCGAGCGCGCGGCGGCGGC 180
QY 181 GTGCGCGCCGAGCAGCAGCGCGGAGGAGCGCGGTGAAGAGCGCGCGGTTCAGTG 240
DB 181 GTGCGCGCCGAGCAGCAGCGCGGAGGAGCGCGGTGAAGAGCGCGCGGTTCAGTG 240
QY 241 CCGTGGCTTTGCGTTGGTGGGGGATGCGACCCACGATGTTCCCGCGGGA 300
DB 241 CCGTGGCTTTGCGTTGGTGGGGGATGCGACCCACGATGTTCCCGCGGGA 300
QY 301 GAACGACTGGCAGAGCGAGAAAGCCCTGAGCGCCTACTTCGAGCTGCCAGAGAACGACA 360
DB 301 GAACGACTGGCAGAGCGAGAAAGCCCTGAGCGCCTACTTCGAGCTGCCAGAGAACGACA 360
QY 361 AGGTGGCGCGCCAGCTCCCAAGTCTTCAAGTCCGAGGCGCTATGTTGATCTAACCA 420
DB 361 AGGTGGCGCGCCAGCTCCCAAGTCTTCAAGTCCGAGGCGCTATGTTGATCTAACCA 420
QY 421 CGAGGATGCAATGATACAAACATTTAGAGCCAGTCCATCTGGAACCTCTCTAGAGA 480
DB 421 CGAGGATGCAATGATACAAACATTTAGAGCCAGTCCATCTGGAACCTCTCTAGAGA 480
QY 481 TAGCAGCACTATTTCTTTCATTTACCTGGATATTGATGGATGATGATGCAATCTGCC 540
DB 481 TAGCAGCACTATTTCTTTCATTTACCTGGATATTGATGGATGATGATGCAATCTGCC 540

QY 541 CGAGAGGGCTCGAGGGGTGTGTTCTCCTAGCTTTGTATAGTCCAGATGGTATTCT 600
DB 541 CGAGAGGGCTCGAGGGGTGTGTTCTCCTAGCTTTGTATAGTCCAGATGGTATTCT 600
QY 601 ACAGGAAGTTATCCCCCATACTGTGCTACCTAAAGAGAGACGACCAAGTTACACAAT 660
DB 601 ACAGGAAGTTATCCCCCATACTGTGCTACCTAAAGAGAGACGACCAAGTTACACAAT 660
QY 661 TATTACAGGTAATGAAGAAGGATATTTTACAGCTATATTTGAAGAAAGAGAGTGAA 720
DB 661 TATTACAGGTAATGAAGAAGGATATTTTACAGCTATATTTGAAGAAAGAGAGTGAA 720
QY 721 ATTTAAAGTCAGAGATTTCTTTTCCAAATACCAAAATGATGAGAAACCTGCTATG 780
DB 721 ATTTAAAGTCAGAGATTTCTTTTCCAAATACCAAAATGATGAGAAACCTGCTATG 780
QY 781 CGTAAATGTCAGTTTGGTGGTGAATGAATTTTGGCTTATGACATCCCATTTGGAGAGCAC 840
DB 781 CGTAAATGTCAGTTTGGTGGTGAATGAATTTTGGCTTATGACATCCCATTTGGAGAGCAC 840
QY 841 CAGAGAACATTTCTCGGGAACGAATAAGACAATTTAAAACTGTTCTTGAAAAATGCAAGA 900
DB 841 CAGAGAACATTTCTCGGGAACGAATAAGACAATTTAAAACTGTTCTTGAAAAATGCAAGA 900
QY 901 GGCTCCAGATTCACACCGGTTATTTTGCAGGAGATACAAATTTAAGAGATCAAGAAT 960
DB 901 GGCTCCAGATTCACACCGGTTATTTTGCAGGAGATACAAATTTAAGAGATCAAGAAT 960
QY 961 TATCAATGTGCTGTTTACCTGACAAAGTTTGTGCTGCTGGGAATTTTGTAGCAAAACC 1020
DB 961 TATCAATGTGCTGTTTACCTGACAAAGTTTGTGCTGCTGGGAATTTTGTAGCAAAACC 1020
QY 1021 TAAACATTTGCCAGTATACATGGGATAGGAAAGCAAAATAACAACCTCAGGATCCCTGTGC 1080
DB 1021 TAAACATTTGCCAGTATACATGGGATAGGAAAGCAAAATAACAACCTCAGGATCCCTGTGC 1080
QY 1081 TTATAAGCATCGTTTTCGATCGAATTTTTCAGAGCAGAGAGGGGACCTTATTCCTCA 1140
DB 1081 TTATAAGCATCGTTTTCGATCGAATTTTTCAGAGCAGAGAGGGGACCTTATTCCTCA 1140
QY 1141 AAGTTTACAGCTTCTGGTTGGAAACCTGCACTGTGTTAGATTTCCGAGTGATCACTG 1200
DB 1141 AAGTTTACAGCTTCTGGTTGGAAACCTGCACTGTGTTAGATTTCCGAGTGATCACTG 1200
QY 1201 GGGGCTCTTGTGCACCTTGAATGTAGTATTTGTAAGAAAGCTTCCACCTTGCAGCTTTACAC 1260
DB 1201 GGGGCTCTTGTGCACCTTGAATGTAGTATTTGTAAGAAAGCTTCCACCTTGCAGCTTTACAC 1260
QY 1261 GTTTGTAGCACTAGTCTGAAATTTGTAGAGTCTCAACCTTTTACAGGACATC 1312
DB 1261 GTTTGTAGCACTAGTCTGAAATTTGTAGAGTCTCAACCTTTTACAGGACATC 1312

RESULT 2
ADD34375/c
ID ADD34375 standard; DNA; 774 BP.
XX
AC ADD34375;
XX
XX 15-JAN-2004 (first entry)
XX
XX Mouse mitochondrial DNA sequence SEQ ID NO:2153.
XX ds; mouse; array; mitochondrial; hybridisation; energy-metabolism;
KW mitochondrial disease; oxidative phosphorylation dysfunction;
KW oxidative stress; apoptosis; aging.
XX
XX Mus musculus.
XX
XX WO2003020220-A2.
XX
XX 13-MAR-2003.
PD

385	56.4	4.3	688	10	ADG30855	Adg30855 Liver tox	458	56	4.3	665	6	ABT09305	Abt09305 Phase-1 R
386	56.4	4.3	688	12	ADG45414	Adg45414 Liver inf	459	56	4.3	665	10	ADG31022	Adg31022 Liver tox
387	56.4	4.3	688	12	ADH22715	Adh22715 Partial D	460	56	4.3	665	12	ADG45666	Adg45666 Liver inf
388	56.4	4.3	688	13	ADR91074	Adr91074 Spleen ne	461	56	4.3	690	6	ABT09267	Abt09267 Phase-1 R
389	56.4	4.3	705	6	ADG30961	Adg30961 Liver tox	462	56	4.3	690	10	ADG31008	Adg31008 Liver tox
390	56.4	4.3	705	10	ADG30961	Adg30961 Liver tox	463	56	4.3	690	12	ADG45642	Adg45642 Liver inf
391	56.4	4.3	705	12	ADG45572	Adg45572 Liver inf	464	56	4.3	690	12	ADH22928	Adh22928 Partial D
392	56.2	4.3	80	14	ACL60434	ACL60434 Human col	465	56	4.3	704	6	ABT09054	Abt09054 Phase-1 R
393	56.2	4.3	655	6	ABT09251	Abt09251 Phase-1 R	466	56	4.3	704	10	ADG31075	Adg31075 Liver tox
394	56.2	4.3	655	6	ABT09142	Abt09142 Phase-1 R	467	56	4.3	704	12	ADG45755	Adg45755 Liver inf
395	56.2	4.3	655	10	ADG31053	Adg31053 Liver tox	468	56	4.3	724	6	ABT08971	Abt08971 Phase-1 R
396	56.2	4.3	655	12	ADH22921	Adh22921 Partial D	469	56	4.3	724	10	ADG30888	Adg30888 Liver tox
397	56.2	4.3	655	12	ADH22982	Adh22982 Partial D	470	56	4.3	724	12	ADG45464	Adg45464 Liver inf
398	56.2	4.3	655	13	ADR91241	Adr91241 Spleen ne	C 471	55.8	4.3	492	6	ABT09059	Abt09059 Phase-1 R
399	56.2	4.3	667	6	ABT08955	Abt08955 Phase-1 R	C 472	55.8	4.3	492	12	ADG45767	Adg45767 Liver inf
400	56.2	4.3	667	10	ADG30874	Adg30874 Liver tox	C 473	55.8	4.3	492	12	ADH23034	Adh23034 Partial D
401	56.2	4.3	673	6	ABT09178	Abt09178 Phase-1 R	C 474	55.8	4.3	560	10	ADH56910	Adh56910 Toxicity-
402	56.2	4.3	673	12	ADG45576	Adg45576 Liver inf	C 475	55.8	4.3	560	10	ADH51471	Adh51471 Primary r
403	56.2	4.3	673	12	ADH22874	Adh22874 Partial D	C 476	55.8	4.3	560	13	ADV40301	Adv40301 Rat cardi
404	56.2	4.3	685	6	ABT09058	Abt09058 Phase-1 R	C 477	55.8	4.3	565	3	AAA45987	Aaa45987 Human met
405	56.2	4.3	685	12	ADG45509	Adg45509 Liver inf	478	55.8	4.3	578	14	ACL63365	ACL63365 Human col
406	56.2	4.3	685	12	ADH23033	Adh23033 Partial D	C 479	55.8	4.3	578	11	ACN87139	ACN87139 Breast ca
407	56.2	4.3	686	6	ABT09000	Abt09000 Phase-1 R	C 480	55.8	4.3	631	5	ADL63376	ADL63376 Human ova
408	56.2	4.3	686	10	ADG30921	Adg30921 Liver tox	C 481	55.8	4.3	631	6	ABT09036	Abt09036 Phase-1 R
409	56.2	4.3	686	12	ADH22808	Adh22808 Partial D	482	55.8	4.3	631	12	ADG45733	Adg45733 Liver inf
410	56.2	4.3	686	13	ADR91154	Adr91154 Spleen ne	483	55.8	4.3	653	6	ABT09133	Abt09133 Phase-1 R
411	56.2	4.3	688	6	ABT09165	Abt09165 Phase-1 R	484	55.8	4.3	653	12	ADG45712	Adg45712 Liver inf
412	56.2	4.3	688	12	ADG45566	Adg45566 Liver inf	485	55.8	4.3	653	13	ADR91293	ADR91293 Spleen ne
413	56.2	4.3	689	6	ABT09183	Abt09183 Phase-1 R	486	55.8	4.3	667	6	ABT09097	Abt09097 Phase-1 R
414	56.2	4.3	689	12	ADG30965	Adg30965 Liver tox	487	55.8	4.3	667	10	ADG31032	Adg31032 Liver tox
415	56.2	4.3	689	12	ADG45579	Adg45579 Liver inf	488	55.8	4.3	667	12	ADG45682	Adg45682 Liver inf
416	56.2	4.3	689	12	ADH22875	Adh22875 Partial D	489	55.8	4.3	667	12	ADH22958	Adh22958 Partial D
417	56.2	4.3	691	6	ABT09065	Abt09065 Phase-1 R	490	55.8	4.3	668	6	ABT09019	Abt09019 Phase-1 R
418	56.2	4.3	691	6	ABT09222	Abt09222 Phase-1 R	491	55.8	4.3	668	6	ABT09088	Abt09088 Phase-1 R
419	56.2	4.3	691	10	ADG30985	Adg30985 Liver tox	492	55.8	4.3	668	12	ADG45534	Adg45534 Liver inf
420	56.2	4.3	691	12	ADG45779	Adg45779 Liver inf	493	55.8	4.3	668	12	ADG45674	Adg45674 Liver inf
421	56.2	4.3	691	12	ADG45610	Adg45610 Liver inf	494	55.8	4.3	668	12	ADH22839	Adh22839 Partial D
422	56.2	4.3	691	12	ADH23046	Adh23046 Partial D	495	55.8	4.3	668	13	ADR91176	ADR91176 Spleen ne
423	56.2	4.3	691	12	ADH22905	Adh22905 Partial D	496	55.8	4.3	669	6	ABT09167	Abt09167 Phase-1 R
424	56.2	4.3	691	13	ADR91225	ADR91225 Spleen ne	497	55.8	4.3	669	12	ADG45568	Adg45568 Liver inf
425	56.2	4.3	693	6	ABT09302	Abt09302 Phase-1 R	498	55.8	4.3	669	13	ADR91196	ADR91196 Spleen ne
426	56.2	4.3	693	10	ADG31019	Adg31019 Liver tox	499	55.8	4.3	673	6	ABT09090	Abt09090 Phase-1 R
427	56.2	4.3	693	12	ADG45662	Adg45662 Liver inf	500	55.8	4.3	673	12	ADG45676	Adg45676 Liver inf
428	56.2	4.3	693	12	ADH22948	Adh22948 Partial D							
429	56.2	4.3	695	6	ABT09268	Abt09268 Phase-1 R							
430	56.2	4.3	698	6	ABT09003	Abt09003 Phase-1 R							
431	56.2	4.3	698	10	ADG30923	Adg30923 Liver tox							
432	56.2	4.3	698	12	ADG45511	Adg45511 Liver inf							
433	56.2	4.3	698	12	ADH22813	Adh22813 Partial D							
434	56.2	4.3	698	13	ADR91156	ADR91156 Spleen ne							
435	56.2	4.3	699	6	ABT08950	Abt08950 Phase-1 R							
436	56.2	4.3	699	13	ADR91088	ADR91088 Spleen ne							
437	56.2	4.3	700	6	ABT09129	Abt09129 Phase-1 R							
438	56.2	4.3	700	10	ADG31047	Adg31047 Liver tox							
439	56.2	4.3	700	12	ADG45708	Adg45708 Liver inf							
440	56.2	4.3	700	13	ADR91290	ADR91290 Spleen ne							
441	56.2	4.3	701	6	ABT08965	Abt08965 Phase-1 R							
442	56.2	4.3	701	10	ADG30884	Adg30884 Liver tox							
443	56.2	4.3	701	12	ADG45454	Adg45454 Liver inf							
444	56.2	4.3	702	6	ABT09248	Abt09248 Phase-1 R							
445	56.2	4.3	702	6	ABT09204	Abt09204 Phase-1 R							
446	56.2	4.3	702	12	ADG45596	Adg45596 Liver inf							
447	56.2	4.3	702	12	ADH22894	Adh22894 Partial D							
448	56.2	4.3	702	13	ADR91239	ADR91239 Spleen ne							
449	56.2	4.3	705	6	ABT09013	Abt09013 Phase-1 R							
450	56.2	4.3	705	12	ADG45527	Adg45527 Liver inf							
451	56.2	4.3	709	6	ABT09125	Abt09125 Phase-1 R							
452	56.2	4.3	709	12	ADH22974	Adh22974 Partial D							
453	56.2	4.3	719	6	ABT08917	Abt08917 Phase-1 R							
454	56.2	4.3	719	12	ADH22681	Adh22681 Partial D							
455	56.2	4.3	719	13	ADR91049	ADR91049 Spleen ne							
456	56.2	4.3	768	2	AAx56830	Aax56830 Human phd							
457	56	4.3	510	14	ACL60196	ACL60196 Human col							

ALIGNMENTS

RESULT 1

AAZ47119
ID AAZ47119 standard; cDNA; 1312 BP.

XX AAZ47119;

XX 15-MAR-2000 (first entry)

DT Mouse CD40 receptor associated protein gene.

XX Antiarteriosclerotic; antiarthritic; neuroprotective; dermatological;
KW immunosuppressive; antiinflammatory; immunosuppressive; antiallergic;
KW mouse; CD40 receptor associated protein; CRAP; cytoplasmic domain;
KW tumour necrosis factor; TNF; receptor; superfamily; CD30; homology;
KW TNF receptor associated factor; TRAF; modulator; signalling pathway;
KW diagnosis; NF-kappaB; Jun; kinase; atherosclerosis; multiple sclerosis;
KW arthritis; systemic lupus erythematosus; graft rejection; allergy;
KW graft versus host disease; autoimmune disease; ds.

OS Mus musculus.

XX WO9955859-A2.

PN 04-NOV-1999.

XX

239	57.2	4.4	422	10	ADG30970	Adg30970 Liver tox	312	56.8	4.3	688	10	ADG30883	Adg30883 Liver tox
240	57.2	4.4	422	12	ADG45587	Adg45587 Liver inf	313	56.8	4.3	688	12	ADG45567	Adg45567 Liver inf
241	57.2	4.4	422	12	ADH22885	Adh22885 Partial D	314	56.8	4.3	688	12	ADG45452	Adg45452 Liver inf
242	57.2	4.4	422	13	ADR91211	Adr91211 Spleen ne	315	56.8	4.3	688	12	ADH22759	Adh22759 Partial D
243	57.2	4.4	422	13	ACL63454	Ac163454 Human col	316	56.8	4.3	688	13	ADR91109	Adr91109 Spleen ne
244	57.2	4.4	586	6	ABT08963	Abt08963 Phase-1 R	317	56.8	4.3	689	6	ABT08952	Abt08952 Phase-1 R
245	57.2	4.4	630	6	ABT09289	Abt09289 Phase-1 R	318	56.8	4.3	689	12	ADH22730	Adh22730 Partial D
246	57.2	4.4	630	12	ADG45655	Adg45655 Liver inf	319	56.8	4.3	689	13	ADR91089	Adr91089 Spleen ne
247	57.2	4.4	634	6	ABT09208	Abt09208 Phase-1 R	320	56.8	4.3	690	6	ABT08973	Abt08973 Phase-1 R
248	57.2	4.4	634	12	ADG45598	Adg45598 Liver inf	321	56.8	4.3	690	12	ADG45466	Adg45466 Liver inf
249	57.2	4.4	634	12	ADH22898	Adh22898 Partial D	322	56.8	4.3	690	12	ADH22771	Adh22771 Partial D
250	57.2	4.4	635	6	ABT08986	Abt08986 Phase-1 R	323	56.8	4.3	692	6	ABT09107	Abt09107 Phase-1 R
251	57.2	4.4	635	12	ADH22794	Adh22794 Partial D	324	56.8	4.3	692	12	ADG45690	Adg45690 Liver inf
252	57.2	4.4	655	6	ABT09263	Abt09263 Phase-1 R	325	56.8	4.3	693	6	ABT09106	Abt09106 Phase-1 R
253	57.2	4.4	656	12	ADH22924	Adh22924 Partial D	326	56.8	4.3	693	10	ADG31036	Adg31036 Liver tox
254	57.2	4.4	656	12	ADR91247	Adr91247 Spleen ne	327	56.8	4.3	693	12	ADG45689	Adg45689 Liver inf
255	57.2	4.4	684	6	ABT09074	Abt09074 Phase-1 R	328	56.8	4.3	693	12	ADH22964	Adh22964 Partial D
256	57.2	4.4	684	12	ADG45558	Adg45558 Liver inf	329	56.8	4.3	694	6	ABT09051	Abt09051 Phase-1 R
257	57.2	4.4	684	12	ADH22863	Adh22863 Partial D	330	56.8	4.3	695	6	ABT08913	Abt08913 Phase-1 R
258	57.2	4.4	684	13	ADR91190	Adr91190 Spleen ne	331	56.8	4.3	699	6	ABT09197	Abt09197 Phase-1 R
259	57.2	4.4	690	6	ABT09024	Abt09024 Phase-1 R	332	56.8	4.3	699	12	ADG45591	Adg45591 Liver inf
260	57.2	4.4	690	12	ADG30943	Adg30943 Liver tox	333	56.8	4.3	699	12	ADH22889	Adh22889 Partial D
261	57.2	4.4	690	12	ADG45540	Adg45540 Liver inf	334	56.8	4.3	701	6	ABT09123	Abt09123 Phase-1 R
262	57.2	4.4	690	13	ADR91180	Adr91180 Spleen ne	335	56.8	4.3	701	12	ADG45703	Adg45703 Liver inf
263	57.2	4.4	693	6	ABT08968	Abt08968 Phase-1 R	336	56.8	4.3	705	6	ABT09030	Abt09030 Phase-1 R
264	57.2	4.4	693	12	ADG45456	Adg45456 Liver inf	337	56.8	4.3	705	10	ADG30952	Adg30952 Liver tox
265	57.2	4.4	693	12	ADH22761	Adh22761 Partial D	338	56.8	4.3	705	12	ADG45552	Adg45552 Liver inf
266	57.2	4.4	710	6	ABT09239	Abt09239 Phase-1 R	339	56.8	4.3	705	12	ADH22858	Adh22858 Partial D
267	57.2	4.4	710	12	ADH22914	Adh22914 Partial D	340	56.8	4.3	709	6	ABT08957	Abt08957 Phase-1 R
268	57.2	4.4	710	13	ADR91236	Adr91236 Spleen ne	341	56.8	4.3	709	12	ADG45447	Adg45447 Liver inf
269	57.2	4.4	719	6	ABT09137	Abt09137 Phase-1 R	342	56.8	4.3	710	6	ABT09093	Abt09093 Phase-1 R
270	57.2	4.4	719	10	ADG31050	Adg31050 Liver tox	343	56.8	4.3	710	13	ADR91272	Adr91272 Spleen ne
271	57.2	4.4	719	12	ADG45717	Adg45717 Liver inf	344	56.8	4.3	713	6	ABT09145	Abt09145 Phase-1 R
272	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	345	56.8	4.3	713	12	ADG45723	Adg45723 Liver inf
273	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	346	56.8	4.3	713	12	ADG45723	Adg45723 Liver inf
274	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	347	56.8	4.3	717	6	ABT09081	Abt09081 Phase-1 R
275	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	348	56.8	4.3	717	10	ADG30992	Adg30992 Liver tox
276	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	349	56.8	4.3	717	13	ADR91234	Adr91234 Spleen ne
277	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	350	56.8	4.3	721	6	ABT09202	Abt09202 Phase-1 R
278	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	351	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
279	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	352	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
280	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	353	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
281	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	354	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
282	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	355	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
283	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	356	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
284	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	357	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
285	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	358	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
286	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	359	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
287	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	360	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
288	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	361	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
289	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	362	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
290	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	363	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
291	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	364	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
292	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	365	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
293	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	366	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
294	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	367	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
295	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	368	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
296	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	369	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
297	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	370	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
298	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	371	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
299	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	372	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
300	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	373	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
301	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	374	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
302	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	375	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
303	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	376	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
304	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	377	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
305	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	378	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
306	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	379	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
307	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	380	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
308	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	381	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
309	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	382	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
310	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	383	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf
311	57.2	4.4	719	13	ADR91294	Adr91294 Spleen ne	384	56.8	4.3	721	12	ADG45594	Adg45594 Liver inf

93	60.2	4.6	657	10	ADG31029	Adg31029 Liver tox	166	58	4.4	126	14	ACL60557	ACL60557 Human col
94	60.2	4.6	657	12	ADG45679	Adg45679 Liver inf	167	58	4.4	625	6	ABT09062	ABT09062 Phase-1 R
95	60.2	4.6	657	12	ADH22956	Adh22956 Partial D	168	58	4.4	633	10	ADG31084	Adg31084 Liver tox
96	60.2	4.6	657	13	ADR91273	Adr91273 Spleen ne	169	58	4.4	633	12	ADG45774	Adg45774 Liver inf
97	60	4.6	669	6	ABT09158	Abt09158 Phase-1 R	170	58	4.4	666	6	ABT08916	ABT08916 Phase-1 R
98	60	4.6	710	6	ABT09180	Abt09180 Phase-1 R	171	58	4.4	666	10	ADG30826	Adg30826 Liver tox
99	60	4.6	2418	13	ADP23069	Adp23069 PRO polyP	172	58	4.4	666	12	ADG45375	Adg45375 Liver inf
100	59.8	4.6	594	6	ABT09017	Abt09017 Phase-1 R	173	58	4.4	666	12	ADH22680	Adh22680 Partial D
101	59.8	4.6	594	6	ABT09086	Abt09086 Phase-1 R	174	58	4.4	701	6	ABT09099	ABT09099 Phase-1 R
102	59.8	4.6	762	12	ADH22837	Adh22837 Partial D	175	58	4.4	701	14	ACL56825	ACL56825 Human col
103	59.8	4.6	762	12	ADG45658	Adg45658 Liver inf	176	58	4.4	724	6	ABT08931	ABT08931 Phase-1 R
104	59.8	4.6	762	12	ADH22944	Adh22944 Partial D	177	58	4.4	724	12	ADG45399	Adg45399 Liver inf
105	59.8	4.6	762	13	ADR91258	Adr91258 Spleen ne	178	58	4.4	724	12	ADH22701	Adh22701 Partial D
106	59.6	4.5	720	12	ABT09015	Abt09015 Phase-1 R	179	58	4.4	796	4	AAI59391	Aai59391 Human pol
107	59.6	4.5	720	6	ADH22831	Adh22831 Partial D	180	57.8	4.4	634	6	ABT08933	ABT08933 Phase-1 R
108	59.2	4.5	761	6	ABT09294	Abt09294 Phase-1 R	181	57.8	4.4	631	6	ABT09196	ABT09196 Phase-1 R
109	59.2	4.5	761	12	ADH22943	Adh22943 Partial D	182	57.8	4.4	631	12	ADG45590	Adg45590 Liver inf
110	59	4.5	686	6	ABT09162	Abt09162 Phase-1 R	183	57.8	4.4	631	13	ADR91214	Adr91214 Spleen ne
111	59	4.5	686	10	ADG30958	Adg30958 Liver tox	184	57.8	4.4	634	6	ABT08981	ABT08981 Phase-1 R
112	59	4.5	691	10	ADG30844	Adg30844 Liver tox	185	57.8	4.4	634	13	ADR91133	Adr91133 Spleen ne
113	59	4.5	691	12	ADG45395	Adg45395 Liver inf	186	57.8	4.4	670	6	ABT09091	ABT09091 Phase-1 R
114	59	4.5	692	6	ABT08929	Abt08929 Phase-1 R	187	57.8	4.4	670	10	ADG30847	Adg30847 Liver tox
115	59	4.5	695	6	ABT09228	Abt09228 Phase-1 R	188	57.8	4.4	670	10	ADG31027	Adg31027 Liver tox
116	59	4.5	695	10	ADG30989	Adg30989 Liver tox	189	57.8	4.4	670	12	ADG45677	Adg45677 Liver inf
117	59	4.5	695	12	ADG45614	Adg45614 Liver inf	190	57.8	4.4	670	12	ADH22703	Adh22703 Partial D
118	59	4.5	749	6	ABT08988	Abt08988 Phase-1 R	191	57.8	4.4	671	6	ABT08995	ABT08995 Phase-1 R
119	58.8	4.5	627	10	ADG31034	Adg31034 Liver tox	192	57.8	4.4	671	10	ADG30913	Adg30913 Liver tox
120	58.8	4.5	627	10	ADG31021	Adg31021 Liver tox	193	57.8	4.4	671	12	ADG45500	Adg45500 Liver inf
121	58.8	4.5	642	12	ADG45664	Adg45664 Liver inf	194	57.8	4.4	671	12	ADH22802	Adh22802 Partial D
122	58.8	4.5	642	6	ABT09029	Abt09029 Phase-1 R	195	57.8	4.4	671	13	ADR91145	Adr91145 Spleen ne
123	58.8	4.5	642	12	ADH22857	Adh22857 Partial D	196	57.8	4.4	677	6	ABT09292	ABT09292 Phase-1 R
124	58.8	4.5	688	6	ABT09104	Abt09104 Phase-1 R	197	57.8	4.4	677	10	ADG31016	Adg31016 Liver tox
125	58.8	4.5	688	10	ADG31034	Adg31034 Liver tox	198	57.8	4.4	677	12	ADH22942	Adh22942 Partial D
126	58.8	4.5	688	12	ADG45687	Adg45687 Liver inf	199	57.8	4.4	689	6	ABT09266	ABT09266 Phase-1 R
127	58.8	4.5	694	6	ABT09242	Abt09242 Phase-1 R	200	57.8	4.4	689	10	ADG31007	Adg31007 Liver tox
128	58.8	4.5	694	12	ADG45623	Adg45623 Liver inf	201	57.8	4.4	689	12	ADG45641	Adg45641 Liver inf
129	58.8	4.5	704	6	ABT09461	Abt09461 Phase-1 R	202	57.8	4.4	689	12	ADH22927	Adh22927 Partial D
130	58.8	4.5	704	12	ADG45488	Adg45488 Liver inf	203	57.8	4.4	755	6	ABT09235	ABT09235 Phase-1 R
131	58.8	4.5	704	12	ADH22788	Adh22788 Partial D	204	57.8	4.4	755	12	ADH22912	Adh22912 Partial D
132	58.8	4.5	720	6	ABT09100	Abt09100 Phase-1 R	205	57.6	4.4	315	10	ADB56831	ADB56831 Toxicity-
133	58.8	4.5	720	12	ADG45684	Adg45684 Liver inf	206	57.6	4.4	315	10	ADB51380	ADB51380 Primary r
134	58.8	4.5	720	12	ADH22960	Adh22960 Partial D	207	57.6	4.4	315	10	ADB41213	ADB41213 Toxicity
135	58.6	4.5	631	6	ABT09026	Abt09026 Phase-1 R	208	57.6	4.4	315	12	ADP72142	Adp72142 Renal tox
136	58.6	4.5	631	12	ADG30949	Adg30949 Liver tox	209	57.6	4.4	645	12	ADH22856	Adh22856 Partial D
137	58.6	4.5	631	12	ADG45548	Adg45548 Liver inf	210	57.6	4.4	677	6	ABT09170	ABT09170 Phase-1 R
138	58.6	4.5	631	13	ADR91185	Adr91185 Spleen ne	211	57.6	4.4	677	12	ADG45570	Adg45570 Liver inf
139	58.6	4.5	705	6	ABT09205	Abt09205 Phase-1 R	212	57.6	4.4	677	13	ADR91198	Adr91198 Spleen ne
140	58.6	4.5	705	10	ADG30975	Adg30975 Liver tox	213	57.6	4.4	708	6	ABT09121	ABT09121 Phase-1 R
141	58.6	4.5	705	12	ADH22895	Adh22895 Partial D	214	57.6	4.4	708	10	ADG31041	Adg31041 Liver tox
142	58.6	4.5	705	13	ADR91218	Adr91218 Spleen ne	215	57.6	4.4	708	12	ADG45701	Adg45701 Liver inf
143	58.6	4.5	764	4	AAI26662	Aai26662 Human bre	216	57.6	4.4	728	6	ABT09161	ABT09161 Phase-1 R
144	58.6	4.5	764	4	AAI26458	Aai26458 Human bre	217	57.6	4.4	728	10	ADG30957	Adg30957 Liver tox
145	58.6	4.5	846	11	ACN88566	Acn88566 Breast ca	218	57.6	4.4	728	12	ADG45563	Adg45563 Liver inf
146	58.4	4.5	422	11	ACN91843	Acn91843 Breast ca	219	57.6	4.4	728	12	ADH22868	Adh22868 Partial D
147	58.4	4.5	497	14	ACL60583	ACL60583 Human col	220	57.6	4.4	728	13	ADR91194	Adr91194 Spleen ne
148	58.4	4.5	667	6	ABT09174	Abt09174 Phase-1 R	221	57.4	4.4	77	14	ACL60436	ACL60436 Human col
149	58.4	4.5	667	13	ADR91201	Adr91201 Spleen ne	222	57.4	4.4	663	6	ABT09224	ABT09224 Phase-1 R
150	58.4	4.5	692	6	ABT09082	Abt09082 Phase-1 R	223	57.4	4.4	663	10	ADG30986	Adg30986 Liver tox
151	58.4	4.5	692	12	ADG45631	Adg45631 Liver inf	224	57.4	4.4	663	12	ADG45612	Adg45612 Liver inf
152	58.4	4.5	692	12	ADH22920	Adh22920 Partial D	225	57.4	4.4	663	12	ADH22906	Adh22906 Partial D
153	58.4	4.5	730	6	ABT08921	Abt08921 Phase-1 R	226	57.4	4.4	663	13	ADR91227	Adr91227 Spleen ne
154	58.4	4.5	730	12	ADH22686	Adh22686 Partial D	227	57.4	4.4	698	6	ABT08956	ABT08956 Phase-1 R
155	58.4	4.5	730	13	ADR91051	Adr91051 Spleen ne	228	57.4	4.4	705	6	ABT09220	ABT09220 Phase-1 R
156	58.2	4.4	632	6	ABT09047	Abt09047 Phase-1 R	229	57.4	4.4	705	10	ADG30983	Adg30983 Liver tox
157	58.2	4.4	632	12	ADH23008	Adh23008 Partial D	230	57.4	4.4	705	12	ADG45608	Adg45608 Liver inf
158	58.2	4.4	632	13	ADR91319	Adr91319 Spleen ne	231	57.4	4.4	705	12	ADH22903	Adh22903 Partial D
159	58.2	4.4	639	6	ABT09069	Abt09069 Phase-1 R	232	57.4	4.4	709	6	ABT09199	ABT09199 Phase-1 R
160	58.2	4.4	639	12	ADG45673	Adg45673 Liver inf	233	57.4	4.4	709	12	ADH22891	Adh22891 Partial D
161	58.2	4.4	639	13	ADR91269	Adr91269 Spleen ne	234	57.4	4.4	709	13	ADR91216	Adr91216 Spleen ne
162	58.2	4.4	702	6	ABT09116	Abt09116 Phase-1 R	235	57.4	4.4	749	6	ABT09290	ABT09290 Phase-1 R
163	58.2	4.4	702	12	ADG45697	Adg45697 Liver inf	236	57.4	4.4	749	12	ADH22940	Adh22940 Partial D
164	58.2	4.4	702	12	ADH22968	Adh22968 Partial D	237	57.4	4.4	749	13	ADR91257	Adr91257 Spleen ne
165	58.2	4.4	702	13	ADR91282	Adr91282 Spleen ne	238	57.2	4.4	422	6	ABT09192	ABT09192 Phase-1 R

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 06:13:56 ; Search time 806.517 Seconds
(without alignments)
10841.779 Million cell updates/sec

Title: US-10-757-745-3

Perfect score: 1312

Sequence: 1 agctattaatgattcgaatt.....tctcaaccttcaggacatc 1312

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :

N_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2001bs.*
- 6: Geneseq2002as.*
- 7: Geneseq2002bs.*
- 8: Geneseq2003as.*
- 9: Geneseq2003bs.*
- 10: Geneseq2003cs.*
- 11: Geneseq2003ds.*
- 12: Geneseq2004as.*
- 13: Geneseq2004bs.*
- 14: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1312	100.0	1312	3	Aaz47119 Mouse CD4
2	682.8	52.0	774	10	ADD34375
3	682.2	50.9	1920	3	Aaz47118 Human CD4
4	668.2	50.9	1948	4	Aai58997 Human pol
5	668.2	50.9	1948	5	ADQ99219 DNA encod
6	668.2	50.9	1948	9	ADB48979 Novel hum
7	668.2	50.9	1958	4	Aai60783 Human pol
8	668.2	50.9	2499	2	Aax28153 Topoisome
9	668.2	50.9	3152	9	ADA10970 Human cDN
10	667	50.8	1296	3	Aac98160 Human col
11	666.6	50.8	1936	10	ADD19013
12	666.6	50.8	1936	13	ADP25361 PRO polyp
13	666.6	50.8	1940	14	ADX06356 Cyclin-de
14	665	50.7	1898	4	Aai15146 Human cDN
15	600.4	45.8	602	10	ADD34376 Mouse mit
16	493.2	37.6	1088	5	Aas86254 DNA encod
17	490	37.3	1079	2	Aax84209 DNA encod
18	490	37.3	1079	3	AAC79438 cDNA sequ
19	490	37.3	1079	6	ABK28982 Human bre

20	461.6	35.2	674	11	ADT95548
21	461.6	35.2	674	11	ADX42030
22	436.4	33.3	644	11	ADT95551
23	436.4	33.3	644	11	ADX42033
24	428.4	32.7	625	11	ADT95512
25	428.4	32.7	625	11	ADX41994
26	428.4	32.7	633	11	ADT95565
27	428.4	32.7	633	11	ADX42047
28	418	31.9	625	11	ADT95029
29	418	31.9	625	11	ADX41511
30	395.8	29.4	553	11	ADT95464
31	385.8	29.4	553	11	ADX41946
32	377.8	28.8	752	4	AAH08073
33	370.2	22.1	401	11	ADT95844
34	290.2	22.1	401	11	ADX42326
35	231.8	17.7	483	2	AAAX0590
36	198.2	15.1	1227	5	AAAS86255
37	140.8	10.7	391	11	ADT95307
38	140.8	10.7	391	11	ADX41789
39	135.6	10.3	179	6	ABL36461
40	134.4	10.2	176	6	ABK27684
41	134.4	10.2	176	6	ABV95959
42	101.4	7.7	268	6	ABT07150
43	101.4	7.7	268	8	ABX73028
44	75.2	5.7	258	2	AAAX41008
45	74.6	5.7	444	4	AAI15311
46	74.6	5.7	691	4	AAI24484
47	67.4	5.1	705	6	ABT09027
48	67.4	5.1	705	12	ADG45549
49	67.4	5.1	705	12	ADH22854
50	64.8	4.9	631	6	ABT09296
51	64.8	4.9	631	12	ADG45660
52	64.8	4.9	631	12	ADH22946
53	64.8	4.9	631	13	ADR91260
54	63.8	4.9	690	6	ABT09191
55	63.8	4.9	690	10	ADG30969
56	63.8	4.9	690	12	ADG45586
57	63.8	4.9	690	12	ADH22884
58	63.6	4.8	966	4	AAK52001
59	63.2	4.8	966	6	ABT09200
60	63.2	4.8	966	10	ADG30974
61	63.2	4.8	966	12	ADG45593
62	63.2	4.8	966	13	ADR91217
63	63.2	4.8	704	6	ABT09004
64	63.2	4.8	704	10	ADG30925
65	63.2	4.8	704	13	ADR91162
66	62.8	4.8	722	6	ABT09153
67	62.8	4.8	722	12	ADG45729
68	62.2	4.7	630	6	ABT09311
69	62.2	4.7	630	12	ADG45672
70	62.2	4.7	630	13	ADR91268
71	62.2	4.7	1549	3	AAA38745
72	61.6	4.7	701	6	ABT08958
73	61.6	4.7	701	10	ADG30880
74	61.6	4.7	701	12	ADG45448
75	61.6	4.7	701	12	ADH22750
76	61.6	4.7	718	6	ABT09276
77	61.4	4.7	682	6	ABT08928
78	61.4	4.7	682	10	ADG30840
79	61.4	4.7	682	12	ADG45391
80	61.4	4.7	1775	4	AAI57823
81	61.2	4.7	701	6	ABT09046
82	61.2	4.7	956	4	AAI12179
83	61.2	4.7	1404	12	ADG45744
84	60.6	4.6	581	6	ABT09028
85	60.4	4.6	692	6	ABT09022
86	60.4	4.6	692	10	ADG30941
87	60.4	4.6	692	12	ADG45538
88	60.4	4.6	692	12	ADH22844
89	60.4	4.6	706	6	ABT09138
90	60.4	4.6	706	10	ADG31051
91	60.4	4.6	706	12	ADG45718
92	60.2	4.6	657	6	ABT09094

Adt95548	Colon can
Adx42030	Human cDN
Adt95551	Colon can
Adx42033	Human cDN
Adt95512	Colon can
Adx41994	Human cDN
Adt95565	Colon can
Adx42047	Human cDN
Adt95029	Colon can
Adx41511	Human cDN
Adt95464	Colon can
Adx41946	Human cDN
Aah08073	Human cDN
Adt95844	Colon can
Adx42326	Human cDN
Aax0590	Human sec
Aas86255	DNA encod
Adt95307	Colon can
Adx41789	Human cDN
Abi36461	Human col
Abk27684	Human col
Abv95959	Human pan
Abt07150	Human ova
Abx73028	Human ova
Aax41008	Human sec
Aai15311	Probe #52
Aai24484	Probe #14
Abt09027	Phase-1 R
Adg45549	Liver inf
Adh22854	Partial D
Abt09296	Phase-1 R
Adg45660	Liver inf
Adh22946	Partial D
Adx41260	Spleen ne
Abt09191	Phase-1 R
Adg30969	Liver tox
Adg45586	Liver inf
Adh22884	Partial D
Aak52001	Human pol
Abt09200	Phase-1 R
Adg30974	Liver tox
Adg45593	Liver inf
Adx91217	Spleen ne
Abt09004	Phase-1 R
Adg30925	Liver tox
Adx91162	Spleen ne
Abt09153	Phase-1 R
Adg45729	Liver inf
Abt09311	Phase-1 R
Adg45672	Liver inf
Adx91268	Spleen ne
Aaa38745	Murine Hs
Abt08958	Phase-1 R
Adg30880	Liver tox
Adx45448	Liver inf
Adh22750	Partial D
Abt09276	Phase-1 R
Abt08928	Phase-1 R
Adg30840	Liver tox
Adg45391	Liver inf
Aai57823	Human pol
Abt09046	Phase-1 R
Aai12179	Murine 2P
Adg45744	Liver inf
Abt09028	Phase-1 R
Abt09022	Phase-1 R
Adg30941	Liver tox
Adg45538	Liver inf
Adh22844	Partial D
Abt09138	Phase-1 R
Adg31051	Liver tox
Adg45718	Liver inf
Abt09094	Phase-1 R

RESULT 29	BX433489/c	952 bp	mrna	linear	EST 04-MAY-2004
LOCUS	BX433489 Homo sapiens ADULT BRAIN Homo sapiens cdna clone				
DEFINITION	CS0DN005YN02 3-PRIME, mRNA sequence.				
ACCESSION	BX433489				
VERSION	BX433489.2	GI:47002503			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	On May 15, 2003 this sequence version replaced gi:30775195. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: secref@genoscope.cns.fr , Web: www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3474.r For more information about this cluster, see http://www.genoscope.cns.fr/cdna?n=CS0BA1056ZD12_CS05372_1&c=3474.r				
FEATURES	Location/Qualifiers				
source	1..952				
	/organism="Homo sapiens"				
	/mol_type="mrna"				
	/db_xref="taxon:9606"				
	/clone="CS0DN005YN02"				
	/tissue_type="ADULT BRAIN"				
	/dev_stage="adult"				
	/clone_lib="Homo sapiens ADULT BRAIN"				
	/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."				
ORIGIN					
Query Match	43.7%; Score 573; DB 5; Length 952;				
Best Local Similarity	78.5%; Pred. No. 8.5e-145;				
Matches	713; Conservative 0; Mismatches 186; Indels 9; Gaps 2;				
QY	373	CCAGGCTCCCGCTCTCAAGTCGAGCCCTATGTTGATCTAATCAACACGAGGATGCAAA	432		
Db	925	CGAAGCTGAACCATCTCTGAGCCCAAGACCTATGTGACCTAAACCAATGAAGAAACAAC	866		
QY	433	TGATACACCACTTTTAGAGGACAGTCCATCTGGA---ACTCCTCTAGAGATAGCAGCAC	489		
Db	865	GNAATCCACACTTTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCAT	806		
QY	490	TATTTCTTTCTTACTCTGGAATTTATGATGATGATGATGATGATGATGATGATGATGATG	549		
Db	805	GTCTCTCTCATCTGGAATTTATGATGATGATGATGATGATGATGATGATGATGATGATG	746		
QY	550	TCGAGGGTGTGTTCTGCTAGCTTTGTATAGTCAGATGGTGATTTCTTACAGGAAGT	609		
Db	745	TCGAGGGTGTGTTCTGCTAGCTTTGTATAGTCAGATGGTGATTTCTTACAGGAAGT	686		
QY	610	TATCCCCCATCTGCTCTCACTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	669		
Db	685	TATCCCCCATCTGCTCTCACTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	626		
QY	670	TAATGAAGAAGGATATTTTCACAGCTATCTACTATTGAAGAAGAAGAGAGTGAATTTTAAAG	729		
Db	625	TCATGAAGAAGGATATTTTCACAGCTATCTACTATTGAAGAAGAAGAGTGAATTTTAAAG	566		
QY	730	TCAGGAGATTTATCTCTTTTCCAAATACCAAAATGATGAGAAACCTGCTATGCGTAAATGT	789		
Db	565	CCAAGAGATTTATCTCTTTTCCAAATGATGAGAAACCTTTTATGCTGTCATGT	506		
QY	790	GAGTTTGGGTGGAAATGAATTTTCCCTTATGACATCCATTTGGAGAGCACCAGAGACA	849		
Db	505	GAATGTGTCAGGAAATGAGCTTTTCCCTTATGACATCCATTTGGAGAGCACCAGAGGCA	446		
QY	850	TTCTGCGGAAAGGATAGACAAATTAATAAATCTTTTGGAAAAATGCAAGAGGCTCCAGA	909		
Db	445	TGCTGCGGAAAGGATAGATCAATTTTAAAGAAATGGAAGAGGCTCCAGA	386		
QY	910	TTCAACACCGGTTATATTTTGCAGGAGATACAAATTTTAAGAGATCAAGAAGTTTCAATG	969		
Db	385	GTCAAGCTACAGTTATATTTTGCAGGAGATACAAATCTAAGGATCGAGAGTTACCAGATG	326		
QY	970	TGTTGGTTTACCTGACAAAGTTTGTGATGCTGCGGAATTTTATAGGCAAACTTAACATTTG	1029		
Db	325	TGTTGGTTTACCTGACAAAGTTTGTGATGCTGCGGAATTTTATAGGCAAACTTAACATTTG	266		
QY	1030	CCAGTATACATGCGATACGAAGCAATTAACAACCTCAGGATCCCTGCTGCTTATAAGCA	1089		
Db	265	CCAGTATACATGCGATACGAAGCAATTAACAACCTCAGGATCCCTGCTGCTTATAAGCA	206		
QY	1090	TCGTTTGTATCGAATATTTTTCAG-----AGCAGAAGAGGGCACCCTTATTCCTCAAAG	1143		
Db	205	TCGTTTGTATCGAATATTTTTCAGAGCAGCAGCAGAGAGAGGACACATTTATCCCGAAG	146		
QY	1144	TTTAGACCTTGTGGGTGGAAAACTGGAGTGGTAGATTTCGAGTGTATCTACCTGGGG	1203		
Db	145	TTTGGACCTTGTGGATTAGAAAACTGGAGTGGTAGATTTCCTAGTGTATCTACCTGGGG	86		
QY	1204	GCTCTTGTGACCTTGATGTAGTATTGTGAAGAGCTTCCCACTTGCAGCTTACACGTT	1263		
Db	85	TCCTTCTGTCAACTTAGATATATTTGTAATAATGCTTTTCAAGTGGGGTTTTCCTCGA	26		
QY	1264	TGTTAGCA 1271			
Db	25	TTGTTGCA 18			
RESULT 30					
LOCUS	BY708937	936 bp	mrna	linear	EST 16-DEC-2002
DEFINITION	BY708937 RIKEN full-length enriched, adult male tongue Mus musculus				
ACCESSION	BY708937				
VERSION	BY708937.1	GI:27120132			
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 936) Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaudo, I., Osato, N., Saito, R., Suzuki, H., Yamana, A., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Della, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konegaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, I., Pavan, W.J., Perce, G., Pesole, G.,				

/dev_stage="Embryonic day 16.5"
/lab_host="TOPI0"
/clone_lib="Milton Mouse E16 5 Pancreas Library 2 M16B2"
/notes="Organ: Pancreas; Vector: pBluescript II SK; Site 1:
NotI; Site 2: SalI; Library constructed using SuperScript
Plasmid Library kit (Life Technologies). cDNA made by
oligo-dr priming. Size-selected by column fractionation;
average insert size 1.06kb. Primary library,
unamplified."

ORIGIN

Query Match 44.2%; Score 580; DB 3; Length 580;
Best Local Similarity 100.0%; Pred. No. 9e-147;
Matches 580; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 587 GATGTGGTATTCTACAGGAAGTTATCCCCCATCTGTGCTACTTAAGAAGAGAGCA 646
DB 1 GATGTGGTATTCTACAGGAAGTTATCCCCCATCTGTGCTACTTAAGAAGAGAGCA 60

QY 647 GCCAGTTACAAATPATTACAGGTAATGAAGAAGGATATTTACAGCTATATCTATTGAAG 706
DB 61 GCCAGTTACAAATPATTACAGGTAATGAAGAAGGATATTTACAGCTATATCTATTGAAG 120

QY 707 AAAGGAAGAGTCAAAATTTAAAGTCAGGAGATTATCTCTTTCCAAATACCAAAATGATG 766
DB 121 AAAGGAAGAGTCAAAATTTAAAGTCAGGAGATTATCTCTTTCCAAATACCAAAATGATG 180

QY 767 AGAAACCTGCTATGCTGTAATGATGTTGGTGGAAATGAATTTGCTTTATGACATCC 826
DB 181 AGAAACCTGCTATGCTGTAATGATGTTGGTGGAAATGAATTTGCTTTATGACATCC 240

QY 827 CATTTGGAGAGCACAGAGACATCTCTCGGAACGAATAAGACAAATTAATTAATTTA 886
DB 241 CATTTGGAGAGCACAGAGACATCTCTCGGAACGAATAAGACAAATTAATTAATTTA 300

QY 887 GGAAAAATGCAAGAGCTCCAGATTCACACCGGTTATATTGCGAGGAGATACAAATTTA 946
DB 301 GGAAAAATGCAAGAGCTCCAGATTCACACCGGTTATATTGCGAGGAGATACAAATTTA 360

QY 947 AGAGATCAAGAAGTTATCAATGTGCTGTTTACCTGCAACAGTTTTTGATGCTCGGAA 1006
DB 361 AGAGATCAAGAAGTTATCAATGTGCTGTTTACCTGCAACAGTTTTTGATGCTCGGAA 420

QY 1007 TTTTGTAGGCAACCTAAACATTTCCAGTATACATGGATACGAAAGCAAAATTAACACCTC 1066
DB 421 TTTTGTAGGCAACCTAAACATTTCCAGTATACATGGATACGAAAGCAAAATTAACACCTC 480

QY 1067 AGGATCCCTGCTTTAAGCATGTTTGTATCGAATATTTTTCAGAGCAGAGAGGGG 1126
DB 481 AGGATCCCTGCTTTAAGCATGTTTGTATCGAATATTTTTCAGAGCAGAGAGGGG 540

QY 1127 CACCTTATTCCTCAAGTTTACACCTTGTGTTGGTTGGAAA 1166
DB 541 CACCTTATTCCTCAAGTTTACACCTTGTGTTGGTTGGAAA 580

RESULT 27
BX444691 1081 bp mRNA linear EST 04-MAY-2004
LOCUS BX444691 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
DEFINITION CS0DN005YN02 5-PRIME, mRNA sequence.
ACCESSION BX444691
VERSION BX444691.2 GI:47009162
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1081)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)

COMMENT

On May 15, 2003 this sequence version replaced gi:30780264.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CS0DN005DG01QPI&c=3474.r.

FEATURES

source

Location/Qualifiers
1..1081
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DN005YN02"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Query Match 44.1%; Score 579; DB 5; Length 1081;
Best Local Similarity 76.6%; Pred. No. 2e-146;
Matches 784; Conservative 3; Mismatches 223; Indels 13; Gaps 6;

QY 174 GGGCGGCTCGGCGCCGGAAGCAGCACAGGCGGAGGAGCGGCTGAAGAGCGCGCGC 233
DB 46 GGGCGGCGGAGGAGGCGCGGAGGAGGCGGCTGAGGTGAAAAAGCGCGCAC 105

QY 234 TTCAGTGTCTGGGCTTTCGTTTGGTGGGGGATGGACCCACGATGTCCTCCACGGTCC 293
DB 106 TTCTGTGTGGAGTTTTCCTCGGTGCAAGCTGCGATGCGCGAGTGGCTCAGTCTTCC 165

QY 294 TGGCGGAAACGACTGGCAGACGCAAGAACGCCCTGAGCGCTTCTCGAGCTGCCAGAGA 353
DB 166 TGGCGGAAACGACTGGGAGATGGAAGGGCTCTGAACTCTTCTCTCGAGCTCCGGTGG 225

QY 354 ACGACCAAGGGTGGCGCGCCAGCTCCCAAGTCTTCAAGTCCAGGCTATGTTGATC 413
DB 226 AGGAGAGCGCTTGGAAACGCGACCTGAAACCCATCTCTGAGCCCAAGACCTATGTTGACC 285

QY 414 TAACCAACGAGAGTCAAAATGATCAACCAATTTAGAACCCAGTCCATCTGGA ---ACTC 470
DB 286 TAACCAATGAAGAAACAACTGATTCACCACTTTTAAATCAGCCATCTGGAAGATATCTC 345

QY 471 CTCTAGAGATAGCAGACACTATTTCTTTCATTACCTGGAATATTGATGGATTAGATG 530
DB 346 AGCAAGAAATAGGACAGCATGTTCTCTCTCATTTACTCTGGAATATTGATGGATTAGATCTAA 405

QY 531 GCAATCTCCCGAGAGGGCTCGAGGGGTGTGTTCTCTGCTAGCTTTGTATAGTCAGATG 590
DB 406 ACAATCTGTCAAGAGAGGGCTCGAGGGGTGTGTTCTCTTACTTAGCTTTGTACAGCCAGATG 465

QY 591 TGGTATTTCTACAGGAAGTTATCCCGCCACTACTGTCTACCTAAGAGAGAGAGAGCA 650
DB 466 TGATATTTCTACAGGAAGTTATTTCCCGCCATATTTATAGTCTACCTAAGAGAGATCAAGTA 525

QY 651 GTTACACAAATATTACAGGTAAATGAAGAGGATATTTTACAGCTATATCTATTGAAGAAAG 710
DB 526 ATTATGAGATTTATACAGGTCAATGAAGAGGATATTTTACAGCTATATTAATTTGAAGAAAT 585

QY 711 GAAGAGTGAATTTTAAAGAGTCAGGAGATTTATCTCTTTTCCAAATACCAAAATGATGAGAA 770
DB 586 CAAGAGTGAATTTTAAAGAGCCAAAGAGATTTATCTCTTTTCCAAAGTACCAAAATGATGAGAA 645

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Rattus.

1 (bases 1 to 734)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

CONTACT: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Josef Lazar, Dr. Howard J. Jacob, Medical
College of Wisconsin

cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM15744 row: h column: 12

High quality sequence start: 18

High quality sequence stop: 735.

FEATURES

source

1. 734

Location/Qualifiers

/organism="Rattus norvegicus"

/mol_type="mRNA"

/db_xref="taxon:10116"

/clone="IMAGE:7444574"

/tissue_type="whole placenta, 2 pooled"

/lab_host="DH10B Tona"

/clone_lib="NIH MGC 270"

/note="Organ: placenta; vector: pExpress-1; Site: EcorV;
Site 2: NotI; Tissue was collected from two pooled
placentas from the 21st day of pregnancy. 1st strand cDNA
was primed with a Not I - oligo(dT) primer,
double-stranded cDNA was cloned into the Not I and EcorV
sites of pExpress-1. Library was size-selected for >1.25
kb fragments for an average insert size of 2.15 kb.
Library was normalized to Cot7. A non-normalized version
of this library is also available (NIH MGC 269). Library
was constructed by Open Biosystems (Huntsville, AL). Note:
this is a Mammalian Gene Collection library"

ORIGIN

Query Match 44.7%; Score 586.8; DB 7; Length 734;
Best Local Similarity 89.6%; Pred. No. 1.3e-148;
Matches 630; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
Qy 226 GCGGGGCTTCAGTGGCTTGGCTTGGCTGGGGGATGCGACCCGATGGTCCC 285
Db 32 GGGATGGCTTCAGTGGCTTGGCTTGGCTGGGGGATGCGACCTAGCGTGGCTC 91
Qy 286 CAGCGTCTCGGGGAGAACGACTGGCAGACGACGAAAGCCCTGAGCGCTACTTCGAGCT 345
Db 92 CACTTCTCTGCGGAGAACACTGGCAGACGAAAGAGCGTTGAGCGCTTCTTCGAGCA 151
Qy 346 GCCAGAGAACGACCAAGGGTGGCGCGCCGACGCTCCGACGTCCTTCAAGTCCGAGGCGCTA 405
Db 152 GCCAGAGAACGACCTAGCGCGCTCCACGACCTCCGACATCTCCCAAGTCCGAGGACTA 211
Qy 406 TGTGTGATCTACCAACGAGGATGAAATGATACACCAATTTTACAGCCAGTCCATCTGG 465
Db 212 TGTGTGATCTAACCAATGAGGATGAAATGATACCAATTTTACAGCCAGTCCATCTGG 271
Qy 466 AACTCCTCTAGAGATAGCAGCACTATTCTTTTCACTACCTGGAATATTGATGATTAGA 525
Db 272 AACTCCTCTAGAGATAGCAGCACTATTCTTTTCACTACCTGGAATATTGATGATTAGA 331
Qy 526 TGGATGCAATCTGCCCGAGAGGGCTCGAGGGGGTGTTCCTGCGCTAGCTTTGATATAGTCC 585
Db 332 TGGATGCAATCTGCCCGAGAGGGCTCGAGGGGGTGTTCCTGCGCTAGCTTTGATATAGTCC 391

Qy 586 AGATGTGGTATTCTACAGGAAGTATTATCCCCCATACTGCTACCTAAAGAGAGAGC 645
Db 392 GGCAGTGGTATTCTACAGGAAGTATTATCCCCCATACTGCTACCTAAAGAGAGAGC 451
Qy 646 AGCAGTTACACAAATTATTACAGGTAATGAAGAGGATATTTTACAGCTATATTTGAA 705
Db 452 AGCAGTTACACAAATTATTACAGGTAATGAAGAGGATATTTTACAGCTATATTTGAA 511
Qy 706 GAAAGGAAGTGAATAATTTTAAAGTTCAGGAGATTATTCCTTTTCCAAATACCAAAATGAT 765
Db 512 GAAAGGAAGTGAATAATTTTAAAGTTCAGGAGATTATTCCTTTTCCAAATACCAAAATGAT 571
Qy 766 GAGAAACCTGCTATGCTAAATGTGAGTTGGGTGGAATGAATTTTGCCTTATGACATC 825
Db 572 GAGAAACCTTCTGTGTAAATGTGAGTTGGGTGGAATGAATTTTGCCTTATGACATC 631
Qy 826 CATTTTGGAGAGCACCAGAGACATTTCTGGGAGCAATTAAGACCAATTAATAAATCTTCT 885
Db 632 CATTTTGGAGAGCACCAGAGACATTTCTGCTGAGCAATTAATAAATCAATTAATAAATCTGTTT 691
Qy 886 TGGAAATATGCAAGAGGCTCCAGATTCAACACCGTGTATATTT 928
Db 692 TCAAAATATGCAAGAGGCTACAGATTCAACTACTGTATATTT 734

RESULT 26

BMS03555

LOCUS

DEFINITION

BMS03555

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 580

/organism="Mus musculus"

/mol_type="mRNA"

/strain="ICR"

/db_xref="taxon:10090"

/clone="IMAGE:5679061"

/sex="Both"

/tissue_type="Total pancreas"

Qy 653 TACCAATATTACAGGTAAATGAAGAGGATATTTTACAGCTATACTATTGAAGAAGGA 712
Db 68 TACCAATATTATACAGGTAAATGAAGAGGATATTTTACAGCTATACTATTGAAGAAGGA 127
Qy 713 AGAGTGAATTTAAAGTCAGAGATATTCCTTTTCCAAATACCAAAATGATGAGAAAC 772
Db 128 AGAGTGAATTTAAAGTCAGAGATATTCCTTTTCCAAATACCAAAATGATGAGAAAC 187
Qy 773 CTGCTATGCGTAAATGTGAGTTGGTGGAAATGAATTTTCCCTTATGACATCCATTG 832
Db 188 CTGCTATGCGTAAATGTGAGTTGGTGGAAATGAATTTTCCCTTATGACATCCATTG 247
Qy 833 GAGAGCACCAGAACATCTCGCGAAGCAATAGACAAATTAATAAATCTGTTCTGGAAA 892
Db 248 GAGAGCACCAGAACATCTCGCGAAGCAATAGACAAATTAATAAATCTGTTCTGGAAA 307
Qy 893 ATGCAAGAGGCTCCAGATTTCAACACGGTTATATTTGAGGAGATACAAAATTTAAGAGAT 952
Db 308 ATGCAAGAGGCTCCAGATTTCAACACGGTTATATTTGAGGAGATACAAAATTTAAGAGAT 367
Qy 953 CAAGAAGTTATCAATGTGGTGTACCTGACAACTGTTTGTGCTGGAAATTTTGA 1012
Db 368 CAAGAAGTTATCAATGTGGTGTACCTGACAACTGTTTGTGCTGGAAATTTTGA 427
Qy 1013 GGCAAACCTAACATGTCAGTATACATGGGATAGCAAGCAATTAACAACTCAGATC 1072
Db 428 GGCAAACCTAACATGTCAGTATACATGGGATAGCAAGCAATTAACAACTCAGATC 487
Qy 1073 CCGTCTGCTTATAAGCATCTGTTTGCATCGAATATTTTTCAGAGCAGAGAGGGGACCTT 1132
Db 488 CCGTCTGCTTATAAGCATCTGTTTGCATCGAATATTTTTCAGAGCAGAGAGGGGACCTT 547
Qy 1133 ATTCTCTAAAGTTTAGACCTTGTGGGTTGGAAAACTGGAGTGTGGTAGATTTCCGAGT 1192
Db 548 ATTCTCTAAAGTTTAGACCTTGTGGGTTGGAAAACTGGAGTGTGGTAGATTTCCGAGT 607
Qy 1193 GATCACT 1199
Db 608 GATCACT 614

RESULT 24
BF182465
LOCUS 601804232F1 NCI_CGAP_Mam5 621 bp mRNA linear EST 31-OCT-2000
DEFINITION 601804232F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4035319 5',
mRNA sequence.
ACCESSION BF182465
VERSION BF182465.1 GI:11060608
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 621)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM9308 row: p column: 08
High quality sequence stop: 615.
Location/Qualifiers
1..621
/organism="Mus musculus"
/mol_type="mRNA"

/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clones="IMAGE:4035319"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

ORIGIN

Query Match	44.8%	Score 587.4	DB 2	Length 621
Best Local Similarity	99.5%	Pred. No. 8.8e-149		
Matches 610	Conservative 0	Mismatches 1	Indels 2	Gaps 2
Qy 97	GGTGTGTTTGGGGGACCTCGCGGATGCGGCTCTGGCAGCAGATTCCGATGCGGGAGCC	156		
Db 9	GGGGTTTGGGGGACCTCGCGGATGCGGCTCTGGCAGCAGATTCCGATGCGGGAGCC	68		
Qy 157	CGCAGGGCCGCGAGGGCGGGCGGCTCGCGGCCCGAAGCAGCAGCAGCGAGGAGCCG	216		
Db 69	CGCAGGGCCGCGAGGGCGGGCGGCTCGCGGCCCGAAGCAGCAGCAGCGAGGAGCCG	128		
Qy 217	GGTGAAGAGGGCGGGCTTCAGTGCCTGGCTTTGCGTTGGTGGGGGATCGACCCAC	276		
Db 129	GGTGAAGAGGGCGGGCTTCAGTGCCTGGCTTTGCGTTGGTGGGGGATCGACCCAC	188		
Qy 277	GATGCTCCCGAGCTCTCGGGAGAGCAGCTGCGCAGACGAGAAAGCCCTGAGGCGCTA	336		
Db 189	GATGCTCCCGAGCTCTCGGGAGAGCAGCTGCGCAGACGAGAAAGCCCTGAGGCGCTA	248		
Qy 337	CTTCAGAGCTGCCAGAAACGACCAAGGGTGGCGCGCAGCCTCCACGTCCTTCAAGTC	396		
Db 249	CTTCAGAGCTGCCAGAAAGCAAGGGTGGCGCGCAGCCTCCACGTCCTTCAAGTC	307		
Qy 397	CGAGGCTATGTTGATCTAACCAACGAGGATGCAAAATGATACCAACATTTAGAACCCAG	456		
Db 308	CGAGGCTATGTTGATCTAACCAACGAGGATGCAAAATGATACCAACATTTAGAACCCAG	367		
Qy 457	TCCATCTGGAACCTCTTAGAGATAGCAGCAGCTATTTCTTTTCTACCTGGAATATGA	516		
Db 368	TCCATCTGGAACCTCTTAGAGATAGCAGCAGCTATTTCTTTTCTACCTGGAATATGA	427		
Qy 517	TGGATTAGATGATGCAATCTGCCCGAGAGGGCTCGAGGGGTGTGTTCTCGCTAGCTTT	576		
Db 428	TGGATTAGATGATGCAATCTGCCCGAGAGGGCTCGAGGGGTGTGTTCTCGCTAGCTTT	487		
Qy 577	GTATAGTCCAGATGTTGTTTCTACAGGAAGTTATCCCCCCTACTGTGCTACCTAAA	636		
Db 488	GTATAGTCCAGATGTTGTTTCTACAGGAAGTTATCCCCCCTACTGTGCTACCTAAA	547		
Qy 637	GAAGAGAGCCAGCTTACACAATTTTACAGGTAATGAAG-AAGGATATTTTACAGCTA	695		
Db 548	GAAGAGAGCCAGCTTACACAATTTTACAGGTAATGAAGCAAGGATATTTTACAGCTA	607		
Qy 696	TACTATTGAAGAA 708			
Db 608	TACTATTGAAGAA 620			

RESULT 25

CV119018
LOCUS 734 bp mRNA linear EST 30-AUG-2004
DEFINITION AGENCOURT_31557860 NIH_MGC_270 Rattus norvegicus cDNA clone
IMAGE:7444574 5', mRNA sequence.
ACCESSION CV119018
VERSION CV119018.1 GI:51640419
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers

1..703

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="7420437P03"

/sex="female"

/tissue type="in vitro fertilized eggs"

/dev stage="egg"

/lab_host="DH10B"

/clone_lib="RIKEN full-length enriched, in vitro fertilized eggs"

/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTWN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATCTCGAGTTAATTAATTCCTCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

ORIGIN

Query Match 46.6%; Score 612; DB 5; Length 703;
 Beat Local Similarity 97.5%; Pred. No. 1.7e-155;
 Matches 629; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

QY 68 CACGAGGCGGGAACAGCGGTGAAGCGGGTGTGTTTGAAGGGACCCCTGCGCGATGGCG 127
 DB 21 CAGTCGCGCGGAAGCAGCGTGAAGAGCGGGTGTGTTTGAAGGGACCCCTGCGCGATGGCG 80

QY 128 TCTGGCAGCATGTTCCGATCGCGGAGCCCGCAGGCGCGCAGGCGCGCGCGTGGCG 187
 DB 81 TCTGGCAGCATGTTCCGATCGCGGAGCCCGCAGGCGCGCAGGCGCGCGCGTGGCG 139

QY 188 CCGGAGCAGCAGCGGAGGAGGACCGGGTGAAGAGCGCGCGCTTCAGTCCCTGGGC 247
 DB 140 CCGGAGCAGCAGCGGAGGAGGACCGGGTGAAGAGCGCGCGCTTCAGTCCCTGGGC 199

QY 248 TTTGCGTTGGTGGGGATGCGACCCACGATGGTCCCGAGCGTCTTCGCGGAGAACGAC 307
 DB 200 TTTGCGTTGGTGGGGATGCGACCCACGATGGTCCCGAGCGTCTTCGCGGAGAACGAC 259

QY 308 TGGCAGCGCAGAAAGCCCTGAGCGCTTCTCGAGCTGCCAGAGACGACCAAGGGTGG 367
 DB 260 TGGCAGCGCAGAAAGCCCTGAGCGCTTCTCGAGCTGCCAGAGACGACCAAGGGTGG 319

QY 368 CCGCGCCAGCCTCCACGCTCTTCAAGTCCGAGGCGCTATGTTGATCTTAACCAACGAGGAT 427
 DB 320 CCGCGCCAGCCTCCACGCTCTTCAAGTCCGAGGCGCTATGTTGATCTTAACCAACGAGGAT 379

QY 428 GCAATGATACACCAATTTTAGAGCCAGCTCCATCTGGAACTCTCTCTTAGAAGATAGCAGC 487

Db 380 GCAATGATACACCAATTTTAGAGCCAGCTCCATCTGGAACTCTCTTAGAAGATAGCAGC 439
 QY 488 ACTATTTCTTTTCATTACTCTGGAATATTGATGGATTAGATGATGCAATCTGCCGAGAGG 547
 Db 440 ACTATTTCTTTTCATTACTCTGGAATATTGATGGATTAGATGATGCAATCTGCCGAGAGG 499
 QY 548 GCTCAGGGGTGTTCTCTGCTAGCTTTGTATAGTCCAGATGTTGTTATTTCTACAGAA 607
 Db 500 GCTCAGGGGTGTTCTCTGCTAGCTTTGTATAGTCCAGATGTTGTTATTTCTACAGAA 559
 QY 608 GTTATCCCCCATCTGTGCTTACTTAAGAGAGAGCAGCAGTTACACAAATTATTACA 667
 Db 560 NGTATCCCCCATCTGTGCTTACTTAAGAGAGAGCAGCAGTTACACANTATTATACA 619
 QY 668 GGTATGAAGAAGGATATTTTCACAGCTATATCTATTGAAGAAAGGA 712
 Db 620 GGGTATGAAGAAGGATATTTTCACAGCTATATCTATTGAAGAAAGGA 664

RESULT 19

BB609556

LOCUS

DEFINITION

BB609556 RIKEN full-length enriched, 18 days embryo Mus musculus

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 712)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,

Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,

Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,

Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,

Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,

Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

Unpublished (2001)

Contact: Yoshihide Hayashizaki

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The Institute of Physical and Chemical Research (RIKEN)

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Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B.,

Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,

Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.

and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,

Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,

Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and

Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

FEATURES		division of Invitrogen.		Location/Qualifiers	
source		1..1743		/organism="Homo sapiens"	
				/mol_type="mRNA"	
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ORIGIN		Query Match		47.0%; Score 616.6; DB 4; Length 1743;	
		Best Local Similarity		79.7%; Pred. No. 1.3e-156;	
		Matches 756; Conservative 0; Mismatches 184; Indels 9; Gaps 2;			
Qy	317	CAGAAAGCCCTGAGCGCTACTTCGAGCTGCAGACGACCAAGGGTGC	CGCCGCGCAG	376	
Db	32	CAGAGGGCTCTGAATCTCTACTTCGAGCTCCGGTGGAGGAGCGCTT	GGAAACGCCGA	91	
Qy	377	CTCTCCACGCTCTTCAAGTCGAGCGCTATGTTGATCTTAACCAACG	AGGATGCAAAATGAT	436	
Db	92	CTGGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATG	AAGAACCACTGAT	151	
Qy	437	ACAAACCAATTTAGAGCCAGCTCTCTGGA---ACTCCTCTAGAA	GATAGCAGCACTATT	493	
Db	152	TCCACCACTTCTAAATCAGCCCATCTGAAGATACTCAGCAAGAA	ATGGCAGCATGTC	211	
Qy	494	TCCTTCAATCTCGAATATTGATGGATTAGATGGATGCTGCCG	GAGAGGGCTCGA	553	
Db	212	TCCTCTAATCTCGAATATTGATGGATTAGATCTAAACAATCTG	CAGAGAGGGCTCGA	271	
Qy	554	GGGGTGTCTCTGCTAGCTTCTATAGTCCAGATGTGTTATTTCT	PACAGGAAGTTATC	613	
Db	272	GGGGTGTCTCTGCTAGCTTCTATAGTCCAGATGTGTTATTTCT	PACAGGAAGTTATT	331	
Qy	614	CCCCCATCTGTGCTCTACCTAAAGAAGAGCAGCCAGTGTACACA	ATTTATTACAGGTAAT	673	
Db	332	CCCCCATATTATAGTCTACCTAAAGAAGAGATCAAGTAATTAT	GATGATTTATTACAGGTCAT	391	
Qy	674	GAAGAAGATATTTACAGCTATACTATTGAAGAAAGAGAGTGAA	ATTTAAAGTCAG	733	
Db	392	GAAGAAGATATTTACAGCTATATGTTGAAGAAATCAAGAGTGA	ATTTAAAGGCCAA	451	
Qy	734	GAGATTATTCCTTTTCCAAATACCAAAATGATGAGAACCTGCT	ATGCGTAAATGTGAGT	793	
Db	452	GAGATTATTCCTTTTCCAAATGATGAGAACCTTTATGTCATGT	GAAC	511	
Qy	794	TTGGGTGGAATGAATTTTGCTTTATGACATCCCATTTGGAGAG	CACCCAGAGAACATTC	853	
Db	512	GTGTCAGGAATGAGCTTTGCTTTATGACATCCCATTTGGAG	AGCACCAGAGGGCATGCT	571	
Qy	854	CGGAAAGAAATGAAGCAATTAATACTGTTCTTGGAAAAATG	GAAGAGGCTCCAGATCA	913	
Db	572	CGGAAAGCAATGAATGAGTTAAATGTTTAAAGAAAAATGCA	AGAGGCTCCAGAGTCA	631	
Qy	914	ACCAAGTTATTTGAGGAGATACAAATTTAAGAGATCAAGAG	TTATCAATGTGTT	973	
Db	632	GCTACAGTTATTTGAGGAGATACAAATCTAAGGGATCGAG	GGTTACCAAGATGGT	691	
Qy	974	GTTTACCTGACAAAGTTTGTGCTCTGGGAAATTTTGGCAAA	ACCTTAAACATTTGCCAG	1033	
Db	692	GTTTACCAACAATGTTGATGTTCTGGGAGTTTGGGCAAC	CTTAAACATTTGCCAG	751	
Qy	1034	TATCATGGGATACGAAGCAAAATAACCTCAGGATCCCTGCTG	CTTTAATGATCATCGT	1093	
Db	752	TATCATGGGATACGAATGAATCTAATCTTGGAAATAACTG	CTGCTTGTGTAACCTTCGT	811	
Qy	1094	TTTCATCCAATATTTTCAG-----AGCAAGAGGGGCACT	TATTCCTCAAGTTTA	1147	
Db	812	TTTCATCCAATATTTTCAGAGCAGCAGCAAGAGGGACACAT	TATTCCTCCGAGTTTG	871	
Qy	1148	GACCTTGTGGTGTGGAAAAACTGGACTGTGGTATTTCCGAG	TGATCACTGGGGGCTC	1207	

872

GACCTTCTTTGGATTAGAAAAAATGGAAGCTGTGGTAGATTTCTCTAGTCATCACTGGGGTCTT

931

1208

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1256

932

CTGTGCAACTTAGATATAATATTGTAATAATGCTTTTCAAGTGTGGGTTT

980

BY1719852

703 bp

mrna

linear

EST 17-DEC-2002

BY1719852

RIKEN full-length enriched, in vitro fertilized eggs

Mus

BY1719852

musculus cDNA clone 7420437P03 5', mRNA sequence.

BY1719852.1

GI:27132969

EST.

Mus musculus

(house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 703)

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaoka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalia,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grilmond,S., Gustavich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierzki,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Inotani,K., Ishii,Y., Itoh,M., Kigawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shingawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

Analysis of the mouse transcriptome based on functional annotation of 60,720 full-length cDNAs

Nature 420, 563-573 (2002)

1246851

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Fax: 81-45-503-9216

Email: genome-resesc.riken.jp, URL: http://genome.gsc.riken.jp/

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Inotani,K., Ishii,Y., Itoh,M., Kigawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.

Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

QY 493 TTCTTTCACTACCTGGAATATTGATGGATTAGATTGCCGAGAGGGCTCG 552

Db 241 TTTCTCAGGAGTTATCCCCCATATCTGTCCTACCTAAAGAGAGAGCAGCGTTAC 300
Qy 656 ACAATTATTACAGTAATGAAGAGATATTTTACAGCTATATCTATTGAAGAAAGGAGA 715
Db 301 ACAATTATTACAGTAATGAAGAGATATTTTACAGCTATATCTATTGAAGAAAGGAGA 360
Qy 716 GTGAAATTTAAAGCTCAGGAGATTTTCTTTTCCAAATACCAAAATGATGAGAAACCTG 775
Db 361 GTGAAATTTAAAGCTCAGGAGATTTTCTTTTCCAAATACCAAAATGATGAGAGCTG 420
Qy 776 CTATGCGTAATGTAGTTGGGTGGAAATGAATTTTGGCTTATGACATCCATTTGGAG 835
Db 421 CTATGCGTAATGTAGTTGGGTGGAAATGAATTTTGGCTTATGACATCCATTTGGAG 480
Qy 836 AGCACACAGAGACATTTCTGGGACGATAGACAAATTAAGAACTGTTCTTGGAAATG 895
Db 481 AGCACACAGAGACATTTCTGGGACGATAGACAAATTAAGAACTGTTCTTGGAAATG 540
Qy 896 CAAGAGGCTCAGATTTCAACACCGTTTATTTTGCAGGAGATACAAATTTAAGAGATCAA 955
Db 541 CAAGAGGCTCAGATTTCAACACCGTTTATTTTGCAGGAGATACAAATTTAAGAGATCAA 600
Qy 956 GAAGTTATCAATGTGGTGGTTACCTGACAACTTTTGTATGC 999
Db 601 GAAGTTATCAATGTGGTGGTTACCTGACAACTTTTGTATGC 644

RESULT 15
CR592636 1620 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DM007YE11 of Fetal liver of Homo sapiens
DEFINITION (human).
ACCESSION CR592636
VERSION CR592636.1 GI:50473443
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1620)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1620)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail: seque@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. 1620
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM007YE11"
/tissue type="Fetal liver"
/plasmid="pCMVSPORT_6"

FEATURES
source
1. 1620
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM007YE11"
/tissue type="Fetal liver"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 47.6%; Score 625; DB 4; Length 1620;
Best Local Similarity 78.7%; Pred. No. 6.3e-159;
Matches 774; Conservative 0; Mismatches 200; Indels 9; Gaps 2;
Qy 217 GGTGAAGAGCGCGGCTTCAGTCCCTGGGCTTTGGGTTGGTGGGGATCGGACCCAC 276

RESULT 16
CN694288 617 bp mRNA linear EST 18-MAY-2004
LOCUS E0348E09-5 NIA Mouse B10.5 whole embryo cDNA library (Long) Mus
DEFINITION musculus cDNA clone NIA:E0348E09 IMAGE:30863576 5', mRNA sequence.

Db 6 GGTGAAGAGCGCGGCTTCAGTCCCTGGTGGAGTTTGGCTCGGTCGCAAGCTGCGATCGCG 65
Qy 277 GATGGTCCCGAGCGTCTCTGGGAGAACGACTGGCAGACGCGAGAAAGCCCTGAGCGCTA 336
Db 66 AGTGGCTCAGTGTCTCTGGCCGAGAACGACTGGGAGATGGAAAGGGCTCTGAACCTCTA 125
Qy 337 CTTTCGAGCTGCCAGAGAAACGACCAAGGGTGGCCGCGCCAGCCTCCCAACGTCCTTCAAGTC 396
Db 126 CTTTCGAGCTCCCGTGGAGAGAGCGCTTGGAAACGCGCCAGCTTGAACCATCTCTGAGCC 185
Qy 397 CGAGGCTTATGTTGATCTAAACCAACGAGGATGCAATGATACAAACATTTTGAAGCCAG 456
Db 186 CAAGACCTATGTTGACTTAACCAATGAAGAAACAACTGATTCACCACTTCTTAAATCAG 245
Qy 457 TCCATCTGGA--ACTCCTCTAGAGATAGCAGCAGCTATTTCTTCTTATACCTGGATAT 513
Db 246 CCAATCTGAAGATPACTCAGCAAGAAATGGCAGCATGTTCTCTCTCATTTACCTGGAAAT 305
Qy 514 TGATGATTAGATGGATGCAATCTGCCCGAGAGGGCTCGAGGGGTGTGTTCTCTGCTTAGC 573
Db 306 TGATGATTAGATCTAAACAACTCTGTCAGAGGGGCTCGAGGGGTGTGTTCTTACTTAGC 365
Qy 574 TTTGTATAGTCCAGATGTGTATTTCTACAGGAAGTATCCCCCACTACTGTGCTTACCT 633
Db 366 TTTGTACAGCCAGATGTGTATTTCTACAGGAAGTATTTCCCCCACTATTTATAGTACCT 425
Qy 634 AAAGAAGAGAGCAGCCAGTTTACACAATTTATACAGTAAATGAAGAGGATATTTTCACAGC 693
Db 426 AAAGAAGAGATCAAGTAATTTATGAGATTTATACAGTCAATGAAGAGGATATTTTCACAGC 485
Qy 694 TATACTATTGAAGAAAGAGAGTGAATTTAAAGTCAGAGAGATTTTCTCTTTCACAA 753
Db 486 TATATGTTGAAGAAATCAAGAGTGAATTTAAAGCCAGAGATTTTCTTCTTTCACAG 545
Qy 754 TACCAAAATGATCAGAAACCTGCTATGCGTAAATGTGAGTTTGGTGGAAATGAATTTTG 813
Db 546 TACCAAAATGATCAGAAACCTTTTATGTGTGATGTGAACGTGTGAGAAATGAGCTTTG 605
Qy 814 CTTTATGACATCCATTTGGAGAGCAGAGAACATTTCTGCGGAACGATAGACAATT 873
Db 606 CTTTATGACATCCATTTGGAGAGCAGAGAGGGCATGCTGCGGAACGATAGACAATT 665
Qy 874 AAAAAGCTTTTGGAAATCAAGAGGCTCCAGATTTCAACACGCTTATATTTGAGG 933
Db 666 AAAAATGTTTAAAGAAATGCAAGGCTCCAGAGTCCAGTACAGTTATATTTGAGG 725
Qy 934 AGATACAAATTTAAGAGATCAAGAAGTTATCAAAATGTGGTGGTTTACCTCAACAGCTTT 993
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Qy 994 TGATGCTGGAAATTTTAGGCAACCTTAACATTTCCAGTATACATGGGATACGAAGC 1053
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Qy 1054 AAATAACAACCTCAGGATCCCTGCTGTATAAGCATCGTTTGTATGATGCAATATTTTTCAG 1113
Db 846 GAACTCTAATCTTGGATTAATCTGCTGTGTAACCTCGTTTGTATGATGCAATATTTTTCAG 905
Qy 1114 -----AGCAGAAGAGGGGACCTTATTTCTCAAGTTTATAGACTTGTGGTTGGAAAA 1167
Db 906 AGCAGCAGCAGAGAGAGGACACATTTTCCCGAAGTTTGGACCTTCTTGGATTAGAAAA 965
Qy 1168 ACTGGACTGTGGTAGATTTCCGA 1190
Db 966 ACTGGACTGTGGTAGATTTTCCCTA 988

RESULT 16
CN694288 617 bp mRNA linear EST 18-MAY-2004
LOCUS E0348E09-5 NIA Mouse B10.5 whole embryo cDNA library (Long) Mus
DEFINITION musculus cDNA clone NIA:E0348E09 IMAGE:30863576 5', mRNA sequence.

mRNA prepared from 13,500 2-cell stage embryos. Primer: Sali (d1): 5'-CGTGCACCGTCGACCGTCTTTTCTTTT-3'... cDNAs were cloned into the MluI/Sali sites of a modified pBluescribe vector using commercial linkers (NEB). Average insert size: 1.2 kb."

ORIGIN

Query Match 49.3%; Score 647; DB 1; Length 647;
Best Local Similarity 100.0%; Pred. No. 4.7e-165;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 666 CAGGTAAATGAGAGGATATTTCCAGCTACTATTGAAGAAGAGAGTGAAATTTA 725
Db 1 CAGGTAATGAAGAGGATATTTCCAGCTACTATTGAAGAAGAGAGTGAAATTTA 60

QY 756 AAAGTCAGAGATATTTCTTTCCAAATACCAAAATGATGAGAAACCTGCTATGCGTAA 785
Db 61 AAAGTCAGAGATATTTCTTTCCAAATACCAAAATGATGAGAAACCTGCTATGCGTAA 120

QY 786 ATGTGAGTTTGGTGGAAATGAATTTTCCCTTATGACATCCCATTTGGAGAGCACCAGAG 845
Db 121 ATGTGAGTTTGGTGGAAATGAATTTTCCCTTATGACATCCCATTTGGAGAGCACCAGAG 180

QY 846 AACATTCGCGGAACGAATGAGCAATTAATAAATCTGTTCTGGAAAAATGCAAGAGGCTC 905
Db 181 AACATTCGCGGAACGAATGAGCAATTAATAAATCTGTTCTGGAAAAATGCAAGAGGCTC 240

QY 906 CAGATTCAACACCGGTATATTTGAGGAGATACAAATTTAAGAGATCAAGAAGTTATCA 965
Db 241 CAGATTCAACACCGGTATATTTGAGGAGATACAAATTTAAGAGATCAAGAAGTTATCA 300

QY 966 AATGTGGTGGTTTACCTGACAACTGTTTGTATGCTGGGAATTTTGGGCAAACTTAAC 1025
Db 301 AATGTGGTGGTTTACCTGACAACTGTTTGTATGCTGGGAATTTTGGGCAAACTTAAC 360

QY 1026 ATTGCAGTATACATGGGATGAGCAATTAATAAATCTGAGTCCCTGCTGCTTATA 1085
Db 361 ATTGCAGTATACATGGGATGAGCAATTAATAAATCTGAGTCCCTGCTGCTTATA 420

QY 1086 AGCATCGTTTTCATCGAATATTTTTCAGAGAGAGAGGGGACCTTATCTCTCAAGTT 1145
Db 421 AGCATCGTTTTCATCGAATATTTTTCAGAGAGAGAGGGGACCTTATCTCTCAAGTT 480

QY 1146 TAGACCTTTTGGTGGAAAACTGGACTGTGTGATATTTCCGAGTGAATCACTGGGGC 1205
Db 481 TAGACCTTTTGGTGGAAAACTGGACTGTGTGATATTTCCGAGTGAATCACTGGGGC 540

QY 1206 TCTTGTGCACCTTGAATGTAGTATTTGTGAAGAGCTTCCCACTTGACGCTTTACAGTTTG 1265
Db 541 TCTTGTGCACCTTGAATGTAGTATTTGTGAAGAGCTTCCCACTTGACGCTTTACAGTTTG 600

QY 1266 TTAGCACTAGTCTGAATTTGTAGTCTCAACCTTTTCAGGACATC 1312
Db 601 TTAGCACTAGTCTGAATTTGTAGTCTCAACCTTTTCAGGACATC 647

RESULT 14

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BG083167 644 bp mRNA linear EST 18-DEC-2003
H3085C02-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3085C02 5', mRNA sequence.
BG083167
BG083167.2 GI:40069892
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 644)
Tanaka, T.S.; Jaradat, S.A.; Lim, M.K.; Kargul, G.J.; Wang, X.,
Grahovac, M.J.; Pantano, S.; Sano, Y.; Piao, Y.; Nagaraja, R.; Doi, H.,
Wood, W.H. III, Becker, K.G. and Ko, M.S.H.

TITLE

JOURNAL

PUBMED

COMMENT

Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
10922068
On Jan 26, 2001 this sequence version replaced gi:12565735.
Other ESTs: H3085C02-3
Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgaun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit <http://lgaun.grc.nia.nih.gov/cDNA/15k.html> for details.
Plate: H3085 row: C column: 02
Seq primer: -21M13 Reverse
High quality sequence stop: 644
POLYA=No.

FEATURES

source

Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="niaEST:H3085C02-5"
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/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA libraries"
/lab_host="DH10B"
/clone_lib="NIA Mouse 15K cDNA Clone Set"
/note="Vector: pSPORT1; Site 1: Sali; Site 2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

ORIGIN

Query Match 49.0%; Score 642.4; DB 2; Length 644;
Best Local Similarity 99.8%; Pred. No. 8.5e-164;
Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 356 GACCAAGGTTGGCCGCGCCAGCTCTCCACGTCCTTCAAGTCGCGAGCCCTATGTTGATCTA 415
Db 1 GACCAAGGTTGGCCGCGCCAGCTCTCCACGTCCTTCAAGTCGCGAGCCCTATGTTGATCTA 60

QY 416 ACCAAGGAGGATGCAAAATGATACACCACTTTTAGAAGCCAGTCCATCTGGAACCTCTCTA 475
Db 61 ACCAAGGAGGATGCAAAATGATACACCACTTTTAGAAGCCAGTCCATCTGGAACCTCTCTA 120

QY 476 GAAGATAGCAGCAGTATTTCTTTTCATACCTGGAATATTTAGATGATGATGATGATGAT 535
Db 121 GAAGATAGCAGCAGTATTTCTTTTCATACCTGGAATATTTAGATGATGATGATGATGAT 180

QY 536 CTGCCCCGAGAGGCTCGAGGGGTGTTCCTCCCTAGCTTTGTATAGTCCAGATGTGGTA 595
Db 181 CTGCCCCGAGAGGCTCGAGGGGTGTTCCTCCCTAGCTTTGTATAGTCCAGATGTGGTA 240

QY 596 TTTCTACAGGAAGTTATCCCCCATCTGTGCTACCTACCTAAAGAGAGCAGCCAGTTAC 655


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Db 161 TCCTGGCGGAACGACTGGAGATGGAAGGGCTCTGAACTCTACTTTCAGGCTCGG 220
Qy 351 AGAAGCAGCAAGGGTGGCGGCCAGCTCCACGTCCTTCAAGTCCGAGGCCCTATGTTG 410
Db 221 TGGAGGAGAGCGCCTTGGAAACGCGGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTG 280
Qy 411 ATCTAAACCAACGAGATGCAATGATACCAACCATTTTGAAGCCAGTCATCTCGA ---A 467
Db 281 ACCTAACCAATGAAGAAACAACTGATTCACCACTCTTAAATCAGGCCCATCTGAAGATA 340
Qy 468 CTCCTCTAGAGATAGCAGCACTATTTCTTTCATTACCTCGAATATTTGATGATTTAGATG 527
Db 341 CTCAGCAAGAAATGGCGACATGTTCTCTCTCATTTACCTGGAATATTGATGATTTAGATC 400
Qy 528 GATGCAATCTGCCCGAGAGGGCTCGAGGGGTGTGTTCTCTGCTAGCTTTGTTATAGTCCAG 587
Db 401 TAAACAATCTGTACAGAGAGGGCTCGAGGGGTGTGTTCTTACTTGTAGCTTTGTACAGCCAG 460
Qy 588 ATGTGGTATTTCTACAGGAAGTTATCTCCCCCATACTGTGCGCTACCTAAAGAGAGAGCAG 647
Db 461 ATGTGATATTTCTACAGGAAGTTATCTCCCCCATATTTATAGCTACCTAAAGAGAGATCAA 520
Qy 648 CCAGTTACACAAATTTACAGGTAATGAAGAGGATTTTCCAGCTATATCTATTGAGA 707
Db 521 GTAATTATGAGATTATTCAGGTCTATGAAGAGGATATTTCCAGCTATATATGTTGAAGA 580
Qy 708 AAGGAAGAGTGAATTTAAAGTCCAGGAGATTTATCTCTTTCCAAATACCAAAATGATGA 767
Db 581 AATCAAGAGTGAATTTAAAGCCAGAGATTTATCTCTTTTCCAGTACCAAAATGATGA 640
Qy 768 GAAACCTCTATGCTTAATGTAGTTGGTGGGAAATGAATTTTGCCTTATGACATCCC 827
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Qy 828 ATTTGGAGACACAGAGAACATTTCTGGGACGATGAAGCAATTAAGCAATTAAGCAATTTCTG 887
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Qy 888 GAAAAATGCAGAGGCTCCAGATTCAGACGCTTATATTTGCAGGAGATACAAATTTAA 947
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Qy 1008 TTTTAGGCACAACTTAACATTCGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1067
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Qy 1182 GATTTCCGAGTATCACTGGGGGCTTGTGACCTTGAATGATGATGATGATGATGATGATGATGATGAT 1241
Db 1061 GATTTCCCTAGTATCACTGGGGTCTTGTGCAACTTATGATATATATTTGTAATAATGCTT 1120
Qy 1242 CCACCTTGCAGCTTT 1256
Db 1121 TTCAAGTGTGGGTTT 1135
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RESULT 9
BG070243/c
LOCUS
DEFINITION H3085C02-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
714 bp mRNA linear EST 18-DEC-2003
BG070243
H3085C02-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3085C02 3', mRNA sequence.
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BG070243
BG070243.2 GI:40069891
EST.

Mus musculus (house mouse)

REFERENCE

AUTHORS

Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

TITLE

1 (bases 1 to 714)
Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X.,
Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H.,
Wood,W.H. III, Becker,K.G. and Ko,M.S.H.
Genome-wide expression profiling of mid-gestation placenta and
embryo using a 15,000 mouse developmental cDNA microarray

JOURNAL

PUBMED

COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
10922068

On Jan 26, 2001 this sequence version replaced gi:12552812.

Other ESTs: H3085C02-5

Contact: George J. Kargul

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@lgsun.grc.nia.nih.gov

This clone set has been freely distributed to the community. Please
visit <http://lgsun.grc.nia.nih.gov/cDNA/15k.html> for details.

Plate: H3085 row: C column: 02

Seq primer: -21M13 Forward

High quality sequence stop: 714

POLYA=Yes.

Location/Qualifiers

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1. 714
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/mol_type="mRNA"
/strain="C57BL/6J"
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/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
libraries"
/lab_host="DH10B"
/clone_lib="NIA Mouse 15K cDNA Clone Set"
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
clone is among a rearranged set of 15,247 clones from 11
embryo cDNA libraries (including preimplantation stage
embryos from unfertilized egg to blastocyst, embryonic
part of E7.5 embryos, extraembryonic part of E7.5
embryos, and E12.5 female mesonephros/gonad) and one
newborn ovary cDNA library. Average insert size 1.5 kb.
All source libraries are cloned unidirectionally with
Oligo(dT)-Not primers. References include: (1)
Genome-wide expression profiling of mid-gestation
placenta and embryo using a 15,000 mouse developmental
cDNA microarray, 2000, Proc. Natl. Acad. Sci. U.S.A., 97:
9127-9132; (2) Large-scale cDNA analysis reveals phased
gene expression patterns during preimplantation mouse
development, 2000, Development, 127: 1737-1749; (3)
Genome-wide mapping of unselected transcripts from
extraembryonic tissue of 7.5-day mouse embryos reveals
enrichment in the t-complex and under-representation on
the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

ORIGIN

Query Match 50.2%; Score 658.4; DB 2; Length 714;
Best Local Similarity 99.8%; Pred. No. 3.7e-168;
Matches 659; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 653 TACCAATTTACAGGTAATGAAGGATATTTTCAGAGCTATCTATTGAAGAAGGA 712
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Db 711 TACCAATTTATACAGGTAATGAAGGATATTTTCAGAGCTATCTATTGAAGAAGGA 652
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Qy 713 AGAGTGAATTTAAAGTCAGGAGATTTTCCTTTTCCAAATPACCAAAATGATGAAAC 772
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VERSION CR601303.1 GI:50492110
KEYWORDS HTC; CNSLUT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1168)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
REFERENCE 2 (bases 1 to 1168)
AUTHORS Direct Submission
TITLE Genoscope.
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODN005YN02"
/tissue="Adult brain"
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ORIGIN
Query Match 50.8%; Score 666.6; DB 4; Length 1168;
Best Local Similarity 76.9%; Pred. No. 2.5e-170;
Matches 842; Conservative 0; Mismatches 244; Indels 9; Gaps 2;
QY 171 GCGCGCGCGCTCGCGCGCGAAGCAGCAGCAGCGAGGAGGACCGGGTGAAGAGCGCGC 230
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QY 231 GCGTTCACTGCTGCGCTTTCGTTGGTGGGGGATGCGACCCACGATGTCGCCAGC 290
Db 102 GACTTCTGTGTGGAGTTTGCCTCGTTCGCAAGCTGCGATCGCGCAGTGGCTCAGTCT 161
QY 291 TCCTCGGGAGNACACACTGGCAGACGCGAAGCCCTGAGCGCTTCTCGAGCTGCCAG 350
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QY 411 ATCTAACCAACGAGGATCAATGATGATCAACCATTTTAGAAGCCAGTCCATCTGA-- 467
Db 282 ACCTAACCAATGAAGAAACACTGATTCCACCACCTCTTAAATCAGCCCTCTGAAGATA 341
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QY 528 GATGCAATCTGCCGAGAGGGCTCGAGGGGTGTGTTCTCTGCTAGCTTTGTATAGTCAG 587
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QY 588 ATGTGGTATTTCTACAGGAAGTTATCCGCCCATCTGTGCTTACTTAAAGAGAGAGCAG 647
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Db 1122 TTCAAGTGTGGGTTT 1136
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LOCUS full-length cDNA clone CSODK007YK05 of HeLa cells Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR597293
VERSION CR597293.1 GI:50478100
KEYWORDS HTC; CNSLUT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1894)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
REFERENCE 2 (bases 1 to 1894)
AUTHORS Direct Submission
TITLE Genoscope.
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
```


Tissue Procurement: Dr. Jonathan Kuo, NIMH
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LCM2999 row: e column: 24
High quality sequence stop: 600.

FEATURES

1. 815
Location/Qualifiers
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/db_xref="taxon:10090"
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/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH MGC 169"
/note="Organ: Testicles; Vector: pDNR-LIB; Site 1: Sfil
(ggccattatggcc); Site 2: Sfil (ggcgctctggcc); cDNA made
by oligo-dT priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGTATCAACGAGAGTGGCCATTACGGCGGG-3' and
5'-ATTCTAGAGCGGCGGCGGACATG-dt(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in the laboratory of M.
Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 54.3%; Score 712.4; DB 5; Length 815;
Best Local Similarity 99.9%; Pred. No. 7e-183;
Matches 713; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 590 GTGGTATTCTACAGAAAGTTATCCCCCATCTGTGCTACTAAAGAGAGCAGCC 649
DB 1 GGGGTATTCTACAGAAAGTTATCCCCCATCTGTGCTACTAAAGAGAGCAGCC 60
QY 650 AGTTACAAATTTACAGGTAATGAAGAGGATATTTACAGCTATATCTATTGAAGAAA 709
DB 61 AGTTACAAATTTACAGGTAATGAAGAGGATATTTACAGCTATATCTATTGAAGAAA 120
QY 710 GGAAGAGTGAATTTAAAGTCAGGATTTATCTTTTCCAAATACCAATGATGAGA 769
DB 121 GGAAGAGTGAATTTAAAGTCAGGATTTATCTTTTCCAAATACCAATGATGAGA 180
QY 770 AACCTGCTATGCTAAATGTGAGTTTGGGTGGAATGAATTTTGGCTTATGACATCCCAT 829
DB 181 AACCTGCTATGCTAAATGTGAGTTTGGGTGGAATGAATTTTGGCTTATGACATCCCAT 240
QY 830 TTGGAGAGCACAGAGAAATCTCGGGAACGAATAAGACAAATATAAACTGTTCTTGA 889
DB 241 TTGGAGAGCACAGAGAAATCTCGGGAACGAATAAGACAAATATAAACTGTTCTTGA 300
QY 890 AAAATGCAAGAGCTCCAGATTCACACCGGTTATTTTGCAGGAGATACAAATTAAGA 949
DB 301 AAAATGCAAGAGCTCCAGATTCACACCGGTTATTTTGCAGGAGATACAAATTAAGA 360
QY 950 GATCAAGAGTTATCAAAATGTGTTGTTTACCTGCAACAGTTTGTGTCCTGGGAATTT 1009
DB 361 GATCAAGAGTTATCAAAATGTGTTGTTTACCTGCAACAGTTTGTGTCCTGGGAATTT 420
QY 1010 TTAGGCAAACTTAACATTTGCCAGTATACATGGGATACGAAAGCAAAATCAACCTCAGG 1069
DB 421 TTAGGCAAACTTAACATTTGCCAGTATACATGGGATACGAAAGCAAAATCAACCTCAGG 480
QY 1070 ATCCCTGCTGCTTATAAGCATCGTTTGTGATCGAATATTTTTCAGAGCAGAGGGGCAC 1129
DB 481 ATCCCTGCTGCTTATAAGCATCGTTTGTGATCGAATATTTTTCAGAGCAGAGGGGCAC 540
QY 1130 CTTATTTCCTCAAAAGTTTACACCTTGTGGTTGGAAAACTGGACTGTGTTAGATTTCG 1189
DB 541 CTTATTTCCTCAAAAGTTTACACCTTGTGGTTGGAAAACTGGACTGTGTTAGATTTCG 600

QY 1190 AGTGATCACTGGGGCTCTTGTGCACCTTGATAGTATTGTGAAGAGCTTCCCACTTG 1249
DB 601 AGTGATCACTGGGGCTCTTGTGCACCTTGATAGTATTGTGAAGAGCTTCCCACTTG 660
QY 1250 CAGCTTTACACGTTTGTGTAGCACTAGTTCTCAATTTGTGTAGGTTCTCAACCTTT 1303
DB 661 CAGCTTTACACGTTTGTGTAGCACTAGTTCTCAATTTGTGTAGGTTCTCAACCTTT 714

RESULT 4
CX226137
LOCUS MEM01355 Mus Musculus hematopoietic BM-HPC5 cDNA library Mus
DEFINITION musculus cDNA 5', mRNA sequence.
ACCESSION CX226137
VERSION CX226137.1 GI:56881429
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 767)
AUTHORS Williams,C., Wirta,V., Richter,K., Karlsson,C., Lundberg,J. and
Carlsson,L.
Expressed sequence tags of cDNA clones from a hematopoietic stem
cell line expressing Lhx2
Unpublished (2005)
Contact: Williams, C.
Molecular Biotechnology
Institution of Biotechnology
Albanova University Center, KTH-Royal Institute of Technology, 106
91 Stockholm, Sweden
Tel: +46855378332.
Fax: +46855378481
Email: cecilia.williams@biotech.kth.se

TITLE
JOURNAL
COMMENT
Location/Qualifiers
1. 767
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6-cast"
/db_xref="taxon:10090"
/sex="Male and Female"
/tissue_type="Bone Marrow"
/cell_type="Hematopoietic progenitor/stem cells
immortalized by Lhx2"
/cell_line="hematopoietic stem cell-like cell line
BM-HPC5"
/dev_stage="adult"
/clone_lib="Mus Musculus hematopoietic BM-HPC5 cDNA
library"
/note="Organ: Bone Marrow; Vector: pCMVSPORT6.1;
Preamplified custom cDNA library by Invitrogen/ResGen"

FEATURES

source
Query Match 54.2%; Score 710.8; DB 8; Length 767;
Best Local Similarity 99.3%; Pred. No. 1.9e-182;
Matches 745; Conservative 0; Mismatches 2; Indels 3; Gaps 3;
QY 131 GGCAGCAGTTCCGATGCGGCGGAGCCGCGAGCGGCGGCGGCGGCGGCGGCGGCGG 190
DB 1 GGCAGCAGTTCCGATGCGGCGGAGCCCGAGCGGCGGCGGCGGCGGCGGCGGCGG 60
QY 191 GAAGCAGCAGCAGGCGGAGGAGGACCGGGTGAAGAGCGGCGGCTTTCAGTGCCTGGGCTTT 250
DB 61 GAAGCAGCAGCAGGCGGAGGAGGACCGGGTGAAGAGCGGCGGCTTTCAGTGCCTGGGCTTT 120
QY 251 GCGTTGTTGGGGGATGC-GACCCCAACGATGTTCCAGCGTCTCTGCGGGAGAACACTG 309
DB 121 GCGTTGTTGGGGGATGCTGACCCCAACGATGTTCCAGCGTCTCTGCGGGAGAACACTG 180
QY 310 GCAGAGCGCAGAAAGCCCTGAGCGCCCTACTTCGAGCTGCCAGAGAACGACCAAGGTGGCC 369


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QY 1033 GTATACATGGATACGAAAGCAATATACAACTCAGATCCCTGCTCTTATAAGCATCG 1092
Db 959 GTATACATGGATACGAAAGCAATATACAACTCAGATCCCTGCTCTTATAAGCATCG 1018
QY 1093 TTTTGATCGAATATTTTTCAGAGCAGAGAGGGGCACCTTATTCTCAAAAGTTTAGACCT 1152
Db 1019 TTTTGATCGAATATTTTTCAGAGCAGAGAGGGGCACCTTATTCTCAAAAGTTTAGACCT 1078
QY 1153 TGTGGGTGGAAAACTCGACTGTGTAGATTTCGAGTGATCACTGGGGGCTCTTGTG 1212
Db 1079 TGTGGGTGGAAAACTCGACTGTGTAGATTTCGAGTGATCACTGGGGGCTCTTGTG 1138
QY 1213 CACCTTCAATCTAGTATTGTGAAGCTTCCACTTCAGCTTTTACAGCTTTTGTAGCAC 1272
Db 1139 CACCTTCAATCTAGTATTGTGAAGCTTCCACTTCAGCTTTTACAGCTTTTGTAGCAC 1198
QY 1273 TAGTCTCAATTTGTGTAGTCTCAACCTTTTCAGGACATC 1312
Db 1199 TAGTCTCAATTTGTGTAGTCTCAACCTTTTCAGGACATC 1238

RESULT 2
BG298330
LOCUS 602397112F1 NIH_MGC_94 942 bp mRNA linear EST 21-FEB-2001
DEFINITION 602397112F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4511666 5',
mRNA sequence.
ACCESSION BG298330
VERSION BG298330.1 GI:13062875
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 942)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10395 row: h column: 03
High quality sequence stop: 715.
Location/Qualifiers
1. .942
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 54.3%; Score 712.6; DB 2; Length 942;
Best Local Similarity 95.2%; Pred. No. 6.4e-183;
Matches 778; Conservative 0; Mismatches 34; Indels 5; Gaps 4;

QY 86 CGTGAAGACGGGTGTTTTGAGGGGACCCCTCGCGCATGGCGTCTGGCAGCAGTCCGAT 145
Db 1 CGTGAAGACGGGTGTTTTGAGGGGACCCCTCGCGCATGGCGTCTGGCAGCAGTCCGAT 60
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QY 146 GCGGCGAGCCCGCAGGCGCGGCGGCGCGTCCGCGCCCGAAGCAGCACAGGCG 205
Db 61 GCGGCGAGCCCGCAGGCGCGGCGGCGCGTCCGCGCCCGAAGCAGCACAGGCG 120
QY 206 GAGGAGGACCGGGTGAAGAGGCGGCGGCTTCAGTGCCTGGGCTTTGCTGGGGGA 265
Db 121 GAGGAGGACCGGGTGAAGAGGCGGCGGCTTCAGTGCCTGGGCTTTGCTGGGGGA 180
QY 266 TGGACCCACAGTGTCTCCAGCGTCTCGCGGAGAACGACTGGCAGAGCGAAGGCC 325
Db 181 TGGACCCACAGTGTCTCCAGCGTCTCGCGGAGAACGACTGGCAGAGCGAAGGCC 240
QY 326 CTGAGCGCTTACTTCAGCTGCGCAGAGACGACCAAGGGTGGCGCGCAGCCTCCACG 385
Db 241 CTGAGCGCTTACTTCAGCTGCGCAGAGACGACCAAGGGTGGCGCGCAGCCTCCACG 300
QY 386 TCCTTCAAGTCCGAGGCTATGTGATCTAAACCAACGAGGATGCAATGATACAACTT 445
Db 301 TCCTTCAAGTCCGAGGCTATGTGATCTAAACCAACGAGGATGCAATGATACAACTT 360
QY 446 TTAGAAGCCAGTCCATCTGGAACCTCTCTAGAGATAGCAGCACTATTTCTTCATTACC 505
Db 361 TTAGAAGCCAGTCCATCTGGAACCTCTCTAGAGATAGCAGCACTATTTCTTCATTACC 420
QY 506 TGAATATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 565
Db 421 TGAATATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 566 TGCTAGCTTTGTATAGTCCAGATGTTGTTTCTACAGGAAGTTATCCCCCATACTGT 625
Db 481 TGCTAGCTTTGTATAGTCCAGATGTTGTTTCTACAGGAAGTTATCCCCCATACTGT 540
QY 626 GCTTACTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATAT 685
Db 541 GCTTACTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATAT 600
QY 686 TTCACAGCTATCTATT--GAAGAAAGGAAGAGTGAATTTTAAAGTCAGGAGATTTTCC 744
Db 601 TTCACAGCTATCTATT--GAAGAAAGGAAGAGAGAGAGAGAGAGAGAGATTTTCC 660
QY 745 TTTTCAAATPACCAAATGATGAGAAACCTGCTATGCTGTAAT--GTGAGTTGGGTGAA 803
Db 661 TTTTCAAATPACCAAATGATGAGAAACCTGCTATGCTGTAAT--GTGAGTTGGGTGAA 720
QY 804 ATGAATTTTGCCTATGACA--TCCCATTTGGAGAGACCCAGAGACATTT--CTCGGAC 860
Db 721 ATGAATTTTGCCTATGAAA--TCCGATTTGGGGAGGACCCAGAGAAATTTCTGGGGAAC 780
QY 861 GAATAGACAAATTAATAAATCTGTTCTTGGAAAAATGCA 897
Db 781 GGATTAGACACTAATAAATGCTCTGGGACCATTTGCA 817

RESULT 3
BU936308
LOCUS 815 bp mRNA linear EST i8-OCT-2002
DEFINITION AGENCOURT_1052379 NIH_MGC_169 Mus musculus cDNA clone
IMAGE:6704064 5', mRNA sequence.
ACCESSION BU936308
VERSION BU936308.1 GI:24125127
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 815)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
```

Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yanamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000) ✓
11076861

JOURNAL
PUBMED
REFERENCE

4 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.

JOURNAL
PUBMED
REFERENCE

5 Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001) ✓

JOURNAL
PUBMED
REFERENCE

6 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.

JOURNAL
PUBMED
REFERENCE

Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002) ✓
6 (bases 1 to 1289)

JOURNAL
PUBMED
REFERENCE

Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
Direct Submission

JOURNAL
PUBMED
REFERENCE

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp,
URL: <http://genome.gsc.riken.jp/>, Tel:81-45-503-9222,
Fax:81-45-503-9216)
Please visit our web site (<http://genome.gsc.riken.jp/>) for further
details.

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues. First strand cDNA was primed with a primer
[5' GAGAGAGAAGGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was
and subsequently enriched for full-length by cap-trapper. Second
strand cDNA was prepared with the primer adaptor of sequence [5'
GAGAGAGATCTCGAGTTAAATTAATCTCCCCCCCCC 3']. cDNA was cleaved
with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
Host: SOLR.

FEATURES
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/strain="C57BL/6J"
/db_xref="FANTOM DB:2310002D07"
/db_xref="taxon:10090"
/clone="2310002D07"
/sex="male"
/tissue_type="tongue"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
55. 1160
misc_feature
(note="Traf and Tnf receptor associated protein
(MGD|GI:1860486, GB|NM_019551, evidence: BLASTN, 99%,
match=1184)
putative")

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	polya_site	1289	/note="putative"	
ORIGIN				
Query Match	88.2%;	Score 1156.6;	DB 4;	Length 1289;
Best Local Similarity	99.0%;	Pred. No. 4.1e-304;		
Matches 1227;	Conservative	0;	Mismatches	5; Indels
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				6;
Oy	73	GGCGGGGAAGCAGCGTGAAGAGCGCGGTGTTTGGAGGGACCTCGCGGCGATGGCGCTCTGG	132	
Db	7	GGCGGGGAAGCAGCGTGAAGAGCGCGGTGTTTGGAGGGGA-CCTGCGGCGATGGCGCTCTGG	65	
Oy	133	CAGCAGTTCCGATGGCGGAGCGCCGACGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG	192	
Db	66	CAGCAGTTCCGATGGCGGAGCGCCGACGAGCGCGGTGTTTGGAGGGGA-CCTGCGGCGATGGCGCTCTGG	122	
Oy	193	AGCAGCAGCGGCGGAGGAGCGCGGTGAAGAGCGCGGCTTCAGTGCCTGGGCTTTGCG	252	
Db	123	AGCAGCAGCGGCGGAGGAGCGCGGTGAAGAGCGCGGCTTCAGTGCCTGGGCTTTGCG	182	
Oy	253	GTTGGTGGGCGGATGCGACCCCGACGATGGTCCCGACGCGTCTCGCGGAGAACGACTGGCA	312	
Db	183	GTTGGTGGGCGGATGCGACCCCGACGATGGTCCCGACGCGTCTCGCGGAGAACGACTGGCA	242	
Oy	313	GACGAGAAAGCGCTGAGCGCTTCTCGAGCTGCGAGAGAACGACCAAGGCTGGCGCG	372	
Db	243	GACGAGAAAGCGCTGAGCGCTTCTCGAGCTGCGAGAGAACGACCAAGGCTGGCGCGCG	302	
Oy	373	CCAGCTCCCGACGCTCTTCAAGTCGAGCGCTTATGTCATCTAACCAACGAGGATGCCAAA	432	
Db	303	-CAGCTCCCGACGCTCTTCAAGTCGAGCGCTTATGTCATCTAACCAACGAGGATGCCAAA	361	
Oy	433	TGATACAAACCAATTTTAGAAGCGAGTCCATCTGGAACTCCTCTAGAAGATAGCAGCACTAT	492	
Db	362	TGATACAAACCAATTTTAGAAGCGAGTCCATCTGGAACTCCTCTAGAAGATAGCAGCACTAT	421	
Oy	493	TTCTTTTCAATCTCGGAATATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT	552	
Db	422	TTCTTTTCAATCTCGGAATATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT	481	
Oy	553	AGGGGTGTTCTCGCTACGCTTCTATAGTCCAGATGGTATTTCTTACAGAGAGTAT	612	
Db	482	AGGGGTGTTCTCGCTACGCTTCTATAGTCCAGATGGTATTTCTTACAGAGAGTAT	540	
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Db	541	-CCCCCATACATGCTGCTACCTAAAGAGAGAGCAGCCAGTTTACACAATTTATTACAGGTAA	599	
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Db	600	TGAAGAAGGATATTTACAGCTATATCTATTGAAGAAAGAGAGTGAATTTTAAAGTCA	658	
Oy	733	GGAGATTTCTCTTTTCCAAATACCAAAATGATGAGAAACCTGCTATGCGTAAATGTGAG	792	
Db	659	GGAGATTTCTCTTTTCCAAATACCAAAATGATGAGAAACCTGCTATGCGTAAATGTGAG	718	
Oy	793	TTTGGGTGGAAATGAATTTTGGCTTTATGACATCTCCATTTTGGAGAGCACCAGAGAAACATTC	852	
Db	719	TTTGGGTGGAAATGAATTTTGGCTTTATGACATCTCCATTTTGGAGAGCACCAGAGAAACATTC	778	
Oy	853	TCGGAAACGAATTAAGACAAATTAATAAATCTGTTCTTGGAAAAATGCAAGAGGCTCCGATTC	912	
Db	779	TCGGAAACGAATTAAGACAAATTAATAAATCTGTTCTTGGAAAAATGCAAGAGGCTCCGATTC	838	
Oy	913	ACCACGGTTATTTTGGAGGAGATACAAATTTTAAGAGATCAAGAGTTTATCAATGTGG	972	
Db	839	ACCACGGTTATTTTGGAGGAGATACAAATTTTAAGAGATCAAGAGTTTATCAATGTGG	898	
Oy	973	TGGTTTACCTGACAAACGTTTTTGGTGGGAAATTTTGGGAAATTTTGGGAAACCTTAAACATTC	1032	
Db	899	TGGTTTACCTGACAAACGTTTTTGGTGGGAAATTTTGGGAAATTTTGGGAAACCTTAAACATTC	958	

388	169.8	12.9	806	2	BG777197	602664419	461	109	8.3	780	5	BU427896	BU427896	603235039
389	169.6	12.9	640	1	AL854676	AL854676	462	108.6	8.3	703	5	BU336730	BU336730	603868851
390	168.6	12.9	256	1	AA304024	EST16719	463	107.6	8.2	644	3	BM860342	BM860342	fy36h04.y
391	168.6	12.9	728	5	BUI18538	603143186	464	106	8.1	556	3	BM036121	BM036121	ful6b12.y
392	167.2	12.7	354	2	BG949698	RC4-BT062	465	105	8.0	699	1	AL722490	AL722490	AL722490
393	166.8	12.7	373	1	AI118872	uc15b04.x	466	106	8.1	860	7	CO918949	CO918949	AGENCOURT
394	166.2	12.7	857	7	DN017421	AGENCOURT	467	102.8	7.8	149	3	BQ336306	BQ336306	PM1-WT014
395	161.8	12.3	842	8	DN597142	AGENCOURT	468	101.6	7.7	416	8	R14990	R14990	YG45c11.r1
396	161.4	12.3	743	5	BU337201	603515540	469	101.4	7.7	450	1	AA256631	AA256631	zr86b01.x
397	160	12.2	750	5	BU370465	603595629	470	101.4	7.7	527	1	AA425487	AA425487	zr46d01.x
398	159.8	12.2	765	7	CN042095	vii_p41.a	471	101.4	7.7	764	2	BG499332	BG499332	602547407
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401	158	12.0	531	7	CN233559	RJA113f02	474	100	7.6	741	7	CO879805	CO879805	BoVgen.08
402	157	12.0	485	9	AQ999402	RPCI-23-3	475	99.2	7.6	834	7	CO795546	CO795546	AGENCOURT
403	156.8	12.0	615	3	BM425735	pgf2c.pk0	476	98.8	7.5	654	8	CX682762	CX682762	Yde05g08
404	156	11.9	433	2	BF470011	ui-M-BH3-	477	98.4	7.4	599	5	BU199455	BU199455	603950890
405	155	11.8	347	5	BU070038	im09c09.x	478	97.6	7.4	342	2	BI040104	BI040104	CM4-MT028
406	154	11.7	154	10	CG887267	RRS512.Ba	479	96.6	7.4	342	8	CX234290	CX234290	MMB16472
407	152.8	11.6	388	1	AV659558	AV659558	480	96	7.3	162	8	CV572057	CV572057	od20e01.y
408	152	11.6	472	5	BU073441	ik63a06.y	481	93	7.1	121	7	CV572057	CV572057	od20e01.y
409	151	11.5	310	8	T26956	1ld155proj	482	92.2	7.0	747	7	CK956961	CK956961	4097235.B
410	150.6	11.5	503	3	BQ323527	RC1-C1011	483	92	7.0	801	5	BU930537	BU930537	AGENCOURT
411	150.6	11.5	816	7	CK806777	AGENCOURT	484	90.8	6.9	759	7	CV429123	CV429123	AGENCOURT
412	150.2	11.4	718	4	CNS08551	Tetraodon	485	90.8	6.9	1021	5	BQ605070	BQ605070	EST02352
413	148.6	11.3	410	5	BU408003	603482066	486	90.4	6.9	965	7	CO648187	CO648187	ILLUMIGEN
414	148.4	11.3	898	2	BG623866	602649018	487	90	6.9	383	7	CN389327	CN389327	170006001
415	147.2	11.2	378	1	AV655175	AV655175	488	90	6.9	407	8	N49017	N49017	YV77c10.r1
416	145.4	11.1	442	8	DN091360	JGI-CABEA	489	89	6.8	104	10	CW990440	CW990440	AZ0661.Sa
417	143.6	10.9	764	2	BF029501	601765902	490	89	6.8	852	2	BF028675	BF028675	601763912
418	143.4	10.7	718	6	CB512714	88a1rdb54	491	88.2	6.7	195	2	BF893164	BF893164	PM1-WT014
419	140.8	10.6	838	7	CV482470	AGENCOURT	492	88	6.7	577	9	BZ858137	BZ858137	CH240_232
420	137.2	10.5	665	5	BU423439	603954935	493	84.8	6.5	136	1	AA213865	AA213865	zr93h08.x
421	136.2	10.4	668	5	BU398986	603534889	494	84	6.4	159	2	BF364316	BF364316	RC1-NN106
422	135.8	10.4	596	7	CN384000	603534889	495	83	6.3	582	3	BP194502	BP194502	BP194502
423	134.4	10.2	735	7	CV480860	AGENCOURT	496	81	6.2	724	2	BE548823	BE548823	601071834
424	134	10.2	655	8	CX034936	1347507.N	497	80.8	6.2	744	9	CE158280	CE158280	tigr-gss-
425	133.4	10.2	754	6	CD053018	LITHZF000	498	80.4	6.1	153	2	BF992130	BF992130	QV3-GN020
426	131.8	10.0	549	1	AW669835	113421.MA	499	80.2	6.1	480	6	CA777140	CA777140	ip03f10.y
427	131.6	10.0	506	6	CB133935	K-EST0185	500	79.4	6.1	198	1	AL869566	AL869566	AL869566
428	131.4	10.0	415	1	AW147819	da05f07.x								
429	131	10.0	365	7	CR767008	DKF2P469G								
430	130.8	10.0	325	8	T31666	EST36732.Hu								
431	130.8	10.0	853	11	CR149458	Forward.B								
432	129.6	9.9	1236	8	DN716145	CNE111-B0								
433	126.6	9.6	581	3	CK693033	ZF101-F00								
434	126.4	9.6	581	3	BP264149	BP264149								
435	124.8	9.5	563	2	BG496889	602541306								
436	124.4	9.5	736	5	BX306203	BX306203								
437	123	9.4	699	5	BQ572870	UI-M-PD0-								
438	122.4	9.3	477	2	BF556211	UI-R-Al-e								
439	122.4	9.3	1072	5	BX337904	BX337904								
440	122	9.3	864	3	B1334358	B1334358								
441	121.6	9.3	581	3	BP270589	BP270589								
442	121	9.2	121	1	AW227720	up13a07.y								
443	119.6	9.1	827	7	CV482523	AGENCOURT								
444	119.4	9.1	828	1	AM029582	AM029582								
445	119	9.1	918	5	BQ964637	AGENCOURT								
446	117.6	9.0	647	5	BX258257	BX258257								
447	117.4	8.9	156	3	BQ331200	MR4-ET014								
448	115	8.8	324	5	BQ921583	AGENCOURT								
449	114.8	8.8	846	7	CN175478	AGENCOURT								
450	114.4	8.7	536	6	CD731214	CD731214								
451	114.2	8.7	661	5	BQ211599	BQ211599								
452	113.8	8.7	194	2	BF992138	QV3-GN020								
453	113.8	8.7	624	3	BM956789	fy74e06.x								
454	113.6	8.7	343	3	BM860067	fy36h04.x								
455	111.8	8.5	247	2	BF768814	PMO-IT001								
456	111.6	8.5	387	8	R24634	yh36f03.r1								
457	110.2	8.4	409	2	BQ900023	H048-I-G								
458	109.8	8.4	994	5	BX358706	BX358706								
459	109.4	8.3	288	1	AA746345	oa56e01.x								
460	109	8.3	593	1	AL587415	AL587415								

ALIGNMENTS

RESULT 1	AK009089	1289 bp	mRNA	linear	HTC 03-APR-2004
LOCUS	AK009089	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310002D07 product:Traf and Tnf receptor associated protein, full insert sequence.			
DEFINITION	AK009089	1 GI:12843662			
ACCESSION	AK009089	HTC; CAP trapper.			
VERSION	AK009089.1	Mus musculus			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus				
ORGANISM	Mus musculus				
REFERENCE	1	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,				

242	285	21.7	582	3	BP263516	BP263516	315	227.8	17.4	638	1	AL901140	AL901140
243	284.4	21.7	447	2	BF891509	PM1-MT014	316	227.4	17.3	444	1	AW227681	up12e07.Y
244	283.6	21.6	580	3	BP234218	BP234218	317	227.4	17.3	625	5	BU471395	603263114
245	282.8	21.6	580	3	BP274368	BP274368	318	226.8	17.3	438	5	BY263136	BY263136
246	282	21.5	584	3	BP348623	BP348623	319	226.2	17.2	352	6	CB780491	AMGNNUC:N
247	280.6	21.4	558	5	BK258258	BK258258	320	225.4	17.2	886	5	BU328780	603494664
248	280.2	21.4	482	5	BU072078	im4a02.Y	321	225	17.1	321	1	AA243535	ze15f09.X
c 249	279.4	21.3	461	1	A1428166	m147e02.X	322	223	17.0	654	1	AL895081	AL895081
250	275.8	21.0	588	3	BP236074	BP236074	c 322	221.4	16.9	579	2	BF997052	QV3-GN020
251	275.4	21.0	691	7	CK798310	AGENCOURT	323	221.4	16.8	524	3	BP263000	BP263000
252	275	21.0	652	8	W02878	zA06A07.r1	324	221	16.8	751	2	BF243927	601877278
253	274.6	20.9	959	2	B1161201	602865659	325	220.6	16.8	623	2	BG816763	QV3-GN020
254	274	20.9	588	3	BP348796	BP348796	c 326	219.8	16.8	623	2	BG816763	QV3-GN020
255	273.4	20.8	790	2	BG502867	BG502867	c 327	219.4	16.6	296	2	BI016235	MR4-ET014
256	273.4	20.8	796	6	CB317931	AGENCOURT	c 328	217.6	16.6	491	2	BI016235	MR4-ET014
257	273.2	20.8	573	3	BP379251	BP379251	c 329	217.6	16.6	770	2	BG391295	602417344
c 258	272.6	20.8	708	5	BK780010	BK780010	c 330	217	16.5	623	1	AL725543	AL725543
259	270.2	20.6	946	5	BU468774	603371865	331	215.2	16.4	827	8	CV805216	AGENCOURT
260	269	20.5	644	3	B1333830	603999339	332	214.8	16.4	876	7	CK798287	AGENCOURT
261	268.8	20.5	573	1	AU279894	AU279894	333	214.6	16.4	256	2	BB632345	uv87d12.Y
262	267.4	20.4	748	2	B1224035	602942947	c 334	214.4	16.3	486	1	AA259166	ze30b08.X
c 263	267	20.4	467	3	BQ329405	MR3-EN008	c 335	214.4	16.3	368	2	BE694706	PM0-ET075
c 264	266.6	20.3	655	3	B1449441	de28e09.X	336	213.2	16.2	839	5	BU222688	603758084
c 265	265.8	20.3	583	3	BP319548	BP319548	337	211.2	16.1	326	1	AA366358	EST77294
266	265.4	20.2	1077	5	BU131072	603116142	338	211.2	16.1	640	6	CB505136	ssalplnb5
267	264.6	20.2	581	3	BP199948	BP199948	339	210.6	16.1	710	1	AV706680	AV706680
c 268	264	20.1	570	5	BU397611	603534313	340	210.2	16.0	671	3	BJ622975	BJ622975
c 269	263.4	20.1	836	8	CK135661	AGENCOURT	c 341	207.2	15.8	568	1	AL727624	JG1_CABG9
c 270	262.6	20.0	435	3	BQ332331	MR4-ET014	342	207.2	15.8	847	8	DR867246	JG1_CABG9
c 271	261.8	20.0	587	1	AM608908	AM608908	343	207	15.8	306	1	AV083334	AV083334
272	261.8	20.0	587	1	AM608952	AM608952	344	204	15.5	521	3	BJ079453	BJ079453
c 273	260.4	19.8	623	2	BF045278	BF045278	c 345	203.6	15.5	400	6	CB699555	AMGNNUC:M
274	260.4	19.8	623	2	BF045278	BF045278	346	201.6	15.4	324	1	AV139825	AV139825
275	260.2	19.8	277	1	AA647383	vg77b12.S	347	201.4	15.3	581	2	B1067896	pgfin.pk0
276	259.8	19.8	744	7	CK155540	942844.M	c 348	200.4	15.3	695	6	CB443534	694442.MA
c 277	259.2	19.8	640	3	BI449373	de27d10.X	349	198.8	15.2	833	2	BG611757	602613142
278	258.8	19.7	530	3	BM846221	K-EST0125	c 350	197.4	15.0	935	5	BA22490	BA22490
279	257.8	19.6	583	3	BP195721	BP195721	c 351	197.4	15.0	581	3	BI444674	de27d10.Y
280	254.4	19.4	892	5	BU309561	603539613	c 352	195.6	14.9	470	3	BP417720	BP417720
281	254.4	19.4	927	6	CA972607	AGENCOURT	353	194.4	14.8	645	3	BM426270	BM426270
282	254.2	19.4	688	2	BE189858	BE189858	354	192.4	14.7	734	2	BF246577	BF246577
c 283	254	19.3	394	1	AV661333	AV661333	355	192.2	14.6	226	8	B34653	B34653
c 284	253.8	19.3	453	2	BP773259	PM0-IT001	c 356	190	14.5	729	7	CK78287	CK78287
285	253.8	19.3	889	2	BG537046	BG537046	357	189.6	14.5	689	7	CK981492	CK981492
286	253	19.3	473	6	CB120234	K-EST0167	358	189.4	14.4	875	2	BF678894	BF678894
287	252.8	19.3	782	5	BU406549	BU406549	359	189.2	14.4	252	1	AA325145	AA325145
288	252.2	19.2	875	2	BG529201	602558273	360	188	14.3	208	8	CK228487	MEM08207
c 289	246.8	18.8	614	2	BE188941	BE188941	361	186.8	14.2	574	3	BI345352	BI345352
290	245.6	18.7	355	5	BY206732	BY206732	362	186.6	14.2	707	5	BU418830	BU418830
291	245.4	18.7	485	1	AA486032	aa40b10.r	363	186.6	14.2	467	6	CF788416	CF788416
292	245.4	18.7	691	5	BY727267	BY727267	364	186	14.1	746	2	BF140146	BF140146
293	244	18.6	520	6	CB220518	LAB023A09	c 365	185	14.0	477	2	BE948252	BE948252
294	243.8	18.6	679	5	BY722631	BY722631	c 366	184	13.9	520	1	AM380606	AM380606
295	243.4	18.6	662	2	BU111103	603127011	c 367	182.6	13.9	512	1	AM380606	RC2-HT037
296	243.2	18.5	817	5	BU111103	603127011	c 368	182.6	13.9	520	1	AM380606	RC2-HT037
297	239.6	18.3	484	5	BU338911	603406502	c 369	182	13.9	696	2	BE182391	BE182391
298	238	18.1	238	2	BG147459	mac04b12.S	370	181.2	13.8	782	8	CK937111	CK937111
299	236.8	18.0	634	8	DN091361	JG1_CAB94	c 371	181.2	13.8	835	8	CK937111	CK937111
300	236.6	18.0	712	5	BU228796	603199341	c 372	181	13.8	250	1	AM879460	AM879460
301	236	18.0	839	5	EX911124	EX911124	c 373	180.8	13.8	875	2	BF790756	BF790756
302	234.8	17.9	480	1	AI750554	ch04a01.Y	c 374	178.2	13.6	781	7	CV480876	CV480876
303	234.8	17.8	750	8	CK135641	AGENCOURT	c 375	177.6	13.5	304	2	BF992144	BF992144
304	232.8	17.7	529	3	BP243301	BP243301	c 376	177.4	13.5	548	3	BP375391	BP375391
305	232.4	17.7	456	5	BQ582059	BQ582059	377	177	13.5	928	5	BA432088	BA432088
306	231.8	17.7	831	6	CA981108	AGENCOURT	c 378	176.4	13.4	478	1	AA168965	AA168965
c 307	230.8	17.6	437	2	BF768820	PM0-IT001	c 379	176.4	13.4	1174	6	CD509260	CD509260
308	229.6	17.5	422	2	BG982044	MR3-CN014	c 380	175	13.3	313	2	BG977003	BG977003
309	229.6	17.5	471	7	CR543841	DKFp4590	381	174.8	13.3	641	2	CG977096	CG977096
310	229.2	17.5	600	2	BI064472	pgfin.pk0	382	174.2	13.3	625	3	AL858410	AL858410
311	229.2	17.5	866	8	CK843565	JG1_CAAK1	383	173.8	13.2	634	1	AL858410	MR3-CN014
312	228.6	17.4	879	8	CK824886	JG1_CAAK4	c 384	172.2	13.1	461	2	BG982012	BG982012
c 313	228.2	17.4	675	1	AL722584	AL722584	385	172.2	13.1	463	8	DN851694	DN851694
314	228.2	17.4	842	8	CK958091	JG1_CAA09	386	171	13.0	676	3	BM942779	BM942779
							c 387	170.4	13.0	1445	8	DN716144	DN716144

96 408.4 31.1 410 2 BG091909 mac18c11.
97 406.2 31.0 571 6 CB125492 K-EST0174
98 403.8 30.8 570 3 BF258309 BP258309
99 403.8 30.8 739 7 CF791801 DKFZP468J
100 403.6 30.8 704 3 B1334820 60298939
101 403.4 30.7 841 2 BG562430 602581056
102 401.2 30.6 559 2 BE162174 I12-H7044
103 398.8 30.4 546 2 BG541031 602570190
104 396 30.2 581 3 BF349336 BP349336
105 395.8 30.2 657 7 CN298920 170006001
106 395.6 30.2 577 1 AW964871 EST376839
107 393.2 30.0 534 7 CN298921 170005315
108 393 30.0 731 8 CX760857 AGENCOURT
109 392.2 29.9 927 2 BG119064 602347589
110 389.4 29.7 456 1 AA839622 v97e06.r
111 386.2 29.4 683 7 CN789157 4123581.B
112 385.2 29.4 578 1 AV602300 AV602300
113 385 29.3 464 5 BU788428 i181g10.Y
114 384.8 29.3 635 3 BM539358 hb08d09.g
115 382.4 29.1 793 2 BG533717 602562373
116 381.2 29.0 634 6 CB157906 K-EST0217
117 381 29.0 382 5 BY070423 BY070423
118 381 29.0 711 6 CA945317 UI-M-ED0-
119 380 29.0 404 1 AA467625 ve87h03.s
120 377.8 28.8 752 1 AU139147 AU139147
121 375.8 28.6 774 3 B1754101 603027659
122 374.2 28.5 466 2 BB796685 BB796685
123 374.2 28.5 583 3 BP262741 BP262741
124 373.8 28.5 608 7 CK966606 4081935.B
125 372 28.4 937 2 BG541819 602569712
126 367.4 28.0 581 1 AV717253 AV717253
127 366.2 27.9 816 1 AL516230 AL516230
128 358.8 27.3 674 7 CN791432 4126159.B
129 358.8 27.3 860 8 CX958090 JGI_CAAO9
130 358.2 27.3 519 2 BB867803 BB867803
131 358.2 27.3 648 6 CF764797 CES003181
132 357.8 27.3 424 4 AK180792 Mus muscu
133 357.2 27.2 891 1 AL879624 AL879624
134 357.2 27.2 894 5 BX776016 BX776016
135 357.2 27.2 909 5 BX780455 BX780455
136 357 27.2 678 2 BG719113 602699045
137 355.8 27.1 570 3 BM172060 imageg.3
138 355.6 27.1 550 2 BG667432 DRACL809
139 355.4 27.1 475 6 CB728877 AMGNNUC.C
140 355 27.1 552 2 BG148976 uu87b07.Y
141 354.8 27.0 582 3 BP261141 BP261141
142 354.4 27.0 505 9 AZ088920 RPCI-23-3
143 352.8 26.9 361 5 BY028675 BY028675
144 352.8 26.9 581 3 BP270744 BP270744
145 351.8 26.8 581 3 BP207751 BP207751
146 351.8 26.8 750 2 B1184461 UNL-P-FN-
147 350.2 26.7 581 3 BF379659 BP379659
148 348.8 26.6 853 2 BE784416 601473891
149 347.4 26.5 581 6 CB286391 CMD36_C09
150 347 26.4 724 6 CB443087 693950.MA
151 345.6 26.3 491 1 AU681912 AU681912
152 345.4 26.3 583 3 BP262103 BP262103
153 344.8 26.3 379 5 BY036773 BY036773
154 344 26.2 453 2 BB850674 uw21a05.Y
155 343.2 26.2 908 3 BG391213 602417244
156 342.6 26.1 573 2 BP261500 BP261500
157 342.4 26.1 576 3 BP262642 BP262642
158 342 26.1 584 3 BP263059 BP263059
159 340.8 26.0 369 5 BY101168 BY101168
160 340.4 25.9 367 5 BY067359 BY067359
161 340.4 25.9 737 3 BJ639656 BJ639656
162 340 25.9 354 5 BY088879 BY088879
163 339.8 25.9 786 2 EG719977 602691335
164 337.6 25.7 347 5 B150701 B150701
165 335.2 25.5 456 2 BF996980 QV3-GN020
166 335.2 25.5 573 3 BP221260 BP221260
167 334.2 25.5 826 5 BU943127 AGENCOURT
168 334 25.5 440 2 BG982036 MR3-CN014
621 25.5 334 169 BG091909 mac18c11.
566 25.4 333.2 170 CB125492 K-EST0174
440 25.4 333.3 171 BF258309 BP258309
463 25.3 331.6 172 CF791801 DKFZP468J
453 25.2 330.8 173 B1334820 60298939
919 25.2 330.8 174 BG562430 602581056
565 25.2 330.2 175 BE162174 I12-H7044
900 25.2 330.2 176 BG541031 602570190
554 25.1 329.6 177 BF349336 BP349336
896 25.1 329.4 178 CN298920 170006001
799 25.0 327.8 179 AW964871 EST376839
749 25.0 327.6 180 CN298921 170005315
327 24.9 327 181 CX760857 AGENCOURT
614 24.9 327 182 BG119064 602347589
441 24.9 326.4 183 AA839622 v97e06.r
441 24.9 326.4 184 CN789157 4123581.B
688 24.8 326 185 AV602300 AV602300
984 24.7 323.8 186 BU788428 i181g10.Y
634 24.6 323 187 BM539358 hb08d09.g
833 24.6 323 188 BG533717 602562373
332 24.6 322.6 189 CB157906 K-EST0217
602 24.6 322.6 190 BY070423 BY070423
732 24.4 320.6 191 CA945317 UI-M-ED0-
568 24.3 319.2 192 AA467625 ve87h03.s
877 24.3 319.2 193 AU139147 AU139147
570 24.3 318.8 194 B1754101 603027659
582 24.3 318.6 195 BB796685 BB796685
458 24.3 318.2 196 BP262741 BP262741
444 24.2 317 197 CK966606 4081935.B
395 24.0 315.6 198 BG541819 602569712
582 24.0 314.6 199 AV717253 AV717253
454 24.0 314.4 200 AL516230 AL516230
314 23.9 202 CN791432 4126159.B
463 23.9 314 2 CX958090 JGI_CAAO9
534 23.9 313.4 203 BB867803 BB867803
808 23.9 313.2 204 CF764797 CES003181
652 23.9 313 205 AK180792 Mus muscu
581 23.8 312.4 206 AL879624 AL879624
995 23.8 312.4 207 BX776016 BX776016
460 23.5 308.4 208 BX780455 BX780455
580 23.5 308 209 BG719113 602699045
583 23.4 306.6 210 BM172060 imageg.3
749 23.4 306.6 211 BG667432 DRACL809
827 23.4 306.6 212 CB728877 AMGNNUC.C
850 23.4 306.6 213 BG148976 uu87b07.Y
582 23.3 305.6 214 BP261141 BP261141
909 23.3 305.4 215 AZ088920 RPCI-23-3
835 23.3 305.2 216 BY028675 BY028675
413 23.2 305 217 BP270744 BP270744
802 23.1 303.4 218 BP207751 BP207751
577 23.0 301.8 219 B1184461 UNL-P-FN-
308 23.0 301.4 220 BF379659 BP379659
459 23.0 301 221 BE784416 601473891
760 22.9 301 222 CB286391 CMD36_C09
311 22.9 301 223 CB443087 693950.MA
666 22.9 300.4 224 AU681912 AU681912
584 22.7 298.4 225 BP262103 BP262103
626 22.7 298.2 226 BY036773 BY036773
927 22.7 298.2 227 BB850674 uw21a05.Y
471 22.6 297.2 228 BG391213 602417244
879 22.5 296.4 229 BP261500 BP261500
456 22.4 295.8 230 BP262642 BP262642
582 22.4 293.4 231 BP263059 BP263059
407 22.3 293.2 232 BY101168 BY101168
565 22.2 291.8 233 BY067359 BY067359
419 22.2 290.4 234 BJ639656 BJ639656
915 22.1 290.4 235 BY088879 BY088879
581 21.9 287.6 236 EG719977 602691335
572 21.8 286 237 B150701 B150701
425 21.8 285.4 238 BF996980 QV3-GN020
799 21.7 285.2 239 BP221260 BP221260
582 21.7 285 240 BU943127 AGENCOURT
3 BP233592 MR3-CN014


```
QY 1880 CCCCACAGAGAAATTAATAAAGAAATTTATTGGT 1917
Db 1861 CCCCACAGAGAAATTTAAATAAAGAAATTTATTGGT 1898

RESULT 11
AAX28153
ID RAX28153 standard; DNA; 2499 BP.
XX
AC AAX28153;
XX
DT 16-JUN-1999 (first entry)
XX
DE Topoisomerase II binding protein 1 coding sequence.
XX
KW Topoisomerase II binding protein; TopBP; anticancer agent; ds.
XX
OS Homo sapiens.
XX
PN JP11075856-A.
XX
PD 23-MAR-1999.
XX
PF 17-SEP-1997; 97JP-00251544.
XX
PR 17-SEP-1997; 97JP-00251544.
XX
PA (TSURUO T.
PA (CHUS ) CHUGAI PHARM CO LTD.
XX
DR WPI; 1999-257704/22.
DR P-PSDB; AAY03182.
XX
PT New Topoisomerase II- binding protein - useful as an anticancer agent.
XX
PS Disclosure; Page 18-19; 28pp; Japanese.
XX
CC This sequence encodes the topoisomerase II binding protein (TopBP) of the
CC invention. The TopBP protein is useful as an anticancer agent. TopBP can
CC be used as the target molecule for anticancer agent
XX
SQ Sequence 2499 BP; 720 A; 505 C; 587 G; 687 T; 0 U; 0 Other;

Query Match 94.6%; Score 1815.4; DB 2; Length 2499;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1816; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGCAGAGCGCGCAGGAGATGAGTTGGGAGTTGCTGGAGCGCGGGAGGCGGC 60
Db 463 GTGCAGAGCGCGCAGGAGATGAGTTGGGAGTTGCTGGAGCGCGGGAGGCGGC 522
QY 61 GGAGGAAGAGCGCGAGCGCTCAGGTGAAAAAGCGCGACTTCTGTGTGGAGTTGCTC 120
Db 523 GGAGGAAGAGCGCGAGCGCTCAGGTGAAAAAGCGCGACTTCTGTGTGGAGTTGCTC 582
QY 121 GGTGCGAAGCTGGGATGCCGAGTGGCTCAGTGTCTTCTGGCCGAGAACGACTGGAGAT 180
Db 583 GGTGCGAAGCTGGGATGCCGAGTGGCTCAGTGTCTTCTGGCCGAGAACGACTGGAGAT 642
QY 181 GGAAAGGGCTCTGAATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 240
Db 643 GGAAAGGGCTCTGAATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 702
QY 241 ACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGCAAGAAACAACTGA 300
Db 703 ACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGCAAGAAACAACTGA 762
QY 301 TTCACCACTCTTAAATCAGCCCATCTGAAGTACTCAGCAAGAAATGGCAGCATGTT 360
Db 763 TTCACCACTCTTAAATCAGCCCATCTGAAGTACTCAGCAAGAAATGGCAGCATGTT 822
QY 361 CTCTCTCATTCAGTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
```


Db 1903 TAGTTAATATTTAAATAAGTCTTCAAAAGAAAAACATAAGAGATTATTGAGTTCTTGGGA 1962
Qy 1501 CTGGATCCTTTATTTTCAAGTTTCAGATCATCTTAATGAAATGAAATGCCATGATTCTGCA 1560
Db 1963 CTGGATCCTTTATTTTCAAGTTTCAGATCATCTTAATGAAATGAAATGCCATGATTCTGCA 2022
Qy 1561 GTTAAGTAGATGACAGCTATTCTACATCAGACTTGGATTTTGTGAGCTAATTACATAATT 1620
Db 2023 GTTAAGTAGATGACAGCTATTCTACATCAGACTTGGATTTTGTGAGCTAATTACATAATT 2082
Qy 1621 GGTAAAGTAAATTTGAAACCTTTATGCTTTAAATTCCTTAACCTCTTTTGTGATTCATGTT 1680
Db 2083 GGTAAAGTAAATTTGAAACCTTTATGCTTTAAATTCCTTAACCTCTTTTGTGATTCATGTT 2142
Qy 1681 TGTAGTCATGTTCTCAACAGAGCAAGTTAAGCTTTGATGATGTTTAAATCGGTTTGTAT 1740
Db 2143 TGTAGTCATGTTCTCAACAGAGCAAGTTAAGCTTTGATGATGTTTAAATCGGTTTGTAT 2202
Qy 1741 AGCACCATGGACATTTTAAACAAAAATAAATGATGATGATGATGATGATGATGATGATGAT 1800
Db 2203 AGCACCATGGACATTTTAAACAAAAATAAATGATGATGATGATGATGATGATGATGATGAT 2262
Qy 1801 TTGCTAATTTGTAATGG 1818
Db 2263 TTGCTAATTTGTAATGG 2280

RESULT 12

AAC98160
ID AAC98160 standard; cDNA; 1296 BP.
XX AAC98160;
AC
XX
DT 09-MAR-2001 (first entry)
XX Human colon cancer antigen nucleotide sequence SEQ ID NO:170.
DE
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW identification; cytostatic; cardioactive; neuroprotective; vulnary;
KW immunomodulatory; muscular; gynaecological; gastrointestinal;
KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;
KW neural disorder; immune system disorder; muscular disorder;
KW reproductive disorder; gastrointestinal disorder; renal disorder;
KW infectious disease; cardiovascular disorder; ss.
XX
OS Homo sapiens.
XX
XX WO200055351-A1.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US005883.
XX
XX 12-MAR-1999; 99US-0124270P.
XX
XX (HUMÀ-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2000-587534/55.
XX
XX P-PSDB; AAB53403.
XX
XX Colon cancer associated gene sequences, referred to as colon cancer
XX antigens, useful for the treatment, prevention, and diagnosis of colon
XX disorders such as colon cancer.
XX
XX Claim 1; Page 597; 2104pp; English.
XX
XX AAC97991 to AAC98763 encode the human colon cancer associated proteins,
XX called human colon cancer antigens, given in AAB53234 to AAB54006. The
XX human colon cancer antigens can have cytostatic, cardioactive, muscular;
XX neuroprotective, immunomodulatory, gynaecological, gastrointestinal, and
XX vulnary, nephrotropic, antiinfective and antibacterial activities, and

CC can be used in gene therapy. The colon cancer antigen polynucleotides,
CC proteins and antibodies to the proteins are useful for the prevention,
CC treatment and diagnosis of colon disorders, such as colon cancer. The
CC polynucleotides may be used in diagnostics and research, such as for
CC chromosome identification, and as hybridisation probes. The proteins may
CC also be used to prevent diseases such as neural disorders, immune system
CC disorders, muscular disorders, reproductive disorders, gastrointestinal
CC disorders, wounds, renal disorders, infectious diseases, and
CC cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent
CC sequences used in the exemplification of the present invention

XX Sequence 1296 BP; 376 A; 250 C; 326 G; 333 T; 0 U; 11 Other;

SQ Query Match 64.9%; Score 1246.2; DB 3; Length 1296;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 1242; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCAGAGCGCGCAGAGATGGAGTTGGGAGTTGCTTGGAGGCGGAGGAGGCGCG 60

Db 5 GTGCAGAGCGCGCAGAGATGGAGTTGGGAGTTGCTTGGAGGCGGAGGAGGCGCG 64

Qy 61 GGAGAGAGGCGCGCAGCTGAGTGAAGAGGCGGACTTCTGTGTGTGAGTTGCTTC 120

Db 65 GGAGAGAGGCGCGCAGCTGAGTGAAGAGGCGGACTTCTGTGTGTGAGTTGCTTC 124

Qy 121 GGTGCGAAGCTGCGATGCGCAGTGGCTCAGTGTCTTCTGGCCGAGAACGACTGGGAGAT 180

Db 125 GGTGCGAAGCTGCGATGCGCAGTGGCTCAGTGTCTTCTGGCCGAGAACGACTGGGAGAT 184

Qy 181 GGAAAGGCGCTCTGAACTCTTCTGAGCTCCGCTGGAGGAGGCGCTTGGAAAGCGCG 240

Db 185 GGAAAGGCGCTCTGAACTCTTCTGAGCTCCGCTGGAGGAGGCGCTTGGAAAGCGCG 244

Qy 241 ACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAATGA 300

Db 245 ACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAATGA 304

Qy 301 TTCCACCATCTTAAATCAGCCCTCTCAAGATCTCAGCAAGAAATGGCAGCATGTT 360

Db 305 TTCCACCATCTTAAATCAGCCCTCTCAAGATCTCAGCAAGAAATGGCAGCATGTT 364

Qy 361 CTCTCTCATTTACCTGGAATTTTGTGATTTAGATCTTAAACAATCTCTCAGAGAGGCTCG 420

Db 365 CTCTCTCATTTACCTGGAATTTTGTGATTTAGATCTTAAACAATCTCTCAGAGAGGCTCG 424

Qy 421 AGGGGTGTTCTTCTTACTTGTACCTTTGTACGCCAGATGTATTTCTCAGAGAGTAT 480

Db 425 AGGGGTGTTCTTCTTACTTGTACCTTTGTACGCCAGATGTATTTCTCAGAGAGTAT 484

Qy 481 TCCCCCATATTATAGCTACCTAAAGAGAGATCAAGTAAATTTAGATTTATACAGTCA 540

Db 485 TCCCCCATATTATAGCTACCTAAAGAGAGATCAAGTAAATTTAGATTTATACAGTCA 544

Qy 541 TGAAGAAGGATATTTTCAAGCTATATATGTTGAAGAAATCAAGAGTGAATTTAAAAAGCCA 600

Db 545 TGAAGAAGGATATTTTCAAGCTATATATGTTGAAGAAATCAAGAGTGAATTTAAAAAGCCA 604

Qy 601 AGAGATTTATTTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTTGATGTGAA 660

Db 605 AGAGATTTATTTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTTGATGTGAA 664

Qy 661 TGTGTCAGGAATGAGCTTTGCTTATGATCATCTTGGAGAGCAGCAGAGGCGATGC 720

Db 665 TGTGTCAGGAATGAGCTTTGCTTATGATCATCTTGGAGAGCAGCAGAGGCGATGC 724

Qy 721 TGTGTCAGGAATGAGCTTTGCTTATGATCATCTTGGAGAGCAGCAGAGGCTCCAGATC 780

Db 725 TGTGTCAGGAATGAGCTTTGCTTATGATCATCTTGGAGAGCAGCAGAGGCTCCAGATC 784

Qy 781 AGCTACAGTTATTTTTCAGGAGATCAAAATCTTAAGGATTCGAGAGTTACAGATGTGG 840

Db 785 AGCTACAGTTATTTTTCAGGAGATCAAAATCTTAAGGATTCGAGAGTTACAGATGTGG 844

QY 841 TGGTTTACCACCAACATTTGGATGCTCTGGAGTTTGGGCAACCTAAACATTGCCA 900
DB TGGTTTACCACCAACATTTGGATGCTCTGGAGTTTGGGCAACCTAAACATTGCCA 904
QY 901 GTATACATGGGATACACAAATGAATCTTAATCTTGGAAATACCTGCTGTTGAACTTCG 960
DB GTATACATGGGATACACAAATGAATCTTAATCTTGGAAATACCTGCTGTTGAACTTCG 964
QY 961 TTTTGTATCGAATATTTTTCAGAGCAGCAGCAGAGAGAGGACACATTTATCCCGGAAGTTT 1020
DB TTTTGTATCGAATATTTTTCAGAGCAGCAGCAGAGAGAGGACACATTTATCCCGGAAGTTT 1024
QY 1021 GGACCTTCTGGATTAGAAAACTGGACTGTGGTAGATTTCTTAGTATGATCTGGGCTCT 1080
DB GGACCTTCTGGATTAGAAAACTGGACTGTGGTAGATTTCTTAGTATGATCTGGGCTCT 1084
QY 1081 TCTGTGCAACTTAGATATAATTTCTAAATGCTTTTCAAGTGTGGGTTTTCGCTGATTT 1140
DB TCTGTGCAACTTAGATATAATTTCTAAATGCTTTTCAAGTGTGGGTTTTCGCTGATTT 1144
QY 1141 GTTGCAAATACAAATTTCCACCTTCTGGAAGGTAGTTTGTCTGGAGGAAATATATGAC 1200
DB GTTGCAAATACAAATTTCCACCTTCTGGAAGGTAGTTTGTCTGGAGGAAATATATGAC 1204
QY 1201 TAGATCATGTGCAGAAAAACCAACTATGATTTAGTTGTTGTTTCA 1249
DB TAGATCATGTGCAGAAAAACCAACTATGATTTAGTTGTTGTTTCA 1253

RESULT 13

AA84209/c
ID AA84209 standard; cDNA; 1079 BP.
XX
AC AA84209;
XX
DT 08-SEP-1999 (first entry)
XX
DE DNA encoding human breast tumour protein immunogenic fragment.
XX
KW Breast tumour protein; immunogenic fragment; vaccine; detection;
KW breast cancer development; therapy; ss.
XX
OS Homo sapiens.
XX
PN W09933869-A2.
XX
PD 08-JUL-1999.
XX
PF 22-DEC-1998; 98WO-US027416.
XX
PR 24-DEC-1997; 97US-00998253.
PR 24-DEC-1997; 97US-00998253.
PR 17-JUL-1998; 98US-00118554.
PR 17-JUL-1998; 98US-00118627.

(CORI-) CORIXA CORP.

Reed SG, Xu J;

WPI; 1999-405486/34.

New breast tumor protein genes used, in vaccines for immunotherapy, or for diagnosis of breast cancer.

Claim 3; Page 60; 70pp; English.

This sequence encodes a human breast tumour protein immunogenic fragment of the invention. The polypeptides or nucleic acids encoding them are useful in vaccines and pharmaceutical compositions for manufacture of medicaments for inhibiting the development of breast cancer in a patient. They can also be used to treat breast cancer. Antibodies against these polypeptides can be used to detect and monitor progression of breast cancer in patients. Primers and probes derived from the polynucleotides

CC encoding the breast proteins are useful for detection of breast cancer.
CC peripheral blood cells from a patient incubated in the presence of at
CC least one polypeptide, such that T cells proliferate, are useful in
CC manufacture of a medicament for treating breast cancer in a patient.
CC Antigen presenting cells incubated in the presence of at least one
CC polypeptide are also useful for treating breast cancer

XX SQ Sequence 1079 BP; 327 A; 229 C; 177 G; 346 T; 0 U; 0 Other;

Query Match 55.5%; Score 1066.4; DB 2; Length 1079;
Best Local Similarity 99.8%; Pred. No. 2.2e-271;
Matches 1078; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 423 GGGTGTCTTCTACTAGCTTTGTACAGCCAGATGTGATTTCTACAGGAAGTTATTC 482
DB 1079 GGGTGTCTTCTACTAGCTTTGTACAGCCAGATGTGATTTCTACAGGAAGTTATTC 1020
QY 483 CCCCATATTATAGCTTACCTAAAGAGAGATCAAGTAATATGAGATTATACAGTCAATG 542
DB 1019 CCCCATATTATAGCTTACCTAAAGAGAGATCAAGTAATATGAGATTATACAGTCAATG 960
QY 543 AAGAAGGATATTTCCAGCTATATATGTTGAAGAAATCAAGAGTGAAATTAAGGCCAAG 602
DB 959 AAGAAGGATATTTCCAGCTATATATGTTGAAGAAATCAAGAGTGAAATTAAGGCCAAG 900
QY 603 AGATTATTTCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTAATG 662
DB 899 AGATTATTTCTTTTCCAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTAATG 840
QY 663 TGTGAGGAATGAGCTTTGCTTATGATCATCCCATTTTGGAGAGCACCAGAGGGATGCTG 722
DB 839 TGTGAGGAATGAGCTTTGCTTATGATCATCCCATTTTGGAGAGCACCAGAGGGATGCTG 780
QY 723 CGGAACGAATCAATCAGTTAAATAATGTTTAAAGAAATCAAGAGGCTCCAGAGTCAG 782
DB 779 CGGAACGAATCAATCAGTTAAATAATGTTTAAAGAAATCAAGAGGCTCCAGAGTCAG 720
QY 783 CTACAGTTATATTTTGGAGGATACAAATCTAAGGATCGAGAGTTACCAAGATGCTG 842
DB 719 CTACAGTTATATTTTGGAGGATACAAATCTAAGGATCGAGAGTTACCAAGATGCTG 660
QY 843 GTTTACCCCAACAACATTTGTGGATGCTGGGAGTTTGGGCAAACTAAACATTTGCCAGT 902
DB 659 GTTTACCCCAACAACATTTGTGGATGCTGGGAGTTTGGGCAAACTAAACATTTGCCAGT 600
QY 903 ATACATGGGATACACAAATGAATCTAATCTTGAATAAATCTGCTGTTGTAACCTCGTT 962
DB 599 ATACATGGGATACACAAATGAATCTAATCTTGAATAAATCTGCTGTTGTAACCTCGTT 540
QY 963 TTGATCGAATATTTTTCAGAGCAGCAGAGAGGAGACATTTATTTCCCGGAAGTTTGG 1022
DB 539 TTGATCGAATATTTTTCAGAGCAGCAGAGAGGAGACATTTATTTCCCGGAAGTTT-G 481
QY 1023 ACCTTCTTGGATTAGAAAACTGGACTGTGGTAGATTTTCTAGTATCATCCTGGGCTCTTC 1082
DB 480 ACCTTCTTGGATTAGAAAACTGGACTGTGGTAGATTTTCTAGTATCATCCTGGGCTCTTC 421
QY 1083 TGTGCAACTTAGATATAATTTTGAATAATGCTTTTCAAGTGTGGGTTTGGCTGATGTT 1142
DB 420 TGTGCAACTTAGATATAATTTTGAATAATGCTTTTCAAGTGTGGGTTTGGCTGATGTT 361
QY 1143 TGCAAATACAAATTTTCCAGCTTCTGGAAGAGTAGGTTTGTCTGGAGGAAATATGACTA 1202
DB 360 TGCAAATACAAATTTTCCAGCTTCTGGAAGAGTAGGTTTGTCTGGAGGAAATATGACTA 301
QY 1203 GATCATTTCTCAGAAAAACCAACTATGATTTATGTTGTGTTTTCAGATTCAACATTA 1262
DB 300 GATCATTTCTCAGAAAAACCAACTATGATTTATGTTGTGTTTTCAGATTCAACATTA 241
QY 1263 AAGATTAAATGTTTATTTAAACGAAACACATTTCTGCAATTCAGGATGTAGGCCATTAAATA 1322
DB 240 AAGATTAAATGTTTATTTAAACGAAACACATTTCTGCAATTCAGGATGTAGGCCATTAAATA 181

QY 1323 AAAAGGGCAAAAGCCTGTGACAGATTTTCAAGGTCCTTACAGCTGCCAGCTGGATTCCA 1382
DB 180 AAAAGGGCAAAAGCCTGTGACAGATTTTCAAGGTCCTTACAGCTGCCAGCTGGATTCCA 121
QY 1383 AACAGGTACCCATGCTCTGAGCTAAATGTTTATATATTTTCCATTCAGGCAACCGAATA 1442
DB 120 AACAGGTACCCATGCTCTGAGCTAAATGTTTATATATTTTCCATTCAGGCAACCGAATA 61
QY 1443 GTTAATATTTAAATTAAGTCTTCAAGAAACATTAAGAGATTATTGAGTCTTGGGACT 1502
DB 60 GTTAATATTTAAATTAAGTCTTCAAGAAACATTAAGAGATTATTGAGTCTTGGGACT 1

RESULT 14
AAC79438/c
ID AAC79438 standard; cdna; 1079 BP.
XX AC
XX AAC79438;
XX 07-FEB-2001 (first entry)
XX cdna sequence of human breast tumour clone 1015D11.
XX Human; breast tumour antigen; cytostatic; immunotherapy; breast cancer;
KW vaccine; ss.
XX Homo sapiens.
XX WO200061756-A2.
XX 19-OCT-2000.
XX 10-APR-2000; 2000WO-US009688.
XX 09-APR-1999; 99US-00288950.
XX 02-JUL-1999; 99US-00346327.
XX (CORI-) CORIXA CORP.
XX Reed SG, Xu J, Dillon DC;
XX WPI; 2000-638568/61.
XX A novel isolated polypeptide comprising an immunogenic portion of a
PT breast cancer protein useful in the detection and treatment of breast
PT cancer.
XX Claim 4; Page 77; 95pp; English.

XX The present sequence was isolated from a breast tumour cdna library. It
CC is provided in a specification relating to compounds for immunotherapy
CC and diagnosis of breast cancer. Breast tumour antigens and the
CC polynucleotides that encode them may be used in the production of a
CC pharmaceutical composition to be used in the treatment of breast cancer.
CC Proliferated T cells and incubated antigen presenting cells are also
CC required. The polypeptides and polynucleotides may also be used to
CC produce a vaccine
XX
XX Sequence 1079 BP; 327 A; 229 C; 177 G; 346 T; 0 U; 0 Other;
Query Match 55.5%; Score 1066.4; DB 3; Length 1079;
Best Local Similarity 99.8%; Pred. No. 2.2e-271;
Matches 1078; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 423 GGGTGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATTTTCTACAGGAAGTTATTC 482
DB 1079 GSGTGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATTTTCTACAGGAAGTTATTC 1020
QY 483 CCCCATATTATAGCTACCTAAAGAGAGATCAAGTAAATTTATGAGATTATTACAGGTCATG 542
DB 1019 CCCCATATTATAGCTACCTAAAGAGAGATCAAGTAAATTTATGAGATTATTACAGGTCATG 960
QY 543 AAGAGGATATTTCACAGCTATAATGTTTGAAGAAATCAAGAGTGAAATTTAAAGCAAG 602

DB 959 AAGAGGATATTTCACAGCTATAATGTTTGAAGAAATCAAGAGTGAATTTAAAGCCAAG 900
QY 603 AGATTATTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTATGTGTGCAATGTGAATG 562
DB 899 AGATTATTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTATGTGTGCAATGTGAATG 840
QY 663 TGTGAGGAATGAGCTTTTGCCTTATGACATCCATTTTGGAGAGCAACAGAGGGCATGCTG 722
DB 839 TGTGAGGAATGAGCTTTTGCCTTATGACATCCATTTTGGAGAGCAACAGAGGGCATGCTG 780
QY 723 CGGAACGAATGATCAGTTTAAATGTTTAAAGAAATGCAAGAGGCTCCAGAGTCAAG 782
DB 779 CGGAACGAATGATCAGTTTAAATGTTTAAAGAAATGCAAGAGGCTCCAGAGTCAAG 720
QY 783 CTACAGTTTATATTTTCAGGAGATACAAATCTAAGGGATCGAGAGGTTTACAGATGTGGTG 842
DB 719 CTACAGTTTATATTTTCAGGAGATACAAATCTAAGGGATCGAGAGGTTTACAGATGTGGTG 660
QY 843 GTTTACCCCAACCAATTTGTGGATGCTGCGAGTCTTGGGCAAACTTAAACATTTGCCAGT 902
DB 659 GTTTACCCCAACCAATTTGTGGATGCTGCGAGTCTTGGGCAAACTTAAACATTTGCCAGT 600
QY 903 ATACATGGGATACAAATGAACTCTAATCTTTGGAATACTGCTGCTTGTAACTTCGTT 962
DB 599 ATACATGGGATACAAATGAACTCTAATCTTTGGAATACTGCTGCTTGTAACTTCGTT 540
QY 963 TTTGATCGAATATTTTTCAGAGCAGCAGAGAGAGAGGACACATTTATTTCCCGAAGTTTGG 1022
DB 539 TTTGATCGAATATTTTTCAGAGCAGCAGAGAGAGAGGACACATTTATTTCCCGAAGTTT-G 481
QY 1023 ACCTTCTTTGGATTAGAAAACTGGACTGTGTGATGTTTCTTAGTGATCACTGGGCTTTC 1082
DB 480 ACCTTCTTTGGATTAGAAAACTGGACTGTGTGATGTTTCTTAGTGATCACTGGGCTTTC 421
QY 1083 TGTGCAACTTAGATATAATTTGTAATGCTTTTCAAGTGTGGGTTTTCCTCTGATTTGT 1142
DB 420 TGTGCAACTTAGATATAATTTGTAATGCTTTTCAAGTGTGGGTTTTCCTCTGATTTGT 361
QY 1143 TGCAAATACAAATTTCCACCTCTGGAAGGTAGGTTTGTCTGGAGGAAATATGTTACTA 1202
DB 360 TGCAAATACAAATTTCCACCTCTGGAAGGTAGGTTTGTCTGGAGGAAATATGTTACTA 301
QY 1203 GATCATTGTGACAGAAAAACCAACTATGATTTATGTTGTTTTCAGAAATTCACATTA 1262
DB 300 GATCATTGTGACAGAAAAACCAACTATGATTTATGTTGTTTTCAGAAATTCACATTA 241
QY 1263 AAGATTAAATGTTTATTTAAACGAAACACATTCCTGCAATTCAGGATGTGAGGCCATTA 1322
DB 240 AAGATTAAATGTTTATTTAAACGAAACACATTCCTGCAATTCAGGATGTGAGGCCATTA 181
QY 1323 AAAAGGGCAAAAGCCTGTGACAGATTTTCAAGGTCCTTACAGCTGCCAGCTGGATTCCA 1382
DB 180 AAAAGGGCAAAAGCCTGTGACAGATTTTCAAGGTCCTTACAGCTGCCAGCTGGATTCCA 121
QY 1383 AACAGGTACCCATGCTCTGAGCTAAATGTTTATATATTTTCCATTCAGGCAACCGAATA 1442
DB 120 AACAGGTACCCATGCTCTGAGCTAAATGTTTATATATTTTCCATTCAGGCAACCGAATA 61
QY 1443 GTTAATATTTAAATTAAGTCTTCAAGAAACATTAAGAGATTATTGAGTCTTGGGACT 1502
DB 60 GTTAATATTTAAATTAAGTCTTCAAGAAACATTAAGAGATTATTGAGTCTTGGGACT 1

RESULT 15
ABK28982/c
ID ABK28982 standard; cdna; 1079 BP.
XX XX
XX AC ABK28982;
XX XX
XX DT 23-APR-2002 (first entry)
XX XX
XX DE Human breast tumour polypeptide cdna clone #11.

XX Human; breast tumour polypeptide; gene; ss; breast cancer; cytostatic; immunostimulant.
KW
XX
OS Homo sapiens.
XX
PN WO200198339-A2.
XX
PD 27-DEC-2001.
XX
XX 12-JUN-2001; 2001WO-US019032.
XX
XX 22-JUN-2000; 2000US-00602877.
PR 12-OCT-2000; 2000US-00687507.
PR 06-FEB-2001; 2001US-00778381.
XX
XX (CORI-) CORIXA CORP.
XX
XX Reed SG, Xu J, Dillon DC, Retter MW, Harlocker SL;
XX WPI; 2002-147792/19.
XX
XX Polynucleotides encoding breast tumor polypeptides, useful for treating breast cancer or stimulating an immune response.
XX
XX Claim 1; Page 131; 150pp; English.
XX
XX The invention relates to polynucleotides encoding breast tumour polypeptides. The sequences are useful for treating cancer, preferably breast cancer, in a patient or for stimulating an immune response. The polynucleotides and polypeptides are also useful in the diagnosis and monitoring of breast cancer. A method for detecting the presence of a cancer in a patient, comprises obtaining a biological sample from the patient, contacting the biological sample with a binding agent that binds to a breast tumour polypeptide, detecting in the sample an amount of polypeptide that binds to the binding agent, and comparing the amount of polypeptide to a predetermined cut-off value, therefore determining the presence of a cancer in the patient. Sequences ABK28920-ABK29025 represent cDNA clones encoding human breast tumour polypeptides of the invention
XX
XX Sequence 1079 BP; 327 A; 229 C; 177 G; 346 T; 0 U; 0 Other;
XX
XX Query Match 55.5%; Score 1066.4; DB 6; Length 1079;
XX Best Local Similarity 99.8%; Pred. No. 2.2e-271;
XX Matches 1078; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
XX
QY 423 GGGTGTGTTCTTACTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTC 482
DB 1079 GGGTGTGTTCTTACTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTC 1020
XX
QY 483 CCCCATATTATAGCTTACCTAAGAGAGATCAAGTAATTATGAGATTATTACAGTCAATG 542
DB 1019 CCCCATATTATAGCTTACCTAAGAGAGATCAAGTAATTATGAGATTATTACAGTCAATG 960
XX
QY 543 AAGAAGGATATTTCACAGTATAATTGTTGAAGAAATCAAGAGTGAATAAAGCCCAAG 602
DB 959 AAGAAGGATATTTCACAGTATAATTGTTGAAGAAATCAAGAGTGAATAAAGCCCAAG 900
XX
QY 603 AGATTATTTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTATGTGTGATGTGAATG 662
DB 899 AGATTATTTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTATGTGTGATGTGAATG 840
XX
QY 663 TGTCAGGAATAGAGCTTTTGCCTTATGACATCCCATTTGGAGAGCACCAGAGGGCATGCTG 722
DB 839 TGTCAGGAATAGAGCTTTTGCCTTATGACATCCCATTTGGAGAGCACCAGAGGGCATGCTG 780
XX
QY 723 CGGAACGAATGATCAGTTTAAAGAAATGCAAGAGGCTCCAGAGTCAG 782
DB 779 CGGAACGAATGATCAGTTTAAAGAAATGCAAGAGGCTCCAGAGTCAG 720
XX
QY 783 CTACAGTATTATTTTCAGGAGATCAAAATCTAAGGGATCGAGGTTTACCAGATCTGTG 842
XX

DB 719 CTACAGTATTATTTGTCAGGAGATACAAATCTAAGGGATCGAGAGGTTTACCAGATGTGTG 660
QY 843 GTTTACCCAAACATTTGTGATGTCTGGAGTTTTTGGGCAACCTTAAACATTTGCCAGT 902
DB 659 GTTTACCCAAACATTTGTGATGTCTGGAGTTTTTGGGCAACCTTAAACATTTGCCAGT 600
QY 903 ATACATGGGATACACAAATGAATCTTAATCTTGGAAATACTGCTGCTTGTAAACTTCGTT 962
DB 599 ATACATGGGATACACAAATGAATCTTAATCTTGGAAATACTGCTGCTTGTAAACTTCGTT 540
QY 963 TTGATCGAATATTTTTCAGAGCAGCAGCAGAGAGGAGACACATTTATTTCCCGAAGTTGG 1022
DB 539 TTGATCGAATATTTTTCAGAGCAGCAGCAGAGAGGAGACACATTTATTTCCCGAAGTTT-G 481
QY 1023 ACCTTCTTGGATTAGAAAACTGGACTGTGGTAGATTTCTAGTAGTACACTGGGGTCTTC 1082
DB 480 ACCTTCTTGGATTAGAAAACTGGACTGTGGTAGATTTCTAGTAGTACACTGGGGTCTTC 421
QY 1083 TGTGCAACTTAGATATATATTTGTAATAATGCTTTTCAAGTGTGGGTTTTTGGCCCTGATTTGT 1142
DB 420 TGTGCAACTTAGATATATATTTGTAATAATGCTTTTCAAGTGTGGGTTTTTGGCCCTGATTTGT 361
QY 1143 TGCAAAATACAAATTTCCACCTTCTGGAAGGTAGGTTTCTGTGTGGAGGAAATAATGTACTA 1202
DB 360 TGCAAAATACAAATTTCCACCTTCTGGAAGGTAGGTTTCTGTGTGGAGGAAATAATGTACTA 301
QY 1203 GATCATTGTGCAGAAAAACCACTATGATTTATGTTGTTTTCAGATTTCACACATTA 1262
DB 300 GATCATTGTGCAGAAAAACCACTATGATTTATGTTGTTTTCAGATTTCACACATTA 241
QY 1263 AAGATTATGTTTATTTTAAACGAAACACATTCCTGCATTTCAGGATGTGAGGCCATTTAATA 1322
DB 240 AAGATTATGTTTATTTTAAACGAAACACATTCCTGCATTTCAGGATGTGAGGCCATTTAATA 181
QY 1323 AAAAGGGCACAAGCCCTGTGAGAGTTTTTCAACGGTGTCTTACAGCTGCCAGCTGATTCGA 1382
DB 180 AAAAGGGCACAAGCCCTGTGAGAGTTTTTCAACGGTGTCTTATAGCTGCCAGCTGATTCGA 121
QY 1383 AACAGGTACCCCATGTTCTGAGCTAATGTTTATATATTTTCCATTTCAGGCACCGAATA 1442
DB 120 AACAGGTACCCCATGTTCTGAGCTAATGTTTATATTTTCCATTTCAGGCACCGAATA 61
QY 1443 GTTATATTTTAAATAAGTCTTCAAAAGAAACATAAGAGATTATTGAGTTCTTTGGGACT 1502
DB 60 GTTATATTTTAAATAAGTCTTCAAAAGAAACATAAGAGATTATTGAGTTCTTTGGGACT 1
XX
RESULT 16
AAS86254
ID AAS86254 standard; cDNA; 1088 BP.
XX
AC AAS86254;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #22058.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
XX cDNAs.
XX
XX
PS Claim 1; SEQ ID NO 4908; 2537pp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
XX present invention
XX
SQ Sequence 752 BP; 225 A; 148 C; 200 G; 176 T; 0 U; 3 Other;
Query Match 36.1%; Score 693; DB 4; Length 752;
Best Local Similarity 97.3%; Pred. No. 1.3e-172;
Matches 724; Conservative 0; Mismatches 16; Indels 2; Gaps 2;
QY 20 ATGGAGTTGGGAGTTGCTCGAGGCGGGAGGAGGCGGAGGAGGCGGAGGCGGAGGCGCT 79
DB 1 ATGGAGTTGGGAGTTGCTCGAGGCGGGAGGAGGCGGAGGAGGCGGAGGAGGCGGAGGCGCT 60
QY 80 GAGGTGAAAGAGCGGCGACTTCTGTGTGGAGTTTGGCTCGGTGCGCAAGCTGCGATGCC 139
DB 61 GAGGTGAAAGAGCGGCGACTTCTGTGTGGAGTTTGGCTCGGTGCGCAAGCTGCGATGCC 120
QY 140 GCAGTGGCTCAGTGTCTTCTGCGCGAGAAACGACTGGGAGATGGAAGGGCTCTGAACTCC 199
DB 121 GGGTGGCTCAGTGTCTTCTGCGCGAGAAACGACTGGGAGATGGAAGGGCTCTGAACTCC 180
QY 200 TACTTTCGAGCTCCGCTGGAGAGAGCGCTTGGAAACCGGACCTGAAACCATCTCTGAG 259
DB 181 TGTTCGAGCTCCGCTGGAGAGAGCGCTTGGAAACCGGACCTGAAACCATCTCTGAG 240
QY 260 CCAAGACCTATGTTGACCTAACCAATGAAGAAACAACTGATTCACCACTTCTAAATC 319
DB 241 CCAAGACCTATGTTGACCTAACCAATGAAGAAACAACTGATTCACCACTTCTAAATC 300
QY 320 AGCCCATCTGAAGATACTCAGCAAGAAATGCGAGCATGTTCTCTCATTTACCTGGAAAT 379
DB 301 AGCCCATCTGAAGATACTCAGCAAGAAATGCGAGCATGTTCTCTCATTTACCTGGAAAT 360
QY 380 ATTGATGATTAAGATTAACCAATCTGTCAGAGAGGCTCGAGGGGTGTGCTCACTTA 439
DB 361 ATTGATGATTAAGATTAACCAATCTGTCAGAGAGGCTCGAGGGGTGTGCTCACTTA 420
QY 440 GCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTTCCCCCATATATAGCTAC 499
DB 421 GCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTTCCCCCATATATAGCTAC 480
QY 500 CTAAGAAGAGATCAAGTAATATATGAGATTATTACAGGTCATGAAGAGGATATTTTACA 559

Db 481 CTAAGAAGAGATCAAGTAATATATGAGATTATTACAGGTCATGAAGAGGATATTTTACA 540
QY 560 GCTATATATGTTGAAGAAATCAAGAGTGAATTTAAAAAGCCCAAGAGATTTATTCCTTTTCCA 619
Db 541 GCTATATATGTTGAAGAAATCAAGAGTGAATTTAAAAAGCCCAAGAGATTTATTCCTTTTCCA 600
QY 620 AGTACCAAAATGATGAG-AAAACCTTTTATGTCATGTCATGTCAGGAATGAGCT 678
Db 601 AGTACCAAAATGATGAGAAAACCTTTTATGTCATGTCATGTCAGGAATGAGCT 660
QY 679 TTGCTCTTATGACATCCC-ATTGAGAGACCAAGAGGCGCATGTCGCGAAACGAATGAATC 737
Db 661 TTGCTCTTAAAGACATCCCAATTTGGNGAACCAAGAGGCGCATGTCGCGAAACGAATGAATC 720
QY 738 AGTTAAAAATGGTTTTTAAAGAAA 761
Db 721 AGTTAAAAATGGTTTTTAAANGAA 744
RESULT 18
AAZ47119
ID AAZ47119 standard; cDNA; 1312 BP.
XX
AC AAZ47119;
XX
DT 15-MAR-2000 (first entry)
XX
DE Mouse CD40 receptor associated protein gene.
XX
KW Antiarteriosclerotic; antiarthritic; neuroprotective; dermatological;
KW immunosuppressive; antinflammatory; immunosuppressive; antiallergic;
KW mouse; CD40 receptor associated protein; CRAP; cytoplasmic domain;
KW tumour necrosis factor; TNF; receptor; superfamily; CD30; homology;
KW TNF receptor associated factor; TRAF; modulator; signalling pathway;
KW diagnosis; NF-kappaB; Jun; kinase; atherosclerosis; multiple sclerosis;
KW arthritis; systemic lupus erythematosus; graft rejection; allergy;
KW graft versus host disease; autoimmune disease; ds.
XX
OS Mus musculus.
XX
PN WO9955859-A2.
XX
PD 04-NOV-1999.
XX
PF 28-APR-1999; 99WO-EP003025.
XX
PR 29-APR-1998; 98EP-00201392.
XX
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI Pype SMC, Remacle JEFJG, Huylebroeck DFE;
XX
XX WPI; 2000-062029/05.
DR P-FSDB; AAY56020.
XX
PT Novel proteins used to treat inflammatory diseases, NF-kappaB related
PT diseases and for improvement of anti-tumor treatments.
XX
PS Claim 10; Page 41-43; 48pp; English.
XX
XX This sequence represents the gene encoding mouse CD40 receptor associated
CC protein (CRAP). CRAP is a functional protein capable of interacting with
CC the cytoplasmic domain of CD40 and/or other receptors of the tumour
CC necrosis factor (TNF) receptor superfamily such as CD30 and TNF receptor
CC I, where the protein has no homology to TNF receptor associated factor
CC (TRAF)-proteins. The CD40 binding proteins can be used as modulators of
CC the CD40 signalling pathway, especially to diagnose and treat TRAF-
CC related, CD40-related, NF-kappaB related and/or Jun (kinase)-related
CC diseases, and for the improvement of anti-tumour diseases. Diseases which
CC may be treated include atherosclerosis, arthritis, multiple sclerosis,
CC systemic lupus erythematosus, graft rejection, graft versus host disease,
CC allergy, and autoimmune disease. The proteins can be used to sensitize

CC analysis, nucleic acid purification, isolation of transcriptionally
CC active genes, blocking or transcription factor binding, genome cleavage
CC or in situ hybridisation, and as enhancers of transcription or
CC biomarkers. This sequence represents a human colon cancer associated
CC cDNA. Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at seqdata.uspto.gov
XX
SQ Sequence 674 BP; 213 A; 114 C; 152 G; 191 T; 0 U; 4 Other;
Query Match 33.4%; Score 642; DB 11; Length 674;
Best Local Similarity 99.4%; Pred. No. 3.8e-159;
Matches 653; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 416 GCTCAGAGGGTGTCTTCTACTTGTGTACAGCCAGATGTGATATTCTACAGAA 475
Db 18 GCTCAGAGGGTGTCTTCTACTTGTGTACAGCCAGATGTGATATTCTACAGAA 77
QY 476 GTTATTCCTCCATATTATAGCTTACCTTAAGAGAGATCAAGTAAATTATGAGATTATACA 535
Db 78 GTTATTCCTCCATATTATAGCTTACCTTAAGAGAGATCAAGTAAATTATGAGATTATACA 137
QY 536 GGTCAATGAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAA 595
Db 138 GGTCAATGAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAA 197
QY 596 AGCCAAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGAT 655
Db 198 AGCCAAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGAT 257
QY 656 GTGATGTGTACGAAAGTGTCTTGTCTTATGATCCATCTTGGAGAGCAGAGGG 715
Db 258 GTGAATGTGTACGAAAGTGTCTTGTCTTATGATCCATCTTGGAGAGCAGAGGG 317
QY 716 CATGCTGCGGAACGAATGAATCAGTTTAAAGAAATGAGTAAAGAGGCTCCA 775
Db 318 CATGCTGCGGAACGAATGAATCAGTTTAAAGAAATGAGTAAAGAGGCTCCN 377
QY 776 -GAGTCAGCTACAGTTATATTGTCAGGAGATACAAATCTAAGGGATCGAGAGTTACCAG 834
Db 378 TGAGTCAGCTACAGTTATATTGTCAGGAGATACAAATCTAAGGGATCGAGAGTTACCAG 437
QY 835 ATGTGCTGTTTACCCAAACATTTGGATGTCTGGAGTTTTTGGGCAACCTTAACA 894
Db 438 ATGTGCTGTTTACCCAAACATTTGGATGTCTGGAGTTTTTGGGCAACCTTAACA 497
QY 895 TTGCCAGTATACATGGGATACACAAATCTTAATCTTGAATAAATCTGCTTTGTAA 954
Db 498 TTGCCAGTATACATGGGATACACAAATCTTAATCTTGAATAAATCTGCTTTGTAA 557
QY 955 ACTTCGTTTTGATCGAATATTTTTCAGAGCAGCAGAGAGGACACATTTTCCCG 1014
Db 558 ACTTCGTTTTGATCGAATATTTTTCAGAGCAGCAGAGAGGACACATTTTCCCG 617
QY 1015 AAGTTTGACCTTCTTGGATTAGAAAACCTGACTGTGGTAGATTTCTAGTGATCA 1071
Db 618 AAGTTTGACCTTCTTGGATTAGAAAACCTGACTGTGGTAGATTTCTAGTGATCA 674
RESULT 20
ADX42030
ID ADX42030 standard; cDNA; 674 BP.
XX
AC ADX42030;
XX
DT 21-APR-2005 (first entry)
XX
DE Human cDNA encoding colon cancer protein SEQ ID NO 1067.
XX
KW Cytostatic; Immunostimulant; therapy; diagnosis; colon cancer; neoplasia;
KW ss; gene.
XX
OS Homo sapiens.
XX

PN WO200274156-A2.
XX 26-SEP-2002.
XX 01-FEB-2002; 2002WO-US002870.
XX 02-FEB-2001; 2001US-0267400P.
PR 07-FEB-2001; 2001US-0267382P.
PR 11-MAY-2001; 2001US-0290322P.
PR 12-JUL-2001; 2001US-0305265P.
PR 16-AUG-2001; 2001US-0313077P.
XX (CORI-) CORIYA CORP.
XX Jiang Y, Chenault RA, Xu J, Indrias CY, Lodes MJ, Secrist H;
PI Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;
XX WPI; 2003-040540/03.
XX New isolated nucleic acids and polypeptides capable of eliciting a
PT humoral and/or cellular immune response, useful for diagnosing,
PT preventing or treating cancer, particularly colon cancer.
PS Claim 1; SEQ ID NO 1067; 244pp; English.
XX The invention relates to a new isolated nucleic acid. The nucleic acids,
CC polypeptides, antibodies are useful for diagnosing, preventing or
CC treating cancer, particularly colon cancer. The nucleic acid and
CC polypeptides are also useful in DNA strand invasion, antisense
CC inhibition, mutational analysis, nucleic acid purification, isolation of
CC transcriptionally active genes, blocking or transcription factor binding,
CC genome cleavage or in situ hybridization, and as enhancers of
CC transcription or biomarkers. The kits are useful for detecting antibody
CC binding. The present sequence represents a human cDNA encoding a colon
CC cancer protein.
XX Sequence 674 BP; 213 A; 114 C; 152 G; 191 T; 0 U; 4 Other;
SQ
Query Match 33.4%; Score 642; DB 11; Length 674;
Best Local Similarity 99.4%; Pred. No. 3.8e-159;
Matches 653; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 416 GCTCAGAGGGTGTCTTCTACTTGTGTGTACAGCCAGATGTGATATTCTACAGAA 475
Db 18 GCTCAGAGGGTGTCTTCTACTTGTGTGTACAGCCAGATGTGATATTCTACAGAA 77
QY 476 GTTATTCCTCCATATTATAGCTTACCTTAAGAGAGATCAAGTAAATTATGAGATTATACA 535
Db 78 GTTATTCCTCCATATTATAGCTTACCTTAAGAGAGATCAAGTAAATTATGAGATTATACA 137
QY 536 GGTCAATGAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAA 595
Db 138 GGTCAATGAAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAA 197
QY 596 AGCCAAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGAT 655
Db 198 AGCCAAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGAT 257
QY 656 GTGAATGTGTACGAAAGTGTCTTGTCTTATGATCCATCTTGGAGAGCAGAGGG 715
Db 258 GTGAATGTGTACGAAAGTGTCTTGTCTTATGATCCATCTTGGAGAGCAGAGGG 317
QY 716 CATGCTGCGGAACGAATGAATCAGTTTAAAGAAATGTTTAAAGAAATGCAAGAGGCTCCA 775
Db 318 CATGCTGCGGAACGAATGAATCAGTTTAAAGAAATGTTTAAAGAAATGCAAGAGGCTCCN 377
QY 776 -GAGTCAGCTACAGTTATATTGTCAGGAGATACAAATCTAAGGGATCGAGAGTTACCAG 834
Db 378 TGAGTCAGCTACAGTTATATTGTCAGGAGATACAAATCTAAGGGATCGAGAGTTACCAG 437
QY 835 ATGTGCTGTTTACCCAAACATTTGGATGTCTGGAGTTTTTGGGCAACCTTAACA 894
Db 438 ATGTGCTGTTTACCCAAACATTTGGATGTCTGGAGTTTTTGGGCAACCTTAACA 497
QY 895 TTGCCAGTATACATGGGATACACAAATCTTAATCTTGAATAAATCTGCTTTGTAA 954
Db 498 TTGCCAGTATACATGGGATACACAAATCTTAATCTTGAATAAATCTGCTTTGTAA 557
QY 955 ACTTCGTTTTGATCGAATATTTTTCAGAGCAGCAGAGAGGACACATTTTCCCG 1014
Db 558 ACTTCGTTTTGATCGAATATTTTTCAGAGCAGCAGAGAGGACACATTTTCCCG 617
QY 1015 AAGTTTGACCTTCTTGGATTAGAAAACCTGACTGTGGTAGATTTCTAGTGATCA 1071
Db 618 AAGTTTGACCTTCTTGGATTAGAAAACCTGACTGTGGTAGATTTCTAGTGATCA 674
RESULT 20
ADX42030
ID ADX42030 standard; cDNA; 674 BP.
XX
AC ADX42030;
XX
DT 21-APR-2005 (first entry)
XX
DE Human cDNA encoding colon cancer protein SEQ ID NO 1067.
XX
KW Cytostatic; Immunostimulant; therapy; diagnosis; colon cancer; neoplasia;
KW ss; gene.
XX
OS Homo sapiens.
XX

QY 416 GCTCAGGGGTGTGTTCTCTACTTACAGCCAGATGTGATTTCTACAGAA 475
DB 26 GCTCAGGGGTGTGTTCTCTACTTACAGCCAGATGTGATTTCTACAGAA 85
QY 476 GTTATTTCCCATATATAGCTTAAAGAGAGATCAAGTAATATGAGATTATACA 535
DB 86 GTTATTTCCCATATATAGCTTAAAGAGAGATCAAGTAATATGAGATTATACA 145
QY 536 -GGTCATCAAGAGATATTTTACAGCTATATGTTGAAGAAATCAAGAGTGAATTTAAA 594
DB 146 GGGTCATCAAGAGATATTTTACAGCTATATGTTGAAGAAATCAAGAGTGAATTTAAA 205
QY 595 AAGCCAGAGATATTTCTTTTCCAAATGATGAGAAACCTTTTATGTGTGCA 654
DB 206 AAGCCAGAGATATTTCTTTTCCAAATGATGAGAAACCTTTTATGTGTGCA 265
QY 655 TGTGAATGTGCAGAAATGAGCTTTCCTTTATGACATCCCATTTGGAGAGCACAGAGG 714
DB 266 TGTGAATGTGCAGAAATGAGCTTTCCTTTATGACATCCCATTTGGAGAGCACAGAGG 325
QY 715 GCATCTCGGGAACGAATCACTTAAATGTTTAAAGAAATGCAAGAGGCTCC 774
DB 326 GCATCTCGGGAACGAATCACTTAAATGTTTAAAGAAATGCAAGAGGCTCC 385
QY 775 AGAGTCAGCTACAGTTATTTGCGAGAGATACAAATCTAAGGGATCGAGAGTTACAG 834
DB 386 AGAGTCAGCTACAGTTATTTGCGAGAGATACAAATCTAAGGGATCGAGAGTTACAG 445
QY 835 ATGTGGTGGTTTACCAACACATTTGGATGCTGGAGTTTGGGCAACCTTAACA 894
DB 446 ATGTGGTGGTTTACCAACACATTTGGATGCTGGAGTTTGGGCAACCTTAACA 505
QY 895 TTGCAGATATACATGGGATACACAATCAACTCTTAATCTTGAATAAAGTCTGTGTA 954
DB 506 TTGCAGATATACATGGGATACACAATCAACTCTTAATCTTGAATAAAGTCTGTGTA 565
QY 955 ACTTCGTTTGTGCAATTTTTCAGAGCAGCAGAGAGGAGACATTTATTTCCCG 1014
DB 566 ACTTCGTTTGTGCAATTTTTCAGAGCAGCAGAGAGGAGGACATTTATTTCCCG 625

RESULT 28
ID ADT95512
XX ADT95512 standard; cdna; 625 BP.
AC ADT95512;
XX ADT95512;
XX 16-DEC-2004 (first entry)
XX Colon cancer associated human cDNA sequence #1031.
XX Colon cancer; T cell; tumour protein; C634S; C635S; C637S; C640S; C636S;
KW humoral immune response; cellular immune response; cytostatic;
KW immunostimulant; human; ss.
XX Homo sapiens.
XX US2003087818-A1.
XX 08-MAY-2003.
XX 01-FEB-2002; 2002US-00066543.
XX 02-FEB-2001; 2001US-0267400P.
PR 07-FEB-2001; 2001US-0267382P.
PR 11-MAY-2001; 2001US-0290322P.
PR 12-JUL-2001; 2001US-0305265P.
PR 16-AUG-2001; 2001US-0313077P.
XX (CORI-) CORIXA CORP.
XX Jiang Y, Chenault RA, Xu J, Indirias CY, Lodes MJ, Secretist H;
PI

PI Carter D, Fanger GR, Smith CL, Durham M, Stolk JA;
XX WPI; 2003-040540/03.
XX New isolated nucleic acids and polypeptides capable of eliciting a
PT humoral and/or cellular immune response, useful for diagnosing,
PT preventing or treating cancer, particularly colon cancer.
XX Claim 1; SEQ ID NO 1031; 87pp; English.
PS
XX The invention relates to polynucleotide and polypeptide sequences
CC associated with cancer, particularly colon cancer. Also disclosed are (i)
CC an expression vector comprising the polynucleotide, (ii) a host cell
CC transformed or transfected with the expression vector, (iii) an isolated
CC antibody, or its antigen-binding fragment, which specifically binds to
CC the polypeptide, (iv) a method of detecting or determining the presence
CC of cancer in a patient, (v) a fusion protein comprising at least one of
CC the polypeptides, (vi) an oligonucleotide that hybridises to the
CC polynucleotide sequence under highly stringent conditions, and (vii) a
CC method of stimulating and/or expanding T cells specific for a tumour
CC protein. The polypeptide specifically comprises the amino acid sequence
CC of C634S, C635S, C637S, C640S, C636S or one of the potential open reading
CC frames (ORFs) of C636S. These polypeptides are encoded by the
CC polynucleotide sequences, where both are capable of eliciting a humoral
CC and/or cellular immune response. The polynucleotides, polypeptides, and
CC antibodies are useful for diagnosing, preventing or treating cancer,
CC particularly colon cancer. The polynucleotide and polypeptide sequences
CC are also useful in DNA strand invasion, antisense inhibition, mutational
CC analysis, nucleic acid purification, isolation of transcriptionally
CC active genes, blocking or transcription factor binding, genome cleavage
CC or in situ hybridisation, and as enhancers of transcription or
CC biomarkers. This sequence represents a human colon cancer associated
CC cDNA. Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at seqdata.uspto.gov
XX
SQ Sequence 625 BP; 202 A; 104 C; 144 G; 174 T; 0 U; 1 Other;

Query Match 30.4%; Score 584; DB 11; Length 625;
Best Local Similarity 100.0%; Pred. No. 8.3e-144;
Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 416 GCTCAGGGGTGTGTTCTCTACTTACAGCCAGATGTGATTTCTACAGAA 475
DB 42 GCTCAGGGGTGTGTTCTCTACTTACAGCCAGATGTGATTTCTACAGAA 101
QY 476 GTTATTTCCCATATATAGCTTAAAGAGAGATCAAGTAATATGAGATTATACA 535
DB 102 GTTATTTCCCATATATAGCTTAAAGAGAGATCAAGTAATATGAGATTATACA 161
QY 536 GGTCAATGAAGAGATATTTTACAGCTATATGTTGAAGAAATCAAGAGTGAATTTAAA 595
DB 162 GGTCAATGAAGAGATATTTTACAGCTATATGTTGAAGAAATCAAGAGTGAATTTAAA 221
QY 596 AGCCAGAGATTTTCTTTTCCAAATGATGAGAAACCTTTTATGTGTGAT 655
DB 222 AGCCAGAGATTTTCTTTTCCAAATGATGAGAAACCTTTTATGTGTGAT 281
QY 656 GTGAATGTGTGAGAAATGAGCTTTCCTTTATGACATCCCATTTGGAGAGCACAGAGG 715
DB 282 GTGAATGTGTGAGAAATGAGCTTTCCTTTATGACATCCCATTTGGAGAGCACAGAGG 341
QY 716 CATGCTCGGGAACGAATCAAGTGAATGTTTAAAGAAATCAAGAGGCTCCA 775
DB 342 CATGCTCGGGAACGAATCAAGTGAATGTTTAAAGAAATCAAGAGGCTCCA 401
QY 776 GAGTCAGCTACAGTTATATTTTGCAGAGATACAAATCTAAGGGATCGAGAGTTACCAGA 835
DB 402 GAGTCAGCTACAGTTATATTTTGCAGAGATACAAATCTAAGGGATCGAGAGTTACCAGA 461
QY 836 TGTGGTGGTTTACCCCAACAACTTGTGATGTCTGGGAGTTTTCGGGCAACCTTAACAT 895
DB 462 TGTGGTGGTTTACCCCAACAACTTGTGATGTCTGGGAGTTTTCGGGCAACCTTAACAT 521

xx The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention

xx SQ Sequence 579 BP; 204 A; 97 C; 79 G; 191 T; 0 U; 8 Other;

Query Match 26.7%; Score 513; DB 4; Length 579;
Best Local Similarity 97.2%; Pred. No. 4.9e-125;
Matches 530; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

QY 1374 TGGATTCGAACAGGTACCCCATGCTCTGAGCTAATGTTTATATTTTCCATTCAGGC 1433
DB 545 TGGATTCGAACCCGGTACAACATNTTTTNGAGTTTAATGTTTATATTTTCCATTCAGGC 486

QY 1434 ACCGAATAGTTAATATTTAAATAAGTCTT-CAAAAGAAAACATAAGAGATTATTGAGT 1492
DB 485 ACCGAATAGTTAATATTTTGAATTAAGTCTTNCAAAAGAAAACATAAGAGATTATTGAGT 426

QY 1493 TCTTGGGACTGGATCCTTTATTTCATAAGTTTCAGATCATCTTTAAATGAAAATGCCATGAT 1552
DB 425 TCTTGGGACTGGATCCTTTATTTCATAAGTTTCAGATCATCTTTAAATGAAAATGCCATGAT 366

QY 1553 TATCTGCGAGTTAAGTAGATGACAGCTATCTACATCAGACTTGATTTTGTTCAGCTAATT 1612
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QY 1613 ACATAATTGGTAGAATATAATTGAAACCTTATGGCTTAAATTCCTTAACCTCTTTTGA 1672
DB 305 ACATAATTGGTAGAATATAATTGAAACCTTATGGCTTAAATTCCTTAACCTCTTTTGA 246

QY 1673 TTCATGTTTGTAGTCATGTTGTCACAGAGCAAAAGTTAAGCTTCATGATGGTTAAATC 1732
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QY 1913 TTGGT 1917
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 11:01:36 ; Search time 1618.39 Seconds
(without alignments)
9810.499 Million cell updates/sec

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Post-processing: Minimum Match 0%
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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1905.2	99.2	1940	5	US-10-783-271-28
4	1897.6	98.8	1948	6	US-10-037-270-889
5	1897.6	98.8	1948	6	US-10-117-722-889
6	1897.6	98.8	1948	9	US-10-122-851-889
7	1246.2	64.9	1296	3	US-09-925-299-170
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9	1066.4	55.5	1079	7	US-10-453-919-63
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11	987.2	51.4	1088	9	US-10-757-745-3
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15	600	31.2	633	5	US-10-066-543-1084
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17	584	30.4	625	5	US-10-066-543-1031
18	512	26.7	553	5	US-10-066-543-983
19	493	25.7	547	5	US-10-066-543-2173
20	410.2	21.4	503	5	US-10-066-543-442
21	405.2	21.1	476	5	US-10-066-543-438
22	404.2	21.1	479	5	US-10-066-543-906
23	404.2	21.1	483	5	US-10-066-543-902

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Sequence 21055, A	725	9	US-10-363-483A-21055	3.8	73.6	C	61
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117 42.8 2.2 640681 3 US-09-790-988-1 Sequence 1, Appl
118 42.6 2.2 408 9 US-10-275-332A-13 Sequence 13, Appl
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244	40	2.1	570	3	US-09-814-353-5719	Sequence 5719, Ap	317	39.2	2.0	19087	6	US-10-311-455-766	Sequence 766, App
245	40	2.1	570	3	US-09-814-353-12003	Sequence 12003, A	C 318	39.2	2.0	49600	7	US-10-459-262A-2	Sequence 2, Appli
C 246	40	2.1	704	7	US-10-424-599-97877	Sequence 97877, A	C 319	39.2	2.0	91552	7	US-10-415-058-5	Sequence 5, Appli
C 247	40	2.1	900	4	US-09-925-065A-84685	Sequence 84685, A	C 320	39	2.0	504	4	US-09-925-065A-214199	Sequence 214199,
C 248	40	2.1	983	4	US-09-925-065A-60049	Sequence 60049, A	C 321	39	2.0	552	4	US-09-925-065A-582899	Sequence 582899,
C 249	40	2.1	983	4	US-09-925-065A-60050	Sequence 60050, A	C 322	39	2.0	575	4	US-09-925-065A-91683	Sequence 91683, A
C 250	40	2.1	983	4	US-09-925-065A-60051	Sequence 60051, A	C 323	39	2.0	611	4	US-09-925-065A-285596	Sequence 285596,
251	40	2.1	5324	6	US-10-311-455-1764	Sequence 1764, Ap	324	39	2.0	681	3	US-09-969-034-2532	Sequence 2532, Ap
252	40	2.1	6210	6	US-10-240-453-345	Sequence 345, App	325	39	2.0	739	7	US-10-424-539-66831	Sequence 66831, A
253	40	2.1	6220	6	US-10-311-455-1273	Sequence 1273, Ap	326	39	2.0	1211	8	US-10-425-115-93385	Sequence 93385, A
254	40	2.1	8537	7	US-10-240-589C-76	Sequence 76, Appl	327	39	2.0	5317	5	US-10-087-464-9	Sequence 9, Appli
255	40	2.1	10329	6	US-10-311-455-2095	Sequence 2095, Ap	328	39	2.0	6325	8	US-10-473-126-372	Sequence 372, App
256	40	2.1	15951	6	US-10-311-455-1653	Sequence 1653, Ap	329	39	2.0	7849	7	US-10-240-589C-87	Sequence 87, Appl
257	40	2.1	15951	6	US-10-240-485-133	Sequence 133, App	C 330	39	2.0	8056	8	US-10-473-126-240	Sequence 240, App
C 258	40	2.1	640681	3	US-09-790-988-1	Sequence 1, Appli	C 331	39	2.0	9204	6	US-10-311-455-1102	Sequence 1102, Ap
C 259	39.8	2.1	491	4	US-09-925-065A-383906	Sequence 383906,	332	39	2.0	9204	7	US-10-221-613-154	Sequence 154, App
C 260	39.8	2.1	2529	4	US-09-925-065A-503812	Sequence 503812,	333	39	2.0	9499	6	US-10-311-455-558	Sequence 558, App
261	39.8	2.1	2529	7	US-10-425-114-31103	Sequence 31103, A	334	39	2.0	9888	6	US-10-311-455-1213	Sequence 1213, Ap
262	39.8	2.1	6203	8	US-10-425-115-158547	Sequence 158547,	335	39	2.0	15479	7	US-10-257-166-46	Sequence 46, Appl
263	39.8	2.1	6327	5	US-10-239-678-152	Sequence 152, App	336	39	2.0	17848	5	US-10-239-676-28	Sequence 28, Appl
264	39.8	2.1	6327	6	US-10-240-453-168	Sequence 168, App	337	39	2.0	17848	6	US-10-240-453-38	Sequence 38, Appl
265	39.8	2.1	7047	6	US-10-240-453-259	Sequence 259, App	338	39	2.0	17848	6	US-10-257-166-58	Sequence 58, Appl
266	39.8	2.1	9368	6	US-10-311-455-1573	Sequence 1573, Ap	C 339	39	2.0	50000	8	US-10-706-635-25	Sequence 25, Appl
267	39.8	2.1	34688	7	US-10-433-793-90	Sequence 90, Appl	C 340	39	2.0	54081	5	US-10-087-192-1318	Sequence 1318, Ap
268	39.8	2.1	35962	8	US-10-473-126-98	Sequence 98, Appl	341	39	2.0	58965	6	US-10-298-132-2	Sequence 2, Appli
269	39.8	2.1	35962	8	US-10-473-126-244	Sequence 244, App	342	39	2.0	63588	5	US-10-243-735-3	Sequence 3, Appli
270	39.8	2.1	37007	9	US-10-661-398-21	Sequence 21, Appl	343	39	2.0	63588	7	US-10-730-010-3	Sequence 3, Appli
271	39.6	2.1	463	4	US-09-925-065A-373871	Sequence 373871,	C 344	39	2.0	54025	8	US-10-719-993-6862	Sequence 6862, Ap
C 272	39.6	2.1	614	4	US-09-925-065A-384685	Sequence 384685,	C 345	38.8	2.0	393	3	US-09-960-352-4582	Sequence 4582, Ap
C 273	39.6	2.1	625	4	US-09-925-065A-503811	Sequence 503811,	346	38.8	2.0	536	4	US-09-925-065A-478576	Sequence 478576,
C 274	39.6	2.1	1620	6	US-10-369-324-38	Sequence 38, Appl	347	38.8	2.0	628	4	US-09-925-065A-513081	Sequence 513081, A
C 275	39.6	2.1	1620	7	US-10-607-538-38	Sequence 38, Appl	348	38.8	2.0	630	4	US-09-925-065A-67078	Sequence 67078, A
C 276	39.6	2.1	1620	9	US-10-505-079-38	Sequence 38, Appl	C 349	38.8	2.0	630	4	US-09-925-065A-607400	Sequence 607400, A
277	39.6	2.1	5706	7	US-10-221-613-280	Sequence 280, App	C 350	38.8	2.0	739	5	US-10-027-632-24044	Sequence 24044, A
278	39.6	2.1	12138	6	US-10-311-455-1473	Sequence 1473, Ap	C 351	38.8	2.0	739	5	US-10-027-632-24046	Sequence 24046, A
279	39.6	2.1	12138	6	US-10-311-455-1916	Sequence 1916, Ap	C 352	38.8	2.0	739	6	US-10-027-632-24044	Sequence 24044, A
280	39.6	2.1	12138	6	US-10-240-453-210	Sequence 210, App	C 353	38.8	2.0	739	6	US-10-027-632-24045	Sequence 24045, A
281	39.6	2.1	17534	7	US-10-257-166-107	Sequence 107, App	C 354	38.8	2.0	739	6	US-10-027-632-24046	Sequence 24046, A
282	39.6	2.1	50000	8	US-10-706-635-23	Sequence 23, Appl	C 355	38.8	2.0	739	6	US-10-027-632-24046	Sequence 24046, A
283	39.6	2.1	163382	7	US-10-367-094-179	Sequence 179, App	C 356	38.8	2.0	1296	7	US-10-724-972A-3720	Sequence 3720, Ap
C 284	39.4	2.1	515	4	US-09-925-065A-540309	Sequence 540309,	C 357	38.8	2.0	1380	7	US-10-425-114-6261	Sequence 6261, Ap
C 285	39.4	2.1	549	4	US-09-925-065A-582894	Sequence 582894,	C 358	38.8	2.0	1750	7	US-10-425-114-9133	Sequence 9133, Ap
C 286	39.4	2.1	549	4	US-09-925-065A-582895	Sequence 582895,	C 359	38.8	2.0	1794	7	US-10-424-599-59974	Sequence 59974, A
C 287	39.4	2.1	549	4	US-09-925-065A-582896	Sequence 582896,	C 360	38.8	2.0	2000	3	US-09-938-842A-4130	Sequence 4130, Ap
C 288	39.4	2.1	552	4	US-09-925-065A-582897	Sequence 582897,	361	38.8	2.0	2000	3	US-09-938-842A-4130	Sequence 4130, Ap
C 289	39.4	2.1	552	4	US-09-925-065A-582900	Sequence 582900,	362	38.8	2.0	2139	7	US-10-437-963-42123	Sequence 42123, A
C 290	39.4	2.1	555	4	US-09-925-065A-582901	Sequence 582901,	363	38.8	2.0	6062	6	US-10-311-455-2051	Sequence 2051, Ap
C 291	39.4	2.1	555	4	US-09-925-065A-582902	Sequence 582902,	364	38.8	2.0	6070	7	US-10-311-455-214	Sequence 214, App
292	39.4	2.1	597	5	US-10-027-632-184929	Sequence 184929,	365	38.8	2.0	6070	7	US-10-240-589C-8	Sequence 8, Appli
293	39.4	2.1	597	6	US-10-027-632-184929	Sequence 184929,	C 366	38.8	2.0	6363	6	US-10-311-455-952	Sequence 952, App
294	39.4	2.1	6361	6	US-10-311-455-1113	Sequence 1113, Ap	367	38.8	2.0	7319	6	US-10-311-455-2017	Sequence 2017, Ap
C 295	39.4	2.1	6816	8	US-10-723-860-7676	Sequence 7676, Ap	368	38.8	2.0	9832	6	US-10-239-676-36	Sequence 629, App
C 296	39.4	2.1	9953	5	US-09-764-847-1336	Sequence 1336, Ap	369	38.8	2.0	12405	5	US-10-239-676-36	Sequence 629, App
C 297	39.4	2.1	9953	5	US-10-092-154-1336	Sequence 1336, Ap	370	38.8	2.0	12405	6	US-10-240-453-44	Sequence 44, Appl
C 298	39.4	2.1	11189	3	US-09-764-847-1335	Sequence 1335, Ap	371	38.8	2.0	12405	7	US-10-221-613-102	Sequence 102, App
C 299	39.4	2.1	11189	3	US-10-092-154-1335	Sequence 1335, Ap	372	38.8	2.0	15500	7	US-10-221-714A-329	Sequence 229, App
300	39.4	2.1	11996	6	US-10-240-485-46	Sequence 46, Appl	373	38.8	2.0	15674	6	US-10-311-455-335	Sequence 335, App
301	39.4	2.1	13131	7	US-10-240-589C-57	Sequence 57, Appl	374	38.8	2.0	15674	6	US-10-240-485-29	Sequence 29, Appl
C 302	39.4	2.1	518360	7	US-10-367-094-125	Sequence 125, App	375	38.8	2.0	15853	7	US-10-221-613-421	Sequence 421, App
C 303	39.4	2.1	653182	5	US-10-087-192-226	Sequence 226, App	376	38.8	2.0	56153	7	US-10-221-714A-519	Sequence 519, App
C 304	39.4	2.1	684187	7	US-10-367-094-71	Sequence 71, Appl	377	38.8	2.0	61020	8	US-10-221-714A-514	Sequence 514, App
C 305	39.2	2.0	589	5	US-10-027-632-251963	Sequence 251963,	378	38.8	2.0	81742	8	US-10-719-993-7045	Sequence 7045, Ap
C 306	39.2	2.0	589	5	US-10-027-632-251964	Sequence 251964,	C 379	38.8	2.0	3673778	6	US-10-312-841-2	Sequence 2, Appli
C 307	39.2	2.0	589	6	US-10-027-632-251963	Sequence 251963,	C 380	38.6	2.0	561	4	US-09-925-065A-625280	Sequence 625280,
C 308	39.2	2.0	589	6	US-10-027-632-251964	Sequence 251964,	C 381	38.6	2.0	568	4	US-09-925-065A-572524	Sequence 572524,
C 309	39.2	2.0	620	4	US-09-925-065A-616694	Sequence 616694,	C 382	38.6	2.0	587	4	US-09-925-065A-890247	Sequence 890247,
C 310	39.2	2.0	630	4	US-09-925-065A-607401	Sequence 607401,	C 383	38.6	2.0	632	4	US-09-925-065A-676498	Sequence 676498,
C 311	39.2	2.0	3716	8	US-10-473-126-352	Sequence 352, App	C 384	38.6	2.0	650	4	US-09-925-065A-911828	Sequence 911828,
312	39.2	2.0	5371	6	US-10-311-455-1159	Sequence 1159, Ap	C 385	38.6	2.0	685	2	US-08-927-939-76	Sequence 76, Appl
313	39.2	2.0	674	7	US-10-221-613-133	Sequence 133, App	386	38.6	2.0	1013	7	US-10-424-599-77007	Sequence 77007, A
314	39.2	2.0	13131	7	US-10-340-589C-58	Sequence 58, Appl	387	38.6	2.0	1378	5	US-10-027-632-177035	Sequence 177035,
315	39.2	2.0	16258	7	US-10-257-166-120	Sequence 120, App	388	38.6	2.0	1378	6	US-10-027-632-177035	Sequence 177035,

389	38.6	2.0	1627	5	US-10-027-632-256646	Sequence 256646,	462	38	2.0	517	7	US-10-021-323-11054	Sequence 11054, A
390	38.6	2.0	1627	6	US-10-027-632-256646	Sequence 256646,	463	38	2.0	525	3	US-09-796-692-9038	Sequence 9038, Ap
391	38.6	2.0	1714	5	US-10-027-632-261004	Sequence 261004,	464	38	2.0	525	5	US-10-040-862-9038	Sequence 9038, Ap
392	38.6	2.0	1714	6	US-10-027-632-261004	Sequence 261004,	465	38	2.0	525	6	US-10-057-475B-9038	Sequence 9038, Ap
393	38.6	2.0	1881	3	US-09-814-353-21495	Sequence 21495, A	466	38	2.0	525	6	US-10-154-884B-9038	Sequence 9038, Ap
394	38.6	2.0	4020	6	US-10-369-493-431172	Sequence 431172, A	467	38	2.0	525	8	US-10-764-324-9038	Sequence 9038, Ap
395	38.6	2.0	6050	6	US-10-311-455-1984	Sequence 1984, Ap	c 468	38	2.0	553	4	US-09-925-065A-829435	Sequence 829435
396	38.6	2.0	6291	6	US-10-311-455-2011	Sequence 2011, Ap	469	38	2.0	558	4	US-09-864-761-7880	Sequence 7880, Ap
397	38.6	2.0	6292	7	US-10-221-714A-521	Sequence 521, App	c 470	38	2.0	574	4	US-09-925-065A-812725	Sequence 812725,
398	38.6	2.0	6343	8	US-10-473-126-333	Sequence 333, App	471	38	2.0	589	4	US-09-925-065A-439914	Sequence 439914,
c 399	38.6	2.0	6478	6	US-10-311-455-471	Sequence 471, App	472	38	2.0	596	5	US-10-027-632-203802	Sequence 203802,
400	38.6	2.0	7353	6	US-10-311-455-46	Sequence 46, Appl	473	38	2.0	596	5	US-10-027-632-203803	Sequence 203803,
401	38.6	2.0	10328	6	US-10-311-455-1517	Sequence 1517, App	474	38	2.0	596	5	US-10-027-632-203804	Sequence 203804,
402	38.6	2.0	13420	6	US-10-311-455-890	Sequence 890, App	475	38	2.0	596	6	US-10-027-632-203802	Sequence 203802,
403	38.6	2.0	19734	6	US-10-311-455-1906	Sequence 1906, Ap	476	38	2.0	596	6	US-10-027-632-203804	Sequence 203804,
404	38.6	2.0	98439	8	US-10-741-600-17724	Sequence 17724, A	477	38	2.0	596	6	US-10-027-632-203804	Sequence 203804,
c 405	38.6	2.0	3673778	6	US-10-312-841-1	Sequence 1, Appli	c 478	38	2.0	600	9	US-10-972-079-65668	Sequence 65668, A
c 406	38.4	2.0	528	3	US-09-864-761-7592	Sequence 7592, Ap	479	38	2.0	753	8	US-10-767-795-5199	Sequence 5199, A
407	38.4	2.0	592	7	US-10-767-701-6040	Sequence 6040, Ap	480	38	2.0	883	4	US-09-925-065A-65787	Sequence 65787, A
c 408	38.4	2.0	602	4	US-09-925-065A-764444	Sequence 764444,	481	38	2.0	960	5	US-10-138-846-6381	Sequence 6381, Ap
c 409	38.4	2.0	656	4	US-09-925-065A-859141	Sequence 859141,	482	38	2.0	1193	5	US-10-027-632-203805	Sequence 203805,
c 410	38.4	2.0	657	4	US-09-925-065A-858971	Sequence 858971,	483	38	2.0	1193	6	US-10-027-632-203805	Sequence 203805,
c 411	38.4	2.0	877	4	US-09-925-065A-25978	Sequence 25978, A	c 484	38	2.0	1621	6	US-10-369-324-37	Sequence 37, Appl
412	38.4	2.0	972	8	US-10-357-930-4473	Sequence 4473, Ap	c 485	38	2.0	1621	7	US-10-607-538-37	Sequence 37, Appl
413	38.4	2.0	993	8	US-10-774-355A-772	Sequence 772, App	c 486	38	2.0	1621	9	US-10-505-079-37	Sequence 37, Appl
414	38.4	2.0	2739	7	US-10-433-793-206	Sequence 206, App	c 487	38	2.0	1866	4	US-09-925-065A-49427	Sequence 49427, A
c 415	38.4	2.0	5743	6	US-10-311-455-2041	Sequence 2041, Ap	c 488	38	2.0	1866	4	US-09-925-065A-54334	Sequence 54334, A
416	38.4	2.0	6130	7	US-10-221-613-373	Sequence 373, App	c 489	38	2.0	2386	10	US-11-097-143-31333	Sequence 31333, A
417	38.4	2.0	6130	7	US-10-221-714A-447	Sequence 447, App	c 490	38	2.0	2406	7	US-10-437-963-44929	Sequence 44929, A
418	38.4	2.0	19634	8	US-10-473-126-302	Sequence 302, App	c 491	38	2.0	2535	3	US-09-796-089-8	Sequence 8, Appli
c 419	38.4	2.0	50000	8	US-10-706-635-24	Sequence 24, Appl	c 492	38	2.0	2535	8	US-10-737-450-55	Sequence 55, Appl
c 420	38.4	2.0	96589	7	US-10-052-482-214	Sequence 214, App	c 493	38	2.0	3351	4	US-09-925-065A-70849	Sequence 70849, A
c 421	38.2	2.0	475	4	US-09-925-065A-278709	Sequence 278709,	c 494	38	2.0	3716	8	US-10-473-126-206	Sequence 206, App
c 422	38.2	2.0	475	4	US-09-925-065A-278710	Sequence 278710,	c 495	38	2.0	3856	7	US-10-751-014-4	Sequence 4, Appli
c 423	38.2	2.0	566	4	US-09-925-065A-278711	Sequence 278711,	c 496	38	2.0	4172	6	US-10-311-455-688	Sequence 688, App
c 424	38.2	2.0	601	4	US-09-925-065A-272169	Sequence 272169,	c 497	38	2.0	5882	6	US-10-311-455-518	Sequence 518, App
425	38.2	2.0	613	4	US-09-925-065A-731148	Sequence 731148,	c 498	38	2.0	5987	6	US-10-311-455-1536	Sequence 1536, Ap
426	38.2	2.0	613	4	US-09-925-065A-731149	Sequence 731149,	499	38	2.0	5987	7	US-10-433-793-132	Sequence 132, App
c 427	38.2	2.0	650	4	US-09-925-065A-887247	Sequence 887247,	500	38	2.0	6033	7	US-10-240-454-31	Sequence 31, Appl
c 428	38.2	2.0	656	4	US-09-925-065A-653774	Sequence 653774,							
c 429	38.2	2.0	1131	7	US-10-437-963-33755	Sequence 33755, A							
c 430	38.2	2.0	1330	9	US-10-956-157-281	Sequence 281, App							
431	38.2	2.0	1330	9	US-10-956-157-5516	Sequence 5516, Ap							
432	38.2	2.0	1345	5	US-10-027-632-124330	Sequence 124330,							
433	38.2	2.0	1345	5	US-10-027-632-124331	Sequence 124331,							
434	38.2	2.0	1345	6	US-10-027-632-124331	Sequence 124330,							
435	38.2	2.0	1345	6	US-10-027-632-124331	Sequence 124331,							
436	38.2	2.0	1372	7	US-10-425-114-24638	Sequence 24638, A							
c 437	38.2	2.0	1446	7	US-10-437-963-47464	Sequence 47464, A							
c 438	38.2	2.0	2029	5	US-10-027-632-264047	Sequence 264047,							
c 439	38.2	2.0	2029	6	US-10-027-632-264047	Sequence 264047,							
c 440	38.2	2.0	2217	7	US-10-437-963-63750	Sequence 63750, A							
441	38.2	2.0	2652	6	US-10-108-260A-356	Sequence 356, App							
442	38.2	2.0	2739	8	US-10-425-115-136011	Sequence 136011,							
443	38.2	2.0	5033	8	US-10-473-126-139	Sequence 139, App							
c 444	38.2	2.0	5286	6	US-10-311-455-324	Sequence 324, App							
c 445	38.2	2.0	5682	6	US-10-311-455-545	Sequence 545, App							
c 446	38.2	2.0	5822	6	US-10-240-485-53	Sequence 53, Appl							
447	38.2	2.0	5822	6	US-10-311-455-1070	Sequence 1070, Ap							
448	38.2	2.0	6311	6	US-10-311-455-1936	Sequence 1936, Ap							
449	38.2	2.0	7165	6	US-10-311-455-723	Sequence 723, App							
450	38.2	2.0	7631	6	US-10-311-455-833	Sequence 833, App							
451	38.2	2.0	8033	7	US-10-221-613-73	Sequence 73, Appl							
452	38.2	2.0	8033	7	US-10-221-714A-29	Sequence 29, Appl							
453	38.2	2.0	8634	6	US-10-311-455-1029	Sequence 1029, Ap							
454	38.2	2.0	9483	6	US-10-311-455-350	Sequence 350, App							
455	38.2	2.0	9483	7	US-10-221-613-48	Sequence 48, Appl							
c 456	38.2	2.0	18434	6	US-10-311-455-1980	Sequence 1980, Ap							
457	38.2	2.0	19659	6	US-10-311-455-740	Sequence 740, App							
458	38.2	2.0	32392	8	US-10-706-635-27	Sequence 27, Appl							
459	38.2	2.0	113515	6	US-10-311-455-2148	Sequence 2148, Ap							
c 460	38.2	2.0	1790242	8	US-10-719-993-6940	Sequence 6940, Ap							
c 461	38	2.0	402	4	US-09-925-065A-279607	Sequence 279607,							

ALIGNMENTS

RESULT 1

US-10-757-745-1

; Sequence 1, Application US/10757745

; Publication No. US20050101769A1

; GENERAL INFORMATION:

; APPLICANT: Vlaams Interuniversitair Instituut Voor Biotechnologie VZW

; TITLE OF INVENTION: CD-40 INTERACTING AND TRAF-INTERACTING PROTEINS

; FILE REFERENCE: 2676-4555US

; CURRENT APPLICATION NUMBER: US/10757,745

; PRIOR FILING DATE: 2004-01-15

; PRIOR APPLICATION NUMBER: US/09/697,863A

; PRIOR FILING DATE: 2000-10-27

; PRIOR APPLICATION NUMBER: PCT/EP99/03025

; PRIOR FILING DATE: 1999-04-28

; PRIOR APPLICATION NUMBER: EPO 98201392.2

; PRIOR FILING DATE: 1998-04-29

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 1920

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1627)..(1627)

; OTHER INFORMATION: N stands for any nucleotide.

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (20)..(1108)

OTHER INFORMATION:

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1849)..(1849)

OTHER INFORMATION: N stands for any nucleotide.

US-10-757-745-1

Query Match

Best Local Similarity 99.9%; Score 1918; DB 9; Length 1920;

Matches 1920; Conservative 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GTGCAGAGCGCGCAGGAAGATGAGTTGGGGAGTTGCCTGGAGGGCGGAGGAGCGGC	60
DB	1	GTGCAGAGCGCGCAGGAAGATGAGTTGGGGAGTTGCCTGGAGGGCGGAGGAGCGGC	60
QY	61	GGAGGAAGAGGGCGAGCCCTGAGGTGAAAAAGCGGCGACTTCTGTGTGTGGAGTTGCCTC	120
DB	61	GGAGGAAGAGGGCGAGCCCTGAGGTGAAAAAGCGGCGACTTCTGTGTGTGGAGTTGCCTC	120
QY	121	GGTCGCAAGCTGCGATGCCGAGTGGCTCAGTGTCTTCTGGCGGAGAACGACTGGGAGAT	180
DB	121	GGTCGCAAGCTGCGATGCCGAGTGGCTCAGTGTCTTCTGGCGGAGAACGACTGGGAGAT	180
QY	181	GGAAAGGGCTCTGAACTCTTCTTACCTTCGAGCCTCCGGTGGAGGAGCGCCTTGGAAAGCGCG	240
DB	181	GGAAAGGGCTCTGAACTCTTCTTACCTTCGAGCCTCCGGTGGAGGAGCGCCTTGGAAAGCGCG	240
QY	241	ACCTGAAACCATCTCTGAGCCCAAGACCTATGTGTAACCAATGAAGAAACAACTGA	300
DB	241	ACCTGAAACCATCTCTGAGCCCAAGACCTATGTGTAACCAATGAAGAAACAACTGA	300
QY	301	TTCCACACATCTTAAATTCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATGTT	360
DB	301	TTCCACACATCTTAAATTCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATGTT	360
QY	361	CTCTCTCATTACCTGGAAATTCATGATGATCTTAAACAAATCTGTGAGAGGGCTCG	420
DB	361	CTCTCTCATTACCTGGAAATTCATGATGATCTTAAACAAATCTGTGAGAGGGCTCG	420
QY	421	AGGGGTGTGTTCTTACTTGTGTACAGCCAGATGTGATATTTCTACAGGAAGTTAT	480
DB	421	AGGGGTGTGTTCTTACTTGTGTACAGCCAGATGTGATATTTCTACAGGAAGTTAT	480
QY	481	TCGCCCATATATATAGCTACTTAAAGAGAGATCAAGTAATTTAGATTTATACAGGTCA	540
DB	481	TCGCCCATATATATAGCTACTTAAAGAGAGATCAAGTAATTTAGATTTATACAGGTCA	540
QY	541	TGAAGAGGATATTTACAGCTATATGTTTGAAGAAATCAAGAGTGAATTTAAAGAGCCA	600
DB	541	TGAAGAGGATATTTACAGCTATATGTTTGAAGAAATCAAGAGTGAATTTAAAGAGCCA	600
QY	601	AGAGATTATTTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAA	660
DB	601	AGAGATTATTTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAA	660
QY	661	TGTGTACGAAATGAGCTTTGCTTATGATCATCCCATTTTGGAGAGCACCAGAGGGCATGC	720
DB	661	TGTGTACGAAATGAGCTTTGCTTATGATCATCCCATTTTGGAGAGCACCAGAGGGCATGC	720
QY	721	TGCGGAACGATGATCAAGTTAAATGTTTAAAGAAATCAAGAGTGAATTTAAAGAGCCA	780
DB	721	TGCGGAACGATGATCAAGTTAAATGTTTAAAGAAATCAAGAGTGAATTTAAAGAGCCA	780
QY	781	AGCTACAGTTATATTTTCAGGAGATCAAAATCTAAGGGATCGAGAGTTACCAAGATGTGG	840
DB	781	AGCTACAGTTATATTTTCAGGAGATCAAAATCTAAGGGATCGAGAGTTACCAAGATGTGG	840
QY	841	TGTTTACCCCAACAACTTGTGATGTCTGGAGTTTTCGGCAAAACCTTAAACATTTGCCA	900
DB	841	TGTTTACCCCAACAACTTGTGATGTCTGGAGTTTTCGGCAAAACCTTAAACATTTGCCA	900
QY	901	GTATACATGGGATACAAATGAACTCTAATCTTGGAAATCACTGCTGCTGTGTAACCTTCG	960

RESULT 2

US-09-981-353-88

; Sequence 88, Application US/09981353

; Patent No. US2002160382A1

; GENERAL INFORMATION:

; APPLICANT: Lasek, Amy W.

```
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981.353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 88
; LENGTH: 3152
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; FEATURE:
; OTHER INFORMATION: Incyte ID No. US20020160382A1 232992.1
; NAME/KEY: unsure
; LOCATION: 1171
; OTHER INFORMATION: a, t, c, g, or other
US-09-981-353-88

Query Match          99.4%; Score 1909; DB 3; Length 3152;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1912; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GTGCAGAGCGCGCAGGAAGATGGACTTCGGGAGTTGCTGGAGGCGCGGAGGGGCGG 60
Db 1233 GTGCAGAGCGCGCAGGAAGATGGAGTTGGGAGTTGCTGGAGGCGCGGAGGGGCGG 1292

Qy 61 GGAGGAAGAGGCGGAGCCTCGAGGTGAAAGCGGCGACTTCGTGTGTGGAGTTTGCC 120
Db 1293 GGAGGAAGAGGCGGAGCCTCGAGGTGAAAGCGGCGACTTCGTGTGTGGAGTTTGCC 1352

Qy 121 GGTGCGAAGCTGCGATGCGGAGTGGCTCAGTGGCTTCCTGCGCGGAGAACGAT 180
Db 1353 GGTGCGAAGCTGCGATGCGGAGTGGCTCAGTGGCTTCCTGCGCGGAGAACGAT 1412

Qy 181 GGAAAGGCTCTGAACTCTCTTCGAGCCTCCGGTGGAGGAGAGCGCTTTGGAAAGCGCG 240
Db 1413 GGAAAGGCTCTGAACTCTCTTCGAGCCTCCGGTGGAGGAGAGCGCTTTGGAAAGCGCG 1472

Qy 241 ACCTGAAACCACTCTCGAGCCCAAGACCTATGTTGACCTAAACCAATGAAGAAACAACTGA 300
Db 1473 ACCTGAAACCACTCTCGAGCCCAAGACCTATGTTGACCTAAACCAATGAAGAAACAACTGA 1532

Qy 301 TTCACCACTTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGCAGATGTT 360
Db 1533 TTCACCACTTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGCAGATGTT 1592

Qy 361 CTCTCTCATTTACCTGGAATATTGATGGATTAGATCTAAACCAATCTGTCAGAGAGGGCTCG 420
Db 1593 CTCTCTCATTTACCTGGAATATTGATGGATTAGATCTAAACCAATCTGTCAGAGAGGGCTCG 1652

Qy 421 AGGGGTGTGTTCTCTACTTTAGCTTTGTACAGCCCGAGATGTGATATTCTACAGGAAGTTAT 480
Db 1653 AGGGGTGTGTTCTCTACTTTAGCTTTGTACAGCCCGAGATGTGATATTCTACAGGAAGTTAT 1712

Qy 481 TCCCCCATATTATAGCTACCTAAAGAGAGATCAAGTAATTATGAGATTTATCAGGTCA 540
Db 1713 TCCCCCATATTATAGCTACCTAAAGAGAGATCAAGTAATTATGAGATTTATCAGGTCA 1772

Qy 541 TGAAGAAGGATATTTACAGCTATATAATGTTGAAGAAATCAAGAGTGAATTTAAAGGCA 600
Db 1773 TGAAGAAGGATATTTACAGCTATATAATGTTGAAGAAATCAAGAGTGAATTTAAAGGCA 1832

Qy 601 AGAGATTTCTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTGAA 660
Db 1833 AGAGATTTCTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTGAA 1892

Qy 661 TGTGTCAGAAATGAGCTTTGCTTTATGACATCCCATTTGGAGACCACAGAGGCGATGC 720
Db 1893 TGTGTCAGAAATGAGCTTTGCTTTATGACATCCCATTTGGAGACCACAGAGGCGATGC 1952

Qy 721 TGCAGAACGAATGAATCAGTTTAAATGTTTAAAGAAATGCAAGAGGCTCCAGAGTGC 780
Db 721 TGCAGAACGAATGAATCAGTTTAAATGTTTAAAGAAATGCAAGAGGCTCCAGAGTGC 3092
```

QY 1861 CTTTAAAGAAATATTTTCCCCACAGAGAAATTTAAATAAAGAAATTTTATTGGTAA 1919
Db |||||
3093 CTTTAAAGAAATATTTTCCCCACAGAGAAATTTAAATAAAGAAATTTTATTGGTTA 3151
Db |||||

RESULT 3
US-10-783-271-28
; Sequence 28, Application US/10783271
; Publication No. US20050186577A1
; GENERAL INFORMATION:
; APPLICANT: Veridex, LLC
; APPLICANT: Wang, Yixin
; TITLE OF INVENTION: BREAST CANCER PROGNOSTICS
; FILE REFERENCE: VDX-5003 USNP
; CURRENT APPLICATION NUMBER: US/10/783,271
; CURRENT FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 1940
; TYPE: DNA
; ORGANISM: human
US-10-783-271-28

Query Match 99.2%; Score 1905.2; DB 9; Length 1940;
Best Local Similarity 99.5%; Pred. No. 0; Mismatches 10; Indels 0; Gaps 0;
Matches 1910; Conservative 0; Gaps 0;
QY 1 GTGCAGAGCGGCGAGCAAGATGGAGTTGGGGAGTTGCCCTGGAGGGCGGAGGAGCGGC 60
Db |||||
7 GTGCAGAGCGGCGAGCAAGATGGAGTTGGGGAGTTGCCCTGGAGGGCGGAGGAGCGGC 66
QY 61 GGAGGAAGAGGGCGAGCGCTGAGGTGAAAGAGCGGCGACTTCTGTGTGTGGAGTTGCCTC 120
Db |||||
67 GGAGGAAGAGGGCGAGCGCTGAGGTGAAAGAGCGGCGACTTCTGTGTGTGGAGTTGCCTC 126
QY 121 GGTGCGAAGTGGGATGCGCGAGTGGCTCAGTGTCTTCTGGCGGAGAACGACTGGGAGAT 180
Db |||||
127 GGTGCGAAGTGGGATGCGCGAGTGGCTCAGTGTCTTCTGGCGGAGAACGACTGGGAGAT 186
QY 181 GGAAAGGGCTCTGAACTCTTACCTTCGAGCGCTCGGTGGAGGAGCGCTTGGAAAGCGCG 240
Db |||||
187 GGAAAGGGCTCTGAACTCTTACCTTCGAGCGCTCGGTGGAGGAGCGCTTGGAAAGCGCG 246
QY 241 ACCTGAAACCATCTCTGAGCGGCAAGACCTATGTGTGACCTAAACCAATGAAGAAACAAC 300
Db |||||
247 ACCTGAAACCATCTCTGAGCGGCAAGACCTATGTGTGACCTAAACCAATGAAGAAACAAC 306
QY 301 TTCACCACTTTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATGTT 360
Db |||||
307 TTCACCACTTTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATGTT 366
QY 361 CTCTCTACCTTACCTGGAATTTGATGATAGATCTAAACAACTCTGTGAGAGGGCTCG 420
Db |||||
367 CTCTCTACCTTACCTGGAATTTGATGATAGATCTAAACAACTCTGTGAGAGGGCTCG 426
QY 421 AGGGGTGTGTTCTCTACTTGTGTACAGCCCGAGATGTGATATTTCTACAGGAATTTAT 480
Db |||||
427 AGGGGTGTGTTCTCTACTTGTGTACAGCCCGAGATGTGATATTTCTACAGGAATTTAT 486
QY 481 TCCCCCATATTTAGCTTACCTTAAAGAGAGATCAAGTAATTTATGAGATTTATACAGGTCA 540
Db |||||
487 TCCCCCATATTTAGCTTACCTTAAAGAGAGATCAAGTAATTTATGAGATTTATACAGGTCA 546
QY 541 TGAAGAGGATATTTTACAGCTTAATGTTTGAAGAAATCAAGAGTGAATTTAAAGAGCCCA 600
Db |||||
547 TGAAGAGGATATTTTACAGCTTAATGTTTGAAGAAATCAAGAGTGAATTTAAAGAGCCCA 606
QY 601 AGAGATTATTTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAA 660
Db |||||
607 AGAGATTATTTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAA 666

QY 661 TGCTCAGGAAATGAGGCTTTGCCCTTATGCAATCCCATTTGGAGAGCACACAGAGGCATGC 720
Db |||||
667 CGTGTCAAGAAATGAGCTTTGCCCTTATGCAATCCCATTTGGAGAGCACACAGAGGCATGC 726
QY 721 TGCGGAACGAATGAATCAGTTTAAAGTGTGTTTAAAGAAATGCAAGAGGCTCCAGAGTC 780
Db |||||
727 TGCGGAACGAATGAATCAGTTTAAAGTGTGTTTAAAGAAATGCAAGAGGCTCCAGAGTC 786
QY 781 AGCTACAGTTTATTTGAGGAGATACAAATCTTAAGGATCGAGAGGTTACAGATGTGG 840
Db |||||
787 AGCTACAGTTTATTTGAGGAGATACAAATCTTAAGGATCGAGAGGTTACAGATGTGG 846
QY 841 TGGTTTACCACCAACATTTGGATGCTGGAGTTTTTGGGCAACCTTAACATTTGCCA 900
Db |||||
847 TGGTTTACCACCAACATTTGGATGCTGGAGTTTTTGGGCAACCTTAACATTTGCCA 906
QY 901 GTATACATGGGATACACAAATGAACTCTTAATCTTGGAAATAACTGCTGTGTTAAACTTCG 960
Db |||||
907 GTATACATGGGATACACAAATGAACTCTTAATCTTGGAAATAACTGCTGTGTTAAACTTCG 966
QY 961 TTTTGATCGAATATTTTTCAGAGCAGCAGAGAGGAGACACATTTATTTCCCGAAGTTT 1020
Db |||||
967 TTTTGATCGAATATTTTTCAGAGCAGCAGAGAGGAGACACATTTATTTCCCGAAGTTT 1026
QY 1021 GGACCTTCTTGGATTTAGAAAACTCGACTGTGGTATAGATTTCTTAGTGATCACTGGGCTC 1080
Db |||||
1027 GGACCTTCTTGGATTTAGAAAACTCGACTGTGGTATAGATTTCTTAGTGATCACTGGGCTC 1086
QY 1081 TCTGTGCAACTTAGATATATAATTTCTGAAATGCTTTTCAAGTGTGGTTTTTCCCTGATT 1140
Db |||||
1087 TCTGTGCAACTTAGATATATAATTTCTGAAATGCTTTTCAAGTGTGGTTTTTCCCTGATT 1146
QY 1141 GTTGCAAAATACAAATTTCCACCTTCTGGAAAGTAGTGTGCTGTGGAGGAAATTAATGTAC 1200
Db |||||
1147 GTTGCAAAATACAAATTTCCACCTTCTGGAAAGTAGTGTGCTGTGGAGGAAATTAATGTAC 1206
QY 1201 TAGATCATTTGTCAAGAAAAACCAATATGATTTATGTTGTTTTTCAAGATTTCAACAT 1260
Db |||||
1207 TAGATCATTTGTCAAGAAAAACCAATATGATTTATGTTGTTTTTCAAGATTTCAACAT 1266
QY 1261 TAAAGATTAATGTTTTTAAACGACACATTTCTGCAATTCAGGATGTCAGGCAATTTAA 1320
Db |||||
1267 TAAAGATTAATGTTTTTAAACGACACATTTCTGCAATTCAGGATGTCAGGCAATTTAA 1326
QY 1321 TAAAGAGGCAACAAAGCCTGTGAGAGTTTCAACGCTGTACAGCTGCCAGCTGATTTC 1380
Db |||||
1327 TAAAGAGGCAACAAAGCCTGTGAGAGTTTCAACGCTGTATAGCTGCCAGCTGATTTC 1386
QY 1381 CAAACAGGTAACCCCATTTGCTCTGAGCTAATGTTTATATTTTCCATTCAAGCACCAGAA 1440
Db |||||
1387 CAAACAGGTAACCCCATTTGCTCTGAGCTAATGTTTATATTTTCCATTCAAGCACCAGAA 1446
QY 1441 TAGTTAATATTTTAAATAAGTCTTCAAGAAAAACATAAGAGATTTATGAGTTCTTTGGGA 1500
Db |||||
1447 TAGTTAATATTTTAAATAAGTCTTCAAGAAAAACATAAGAGATTTATGAGTTCTTTGGGA 1506
QY 1501 CTGGATCCTTTATTTTCAATAGTTTCAATCATCTTAATGAAATGCAATGATTTATCTGCA 1560
Db |||||
1507 CTGGATCCTTTATTTTCAATAGTTTCAATCATCTTAATGAAATGCAATGATTTATCTGCA 1566
QY 1561 GTTAAGTAGATGACAGCTATTCTTACATCAGACTTGAATTTTGTGACCTAATTAATAAT 1620
Db |||||
1567 GTTAAGTAGATGACAGCTATTCTTACATCAGACTTGAATTTTGTGACCTAATTAATAAT 1626
QY 1621 GGTAAAGTAAATTTGAAACCTTATGGCTTAAATTTCTTAACTCCCTTTTGTATCATGTT 1680
Db |||||
1627 GGTAAAGTAAATTTGAAACCTTATGGCTTAAATTTCTTAACTCCCTTTTGTATCATGTT 1686
QY 1681 TGTAGTTCATGTTGTCAACAGAGCAAGTTTAAAGTGTGATGTTGTTTAAATCGGTTTGTAT 1740
Db |||||
1687 TGTAGTTCATGTTGTCAACAGAGCAAGTTTAAAGTGTGATGTTTAAATCGGTTTGTAT 1746
QY 1741 AGCACCATGGGACATTTTTTTTAAACAAAAATAAATGCATGAAGAGACATAGCCTTTTAGTT 1800

Db 1747 AGCACCATTGGGACATTTTCTTAACAAATAATATGTCATGAAGAGACATAGCCTTTTAGTT 1806
Qy 1801 TTGCTAAATTGTGAATGGAATGCTTTTACAGGAAGTAAATGCAAAATTANTTTTAAAGTGTG 1860
Db 1807 TTGCTAAATTGTGAATGGAATGCTTTTACAGGAAGTAAATGCAAAATTACTTTTAAAGTGTG 1866
Qy 1861 CTTTAAAGAAAAATATTTTCCCCACAGAGAAATTTAAATAAAGAAATTTTATTTGGTAAA 1920
Db 1867 CTTTAAAGAAAAATATTTTCCCCACAGAGAAATTTAAATAAAGAAATTTTATTTGTTTAA 1926

RESULT 4

US-10-037-270-889
; Sequence 889, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghaast, John
; APPLICANT: Drmanac, Radolje T.
; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 889
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(1127)
US-10-037-270-889

Query Match 98.8%; Score 1897.6; DB 5; Length 1948;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1900; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 15 GGAAGATGGAGTTGGGAGTTGCCCTGGAGGCGGAGGAGGCGGCGGAGGAAGAGGCG 74
Db 34 GGAAGATGGAGTTGGGAGTTGCCCTGGAGGCGGAGGAGGCGGCGGAGGAAGAGGCG 93
Qy 75 AGCCTGAGGTGAAAAAGCGGCGACTTCTGTGTGTGGAGTTTGCCTCGGTGCGCAAGCTGCG 134
Db 94 AGCCTGAGGTGAAAAAGCGGCGACTTCTGTGTGTGGAGTTTGCCTCGGTGCGCAAGCTGCG 153
Qy 135 ATGCCGAGTGGCTCAGTGTCTTCGCGCGAGAACGACGTGGAGATGGAAGGGCTCTGA 194
Db 154 ATGCCGAGTGGCTCAGTGTCTTCGCGCGAGAACGACGTGGAGATGGAAGGGCTCTGA 213
Qy 195 ACTCTCTACTTCGAGCTCCGGTGGAGGAGGCGCTTGGAAAGCGGCGCTGGAACCATCT 254
Db 214 ACTCTCTACTTCGAGCTCCGGTGGAGGAGGCGCTTGGAAAGCGGCGCTGGAACCATCT 273

Qy 255 CTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACTGATTCCACCACTTCTA 314
Db 274 CTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACTGATTCCACCACTTCTA 333
Qy 315 AAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGCATGTTCTCTCTCATTAACCT 374
Db 334 AAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGCATGTTCTCTCTCATTAACCT 393
Qy 375 GGAATATTGATGATAGATCTTAAACAAATCTGTCTCAGAGAGGCTCGAGGGGTGTGTTCT 434
Db 394 GGAATATTGATGATAGATCTTAAACAAATCTGTCTCAGAGAGGCTCGAGGGGTGTGTTCT 453
Qy 435 ACTTAGCTTTGTACAGCCCGAGATGTGATATTTCTACAGGAAGTTATTTCCCCCATATTATA 494
Db 454 ACTTAGCTTTGTACAGCCCGAGATGTGATATTTCTACAGGAAGTTATTTCCCCCATATTATA 513
Qy 495 GCTACCTAAAGAAAGAGATCAAGTAATTTATGAGATTTATTACAGGTCATGAAGAGATATT 554
Db 514 GCTACCTAAAGAAAGAGATCAAGTAATTTATGAGATTTATTACAGGTCATGAAGAGATATT 573
Qy 555 TCACAGCTATAATTGTTGAAGAAATCAAGAGTGAAATTTAAAGCCAAAGAGATTTTCTCTT 614
Db 574 TCACAGCTATAATTGTTGAAGAAATCAAGAGTGAAATTTAAAGCCAAAGAGATTTTCTCTT 633
Qy 615 TTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCATGTGAATGTGTGAGAAATG 674
Db 634 TTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCATGTGAATGTGTGAGAAATG 693
Qy 675 AGCTTTGCCCTTATGACATCCCATTTGGAGAGCACAGAGGGGCATGTCGCGAAACGAATGA 734
Db 694 AGCTTTGCCCTTATGACATCCCATTTGGAGAGCACAGAGGGGCATGTCGCGAAACGAATGA 753
Qy 735 ATCAGTTAAAAATGCTTTTAAAGAAATGCAAGAGGCTCCAGAGTCAGCTACAGTTATAT 794
Db 754 ATCAGTTAAAAATGCTTTTAAAGAAATGCAAGAGGCTCCAGAGTCAGCTACAGTTATAT 813
Qy 795 TTGAGAGAGATACAAATCTAAGGATCGAGAGGTACAGATGTGGTGTGTTTACCCACAA 854
Db 814 TTGAGAGAGATACAAATCTAAGGATCGAGAGGTACAGATGTGGTGTGTTTACCCACAA 873
Qy 855 ACATTGTGGATGCTGGGAGTTTTTGGGCAAACTTAAACATTTGCCAGTATACATGGGATA 914
Db 874 ACATTGTGGATGCTGGGAGTTTTTGGGCAAACTTAAACATTTGCCAGTATACATGGGATA 933
Qy 915 CACAAATGAACTCTAAATCTTGGAAATACTGCTGCTGTGTAACCTTCGTTTTGATCGAATAT 974
Db 934 CACAAATGAACTCTAAATCTTGGAAATACTGCTGCTGTGTAACCTTCGTTTTGATCGAATAT 993
Qy 975 TTTTCAGAGCAGCAGAGAGAGGAGGACACATTTATCCCGAAAGTTTGGACCTTCTTGAT 1034
Db 994 TTTTCAGAGCAGCAGAGAGAGGAGGACACATTTATCCCGAAAGTTTGGACCTTCTTGAT 1053
Qy 1035 TAGAAAAAATCGGACTGTGGTAGATTTCTAGTGTACTCTGGGGTCTTCTGTGCAACTTAG 1094
Db 1054 TAGAAAAAATCGGACTGTGGTAGATTTCTAGTGTACTCTGGGGTCTTCTGTGCAACTTAG 1113
Qy 1095 ATATAATATTGTAATAATGCTTTTCAAGTGTGGTTTTTGCCTGTGATGTTGTGCAAAATACAAT 1154
Db 1114 ATATAATATTGTAATAATGCTTTTCAAGTGTGGTTTTTGCCTGTGATGTTGTGCAAAATACAAT 1173
Qy 1155 TTCCACCTTCTGGAAAGGTAGGTTTGTGTGGAGGAAATAATGTACTAGATCATTTGTGCAC 1214
Db 1174 TTCCACCTTCTGGAAAGGTAGGTTTGTGTGGAGGAAATAATGTACTAGATCATTTGTGCAC 1233
Qy 1215 AGAAAAACCAACTATGATTTATGTTGTTTTCAGAAATTCAACTTAAAGATTAAATGTT 1274
Db 1234 AGAAAAACCAACTATGATTTATGTTGTTTTCAGAAATTCAACTTAAAGATTAAATGTT 1293
Qy 1275 TATTTAAACGAACACATTTCTGCAATTCAGGATGTGAGGCCATTTTAAATAAAGGGCACA 1334
Db 1294 TATTTAAACGAACACATTTCTGCAATTCAGGATGTGAGGCCATTTTAAATAAAGGGCACA 1353

QY 1335 AGCCTGTGACAGTCTTTCAACGGTGTCTTACAGCTGCAGCTGCAGTCTCCAAACAGAGTACCCC 1394
DB 1354 AGCCTGTGACAGTCTTTCAACGGTGTCTTATAGCTGCAGCTGCAGTCTCCAAACAGAGTACCCC 1413
QY 1395 ATTGTCTCTGACGTAATGTTTATATTTTCCATTCAGGCACCGAAATAGTTAATATTTAA 1454
DB 1414 ATTGTCTCTGACGTAATGTTTATATTTTCCATTCAGGCACCGAAATAGTTAATATTTAA 1473
QY 1455 AATAAGTCTTCAAAAGAAACATATAGAGTATTTAGTCTTTGGGACTGGAATCCTTTATT 1514
DB 1474 AATAAGTCTTCAAAAGAAACATATAGAGTATTTAGTCTTTGGGACTGGAATCCTTTATT 1533
QY 1515 TCATAAGTTCAGATCATCTTAATGAAATGCCATGATTATCTGCAGTTAAGTAGATGAC 1574
DB 1534 TCATAAGTTCAGATCATCTTAATGAAATGCCATGATTATCTGCAGTTAAGTAGATGAC 1593
QY 1575 AGCTATTCTACATCAGACTTGATTTTGTGACGTAATACATAAATGGTAAGNTATAATT 1634
DB 1594 AGCTATTCTACATCAGACTTGATTTTGTGACGTAATACATAAATGGTAAGCTATAATT 1653
QY 1635 GAAACCTTATGGCTTAAATTCCTTAACTCCTTTTGGATTCATGTTGTAGTCATGTTGT 1694
DB 1654 GAAACCTTATGGCTTAAATTCCTTAACTCCTTTTGGATTCATGTTGTAGTCATGTTGT 1713
QY 1695 CAACAGAGCAAGTTAAGCTGATGATGTTTAAATCGTTTGTAGCACCATGGGACA 1754
DB 1714 CAACAGAGCAAGTTAAGCTGATGATGTTTAAATCGTTTGTAGCACCATGGGACA 1773
QY 1755 TTTTCTTAAACAAATTAATGCAATGAAGAGACATAGCCTTTTGTATGTTTCTAATGTGAA 1814
DB 1774 TTTTCTTAAACAAATTAATGCAATGAAGAGACATAGCCTTTTGTATGTTTCTAATGTGAA 1833
QY 1815 ATGAAATGCTTTACAGGAAGTAAATGCAATTAATTTTAAAGTGCTTTTAAAGAAAT 1874
DB 1834 ATGAAATGCTTTACAGGAAGTAAATGCAATTAATTTTAAAGTGCTTTTAAAGAAAT 1893
QY 1875 ATTTTCCCAACAGAGAAATTTAAATAAAGAAATTTTATTTGGTAAA 1920
DB 1894 ATTTTCCCAACAGAGAAATTTAAATAAAGAAATTTTATTTGTTAAA 1939

RESULT 5

US-10-117-722-889
; Sequence 889, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2BCIP
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt FL_genes Version 1.0
; SEQ ID NO 889
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39) .. (1127)

US-10-117-722-889

Query Match 98.8%; Score 1897.6; DB 6; Length 1948;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1900; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 15 GGAAGATGAGTTCGGGAGTTCCTTGGAGGGCGGAGGAGGCGGAGGAGGCGG 74
DB 34 GGAAGATGAGTTCGGGAGTTCCTTGGAGGGCGGAGGAGGCGGAGGAGGCGG 93
QY 75 AGCCTGAGTGAAGGAGGCGGAGCTTCTGTGTGTGAGAGTTCCTTCGTCGCAAGTCGG 134
DB 94 AGCCTGAGTGAAGGAGGCGGAGCTTCTGTGTGTGAGAGTTCCTTCGTCGCAAGTCGG 153
QY 135 ATGCGCGAGTGGCTCAGTCTTCCTGCGCGAGAACGACTGGGAGATGGAAGGGCTCTGA 194
DB 154 ATGCGCGAGTGGCTCAGTCTTCCTGCGCGAGAACGACTGGGAGATGGAAGGGCTCTGA 213
QY 195 ACTCTTACTTCGAGCCTCCGGTGGAGGAGAGGCGCTTGGAAAGCGGAGCTGAAACCATCT 254
DB 214 ACTCTTACTTCGAGCCTCCGGTGGAGGAGAGGCGCTTGGAAAGCGGAGCTGAAACCATCT 273
QY 255 CTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAACTGATTCCACCTTCTA 314
DB 274 CTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAACTGATTCCACCTTCTA 333
QY 315 AAATCAGCCCATCTCAGAGATCTCAGCAAGAAATGGCAGCATGTTCTCTCATTTACCT 374
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QY 375 GGAATATTGATGATTTAGATCTTAAACATCTGTCHAGAGAGGCTCGAGGGGTGTTCCT 434
DB 394 GGAATATTGATGATTTAGATCTTAAACATCTGTCHAGAGAGGCTCGAGGGGTGTTCCT 453
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DB 454 ACTTAGCTTTGACAGCCAGATGTGATATTTCTACAGGAAGTTATTCCTCCCATATTATA 513
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DB 514 GCTTACTAAAGAGAGATCAAGTAATATTAGATTTATTACAGGTCTATGAAGAGGATATT 573
QY 555 TCACAGCTAATATTGTAAGAAATCAAGAGTGAATTTAAAGCCCAAGAGATTTTCCTT 614
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QY 615 TTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAATGTGTACGGAATG 674
DB 634 TTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAATGTGTACGGAATG 693
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DB 694 AGCTTTGCTTATGACATCCCATTTGGAGAGCACAGAGGCGCATGCTGCGGAACGATGA 753
QY 735 ATCAGTTAAATATGGTTTAAAGAAATGCAAGAGCTCCAGAGTCCAGGTACAGTTATAT 794
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DB 934 CACAAATGAATCTAATCTTGGATTAATCTGCTGCTGTTAACTTCGTTTTGATCGAATAT 993
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Qy 1155 TTCCACCTTCTGGAAGTAGTGTGCTGTGGAGGAATAATGTACTAGATCATGTGCAC 1214
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Qy 1515 TCATAAGTTCAGATCATCTTAAATGAAATGCCATGATTAATCTGAGCTTAAGTAGATGAC 1574
Db 1534 TCATAAGTTCAGATCATCTTAAATGAAATGCCATGATTAATCTGAGCTTAAGTAGATGAC 1593
Qy 1575 AGCTATTCTACATCAGACTTGATTTTGTGCTAGCTAAATFACATAATTTGTAAGNTATAATT 1634
Db 1594 AGCTATTCTACATCAGACTTGATTTTGTGCTAGCTAAATFACATAATTTGTAAGNTATAATT 1653
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Qy 1695 CAACAGAGGCAAGTTAAGCTTGATGTTTAAATCGGTTTGTATGACCACCATGGGACA 1754
Db 1714 CAACAGAGGCAAGTTAAGCTTGATGTTTAAATCGGTTTGTATGACCACCATGGGACA 1773
Qy 1755 TTTTCTTAAACAAAAATAAATGCATGACAGACATAGCCCTTTTGTGTTTGTCTAAATTTGTGAA 1814
Db 1774 TTTTCTTAAACAAAAATAAATGCATGACAGACATAGCCCTTTTGTGTTTGTCTAAATTTGTGAA 1833
Qy 1815 ATGGAATGCTTTTACAGGAAGTAAATGCAATTTAAGTGTGCTTTTAAAGAAAAAT 1874
Db 1834 ATGGAATGCTTTTACAGGAAGTAAATGCAATTTAAGTGTGCTTTTAAAGAAAAAT 1893
Qy 1875 ATTTTCCCAACAGAGAAAATTTAAATAAGAAATTTTATTTGGTAAA 1920
Db 1894 ATTTTCCCAACAGAGAAAATTTAAATAAGAAATTTTATTTGTAAA 1939
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RESULT 6
US-10-122-851-889
; Sequence 889, Application US/10122851
; Publication No. US20050239060A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2BDV3

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; CURRENT APPLICATION NUMBER: US/10/122,851  
; CURRENT FILING DATE: 2002-04-12  
; PRIOR APPLICATION NUMBER: 09/620,312  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1104  
; SOFTWARE: pt_FL_genes Version 1.0  
; SEQ ID NO 889  
; LENGTH: 1948  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (39)..(1127)  
US-10-122-851-889
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Query Match 98.8%; Score 1897.6; DB 9; Length 1948;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1900; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 15 GGAAGATGGAGTTGGGAGATTGCTCGAGGCGGAGGCGGCGAGGAGGCGGAGGAGGCGG 74  
Db 34 GGAAGATGGAGTTGGGAGATTGCTCGAGGCGGAGGCGGCGGAGGAGGCGGAGGAGGCGG 93  
Qy 75 AGCCTGAGGTGAAAAAGCGCGACTTCTGTGTGTGGAGTTTGCCTCGGTGCGAAAGCTGCG 134  
Db 94 AGCCTGAGGTGAAAAAGCGCGACTTCTGTGTGTGGAGTTTGCCTCGGTGCGAAAGCTGCG 153  
Qy 135 ATGCGCGAGTGGCTCAGTGTCTTCTGCGCAGAGAACGATCGGAGATGGAAGGGCTCTGA 194  
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Qy 195 ACTCTCACTTTCGAGCCTCCGCTGGAGGAGAGCGCTTTGGAAACGCCGACCTGAAACCATCT 254  
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Db 334 AAATCAGCCCATCTGAAGATACCTCAGCAAGAAAAATGCGAGCATGTTCTCTCTCATTAACCT 393  
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Db 454 ACTTAGCTTTGTACAGCCCGAGATGTGATATTTCTACAGGAAGTTATTTCCCCCATATTATA 513  
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Db 634 TTCCAAGTACAAAATGATGAGAAACCTTTTATGTGTGATGTGAATGTGTGAGAAATG 693  
Qy 675 AGCTTTGCCCTTATGACATCCCATTTGGAGAGCACCGAGGGCATGCTCGCGAAACGAATGA 734  
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Db 754 ATCAGTAAATGCTTTTAAAGAAATGCAAGAGGCTCCAGAGTCAGCTACAGTTATAT 813
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QY 1455 AATAAGTCTTCAAAAGAAACATAAGAGATTTATGAGTTCTTGGGACTGGATCCTTTAT 1514
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Db 1534 TCATAAGTTTCAGATCATCTTAAATGAAATGCAATGATTTATCTGCAATTAAGTAGATGAC 1593
QY 1575 AGCTATTTACATCAGACTGATTTTGTGAGCTAATTAATTAATTTGGTAAGNTAAT 1634
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Db 1714 CAACAGAGGCAAGTTAAGCTTGAATGATGTTTAAATTCGGTTTGTAGTACCAATGGGACA 1773
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Db 1774 TTTTAAACAAAATTAATGCAATGAGACATAGCTTTTATGTTTGTCTAATTTGTGAA 1833
QY 1815 ATGAAATGCTTTTACAGAAATGAAATGCAATTTAATTTAAGTGTGCTTTTAAAGAAAAAT 1874
Db 1834 ATGAAATGCTTTTACAGAAATGAAATGCAATTTAATTTAAGTGTGCTTTTAAAGAAAAAT 1893

QY 1875 ATTTTCCCAACAGAGAAATTTAAATAAAGAAATTTTATTTGGTAAA 1920
Db 1894 ATTTTCCCAACAGAGAAATTTAAATAAAGAAATTTTATTTGTTAAA 1939

RESULT 7
US-09-925-299-170
; Sequence 170, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCY/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 170
; LENGTH: 1296
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1261)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1276)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-170

Query Match 64.9%; Score 1246.2; DB 3; Length 1296;
Best Local Similarity 99.4%; Pred. No. 9.8e-304;
Matches 1242; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCAGAGGCGGACAGAGATCGAGTTGGGAGTTGCCCTGGAGGGCGGAGGAGGCGGC 60
Db 5 GTGCAGAGGCGGACAGAGATCGAGTTGGGAGTTGCCCTGGAGGGCGGAGGAGGCGGC 64
QY 61 CGAGGAAGAGGCGGAGCCCTGAGGTGAAAAGCGGCGACTTCTGTGTGAGGTTCCCTC 120
Db 65 GAGGAGAGGCGGAGCCCTGAGGTGAAAAGCGGCGACTTCTGTGTGAGGTTCCCTC 124
QY 121 GGTCCGCAAGCTCGGATGCCGACAGTGGCTCAGTGTCTTCTGCGCGAGAACGACTGGGAGAT 180
Db 125 GGTCCGCAAGCTCGGATGCCGACAGTGGCTCAGTGTCTTCTGCGCGAGAACGACTGGGAGAT 184
QY 181 GGAAGGGGCTCTGAATCTCTACTTTCGAGCCCTCCGGTGGAGGAGAGCGCTTGGAAACGCCG 240
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Db 245 ACCTGAACCACTCTCTGAGCCCAAGACCTATGTGACCTAAACCAATGAAGAAACAACTGA 304
QY 301 TTCCACCACTTCTAAATCAGCCCATCTGAAAGATCTCAGCAAGAAATGGCAGCATGTT 360
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Db 425 AGGGGTGTCTTCTACTTCTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTAT 484
QY 481 TCCTCCCATATTTAGCTTACCTAAAGAGAGATCAAGTAATTTATGAGATTTATACAGGTCA 540

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RESULT 8

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US-09-925-299-170
; Sequence 170, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US/09/925,299
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 170
; LENGTH: 1296
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (1261)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1276)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-170

Query Match 64.9%; Score 1246.2; DB 3; Length 1296;
Best Local Similarity 99.4%; Pred. No. 9.8e-304;
Matches 1242; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCAGAGGGCGGAGGAGATGGAGTTTGGGAGTTGCTGTGAGGGCGGAGGGAGGGCGGC 60
Db 5 GTGCAGAGGGCGGAGGAGATGGAGTTTGGGAGTTGCTGTGAGGGCGGAGGGAGGGCGGC 64
Qy 61 GGAGGAAGAGGGCGAGCCTGAGGTGAAAAAGCGCGCATCTTGTGTGTGGAGTTTGCTTC 120
Db 65 GGAGGAAGAGGGCGAGCCTGAGGTGAAAAAGCGCGCATCTTGTGTGTGGAGTTTGCTTC 124
Qy 121 GGTCCGAAGCTGCCATGCCAGTGGCTCAGTGCCTTCTGGCCGAGAACGACTGGGAGAT 180
Db 125 GGTCCGAAGCTGCCATGCCAGTGGCTCAGTGCCTTCTGGCCGAGAACGACTGGGAGAT 184
Qy 181 GGAAGGGCTCTGAATCTCTACTTTCGAGCCTCCCGTGGAGGAGAGCGCTTTGGAAACGCCG 240
Db 185 GGAAGGGCTCTGAATCTCTACTTTCGAGCCTCCCGTGGAGGAGAGCGCTTTGGAAACGCCG 244
Qy 241 ACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAAACCAATGAAGAAACAACTGA 300
Db 245 ACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAAACCAATGAAGAAACAACTGA 304
Qy 301 TTCACACATTTTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGSCACATGTT 360
Db 305 TTCCACCACCTTCTAAAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGSCACATGTT 364
Qy 361 CTCTCTCATTAACCTGGAAATATTGATGATTAGATCTTAAACAACTGTCTCAGAGAGGGCTCG 420
Db 365 CTCTCTCATTAACCTGGAAATATTGATGATTAGATCTTAAACAACTGTCTCAGAGAGGGCTCG 424
Qy 421 AGGGGTGTGTTCTTACTTGTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTAT 480
Db 425 AGGGGTGTGTTCTTACTTGTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTAT 484
Qy 481 TCCCCCATATATAGCTACCTTAAAGAGAGATCAAGTAATATGAGATTATACAGGTCA 540
Db 485 TCCCCCATATATATAGCTACCTTAAAGAGAGATCAAGTAATATGAGATTATACAGGTCA 544
Qy 541 TGAAGAAGGATATTTCAAGCTATAATGTTTGAAGAAATCAAGAGTGAATTTAAAAAGCCA 600
Db 545 TGAAGAAGGAKATTTCAAGCTATAATGTTTGAAGAAATCAAGAGTGAATTTAAAAAGCCA 604
Qy 601 AGAGATTAATCTCTTTTCCAACTACCAAAATGATGAGAAACCTTTTATGTGTCATGTGAA 660
Db 605 AGAGATTAATCTCTTTTCCAACTACCAAAATGATGAGAAACCTTTTATGTGTCATGTGAA 664
Qy 661 TGTGTACAGAAATGAGCTTTGCTTATGACATCCCATTTGAGAGACACAGAGGCGATGC 720
Db 665 YGTGTACAGAAATGAGCTTTGCTTATGACATCCCATTTGAGAGACACAGAGGCGATGC 724
Qy 721 TCGGAAACGAATGAATCAAGTATAAATGTTTAAAGAAATGCAAGAGGCTCCAGAGTC 780
Db 725 TCGGAAACGAATGAATCAAGTATAAATGTTTAAAGAAATGCAAGAGGCTCCAGAGTC 784
Qy 781 AGCTACAGTTATATTTGCAGGATACAAATCTAAGGGATCGAGAGGTTACCAAGTGG 840
Db 785 AGCTACAGTTATATTTGCAGGATACAAATCTAAGGGATCGAGAGGTTACCAAGTGG 844
Qy 841 TGGTTATCCCAACAACATTTGTTGGATGCTGGGAGTTTTTGGCAAACTTAAACATTTGCCA 900
Db 845 TGGTTATCCCAACAACATTTGTTGGATGCTGGGAGTTTTTGGGYAAACCTTAAACATTTGCCA 904
Qy 901 GTATACATGGGATACACAAATGAATCTTAATCTTTGGAATAAATCTGCTGTTGTAACCTTCG 960
```

Db 905 GTATACGGGATACACAAATGAACCTAATCTTGAATAACTGCTGCTGTAAACTTCG 964
Qy 961 TTTTGATCGAATATTTTTCAGAGCAGCAGAGAGAGGAGCACAATTTATCCCGAAGTTT 1020
Db 965 TTTTGATCGAATATTTTTCAGAGCAGCAGAGAGAGGAGCACAATTTATCCCGAAGTTT 1024
Qy 1021 GGACCTCTCTGGATTAGAAAAAAGCTGGAGTGTGGTAGATTTCTAGTGATCACTGGGGTCT 1080
Db 1025 GGACCTCTCTGGATTAGAAAAAAGCTGGAGTGTGGTAGATTTCTAGTGATCACTGGGGTCT 1084
Qy 1081 TCTGTGCAACTTAGATATAATATTTGTAATAATCTTTTCAAGTGTGGGTTTGGCCCTGATT 1140
Db 1085 TCTGTGCAACTTAGATATAATATTTGTAATAATCTTTTCAAGTGTGGGTTTGGCCCTGATT 1144
Qy 1141 GTTGCAAAATACAAATTTCCACCTTCTGGAAGAGTAGTTTCTGTGGAGGAATAATGTAC 1200
Db 1145 GTTGCAAAATACAAATTTCCACCTTCTGGAAGAGTAGTTTCTGTGGAGGAATAATGTAC 1204
Qy 1201 TAGATCATTTGTACAGAAAAAACCACCTATGATTTATGTTGTGTTTCA 1249
Db 1205 TAGATCATTTGTACAGAAAAAACCACCTATGATTTATGTTGTGTTTCA 1253

RESULT 9

US-09-745-288-63/c
; Sequence 63, Application US/09745288
; Patent No. US20010018059A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.446D1
; CURRENT APPLICATION NUMBER: US/09/745,288
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-745-288-63

Query Match 55.5%; Score 1066.4; DB 3; Length 1079;
Best Local Similarity 99.8%; Pred. No. 2.3e-258;
Matches 1078; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 423 GGGTGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTC 482
Db 1079 GGGTGTGTTCTTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTC 1020
Qy 483 CCCCATATTATAGTACCTAAAGAAGAGATCAAGTAATTTATGAGATTATTACAGGTCATG 542
Db 1019 CCCCATATTATAGTACCTAAAGAAGAGATCAAGTAATTTATGAGATTATTACAGGTCATG 960
Qy 543 AAGAAGGATATTTACAGCTATTAATGTTGAAGAAATCAAGAGTAAATTAAGAAGCAAG 602
Db 959 AAGAAGGATATTTACAGCTATTAATGTTGAAGAAATCAAGAGTAAATTAAGAAGCAAG 900
Qy 603 AGATTATTCCTTTTCAAGTACCAAAATGATGAAACCTTTTATGTTGTCATGTCAAGT 662
Db 899 AGATTATTCCTTTTCAAGTACCAAAATGATGAAACCTTTTATGTTGTCATGTCAAGT 840
Qy 663 TGTGAGGAATGATTTTGTCTTATGACATCCCATTTGGAGAGCACCAGAGGCGATGCTG 722
Db 839 TGTGAGGAATGATTTTGTCTTATGACATCCCATTTGGAGAGCACCAGAGGCGATGCTG 760
Qy 723 CGGAACGAATGAATCAGTTAAAAATGTTTAAAGAAAAATGCAAGAGGCTCCAGAGTCAG 782
Db 779 CGGAACGAATGAATCAGTTAAAAATGTTTAAAGAAAAATGCAAGAGGCTCCAGAGTCAG 720
Qy 783 CTACAGTTATTTGCGAGGAGATACAAATCTAAGGATCGAGAGTTACCAGATGTGGTG 842

Db 719 CTACAGTTATTTGCGAGGAGATACAAATCTAAGGGATCGAGAGTTTACCAGATGTGGTG 660
Qy 843 GTTTACCCCAACACATTTGTGATGCTGGAGTTTTTTGGGCAAACTTAAACATTTGCCAGT 902
Db 659 GTTTACCCCAACACATTTGTGATGCTGGAGTTTTTTGGGCAAACTTAAACATTTGCCAGT 600
Qy 903 ATACATGGGATACACAAATCTTAATCTTGAATAAATCTGCTGTTGTAACATTTGCTT 962
Db 599 ATACATGGGATACACAAATCTTAATCTTGAATAAATCTGCTGTTGTAACATTTGCTT 540
Qy 963 TTGATCGAATATTTTTCAGAGCAGCAGAGAGGAGGACACATTTATCCCGAAGTTTGG 1022
Db 539 TTGATCGAATATTTTTCAGAGCAGCAGAGAGGAGGACACATTTATCCCGAAGTTT-G 481
Qy 1023 ACCCTTTTGGATTAGAAAAAAGCTGACTGCTGTAGATTTCTTAGTGATCACTGGGGTCTTC 1082
Db 480 ACCCTTTTGGATTAGAAAAAAGCTGACTGCTGTAGATTTCTTAGTGATCACTGGGGTCTTC 421
Qy 1083 TGTGCAACTTAGATATAATATTTGTAATAATCTTTTCAAGTGTGGTTTTTGCCTGATTGT 1142
Db 420 TGTGCAACTTAGATATAATATTTGTAATAATCTTTTCAAGTGTGGTTTTTGCCTGATTGT 361
Qy 1143 TGCAAATACAAATTTCCACCTTCTGGAAGAGTAGTTTCTGCTGAGGAGAAATAATGTACTA 1202
Db 360 TGCAAATACAAATTTCCACCTTCTGGAAGAGTAGTTTCTGCTGAGGAGAAATAATGTACTA 301
Qy 1203 GATCATTTGTACAGAAAAAAGCTGATGATTTATGTTGTTTTCAGAAATTTCAACATTTA 1262
Db 300 GATCATTTGTACAGAAAAAAGCTGATGATTTATGTTGTTTTCAGAAATTTCAACATTTA 241
Qy 1263 AAGATTATGTTTATTTAAACGAAACACATTTCTGCAATTCAGATGTGAGGCAATTAATA 1322
Db 240 AAGATTATGTTTATTTAAACGAAACACATTTCTGCAATTCAGATGTGAGGCAATTAATA 181
Qy 1323 AAAAGGCAAAAGCCTGTGAGTTTCAACGGTCTTACAGCTGCGAGCTGGATTTCCA 1382
Db 180 AAAAGGCAAAAGCCTGTGAGTTTCAACGGTCTTATAGCTGCCAGCTGGATTTCCA 121
Qy 1383 AACAGGTACCCCATGCTCTGAGCTAATGTTTATATTTTCCATTTCAGGCAACCGAATA 1442
Db 120 AACAGGTACCCCATGCTCTGAGCTAATGTTTATATTTTCCATTTCAGGCAACCGAATA 61
Qy 1443 GTTAATATTTAAATAAGTCTTCAAAAGAAACATAGAAGATTTATGAGTTCTTGGACT 1502
Db 60 GTTAATATTTAAATAAGTCTTCAAAAGAAACATAGAAGATTTATGAGTTCTTGGACT 1

RESULT 10

US-10-453-919-63/c
; Sequence 63, Application US/10453919
; Publication No. US20040033230A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.446C7
; CURRENT APPLICATION NUMBER: US/10/453,919
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 1079
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-453-919-63

Query Match 55.5%; Score 1066.4; DB 7; Length 1079;
Best Local Similarity 99.8%; Pred. No. 2.3e-258;

Matches 1078; Conservative 0; Mismatches 1; Indels 1; Gaps 1;			
QY	423	GGGTGTGTCCTACTAGCTTTGTATCAGCCAGATGTGATATTTCTACAGGAAGTTATTC	482
Db	1079	GGGTGTGTCCTACTAGCTTTGTATCAGCCAGATGTGATATTTCTACAGGAAGTTATTC	1020
QY	483	CCCCATATTATAGCTACCTAAAGAAGAGATCAAGTAAATTATGAGATTATTACAGTCAATG	542
Db	1019	CCCCATATTATAGCTACCTAAAGAAGAGATCAAGTAAATTATGAGATTATTACAGTCAATG	960
QY	543	AAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATATTAAGGCCAAG	602
Db	959	AAGAAGGATATTTCACAGCTATAATGTTGAAGAAATCAAGAGTGAATATTAAGGCCAAG	900
QY	603	AGATTATTCCTTTTCCAGTAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAATG	662
Db	899	AGATTATTCCTTTTCCAGTAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAATG	840
QY	663	TGTCAGGAAATGAGCTTTTGCCCTTATGACATCCCATTTGGAGAGCACAGAGGGCATGCTG	722
Db	839	TGTCAGGAAATGAGCTTTTGCCCTTATGACATCCCATTTGGAGAGCACAGAGGGCATGCTG	780
QY	723	CGGAACGAATGAATCAGTTAAAAATGTTTAAAGAAAATCAAGAGGCTCCAGAGTCAG	782
Db	779	CGGAACGAATGAATCAGTTAAAAATGTTTAAAGAAAATCAAGAGGCTCCAGAGTCAG	720
QY	783	CTACAGTTATATTTCAGAGAGATCAAAATCTAAGGGATCGAGAGTTACAGAGTGTGTTG	842
Db	719	CTACAGTTATATTTCAGAGAGATCAAAATCTAAGGGATCGAGAGTTACAGAGTGTGTTG	660
QY	843	GTTTACCACAAACATCTGAGATGTCGGAGTTTTCGGCAAACTTAACATTCGCCAGT	902
Db	659	GTTTACCACAAACATCTGAGATGTCGGAGTTTTCGGCAAACTTAACATTCGCCAGT	600
QY	903	ATACATGGGATACACAAATGAACCTTAATCTTGAATAACTGCTGCTTGTAAACTTCGTT	962
Db	599	ATACATGGGATACACAAATGAACCTTAATCTTGAATAACTGCTGCTTGTAAACTTCGTT	540
QY	963	TGATCGAATATTTTCAGAGAGCAGAGAGAGGGACACATTAATCCCCCGAAGTTTGG	1022
Db	539	TGATCGAATATTTTCAGAGAGCAGAGAGAGGGACACATTAATCCCCCGAAGTTT-G	481
QY	1023	ACCTTCTTTGGATAGAAAACTGGACTGTGTAGATTTTCTAGTATCACCCTGGGCTCTTC	1082
Db	480	ACCTTCTTTGGATAGAAAACTGGACTGTGTAGATTTTCTAGTATCACCCTGGGCTCTTC	421
QY	1083	TGTCAACTTAGATATAATATTGTAAATGCTTTTCAAGTGTGGGTTTTCGCCCTGATTGT	1142
Db	420	TGTCAACTTAGATATAATATTGTAAATGCTTTTCAAGTGTGGGTTTTCGCCCTGATTGT	361
QY	1143	TGCAATACAAATTTCCACCTTCGGAAAGGTAGGTTTTCGCTGTGGAGGAAATAATGTACTA	1202
Db	360	TGCAATACAAATTTTCACCTTCGGAAAGGTAGGTTTTCGCTGTGGAGGAAATAATGTACTA	301
QY	1203	GATCATTGTTCAGAAAAACCAACTATGATTTATGTTGTCTTTTCAGATGTGGGTTTTCGCCCTGATTGT	1262
Db	300	GATCATTGTTCAGAAAAACCAACTATGATTTATGTTGTCTTTTCAGATGTGGGTTTTCGCCCTGATTGT	241
QY	1263	AAGATTAAATGTTTATTTAAACGAAACACATTCCTGCAATTCAGAGTGTGAGGCCATTTAATA	1322
Db	240	AAGATTAAATGTTTATTTAAACGAAACACATTCCTGCAATTCAGAGTGTGAGGCCATTTAATA	181
QY	1323	AAAAGGGCACAAAGCTGTCTAGGTTTTCACCGGTGCTTACAGTGTGCCAGTGTGAATCCA	1382
Db	180	AAAAGGGCACAAAGCTGTCTAGGTTTTCACCGGTGCTTATAGTGTGCCAGTGTGAATCCA	121
QY	1383	AACAGGTACCCCATTTGCTCTGAGCTAATGTTTATATTTTCCATTCAGGCACCCGAATA	1442
Db	120	AACAGGTACCCCATTTGCTCTGAGCTAATGTTTATATTTTCCATTCAGGCACCCGAATA	61
QY	1443	GTTAATATTTAAATAAGTCTTCAAAAGAAACATAAGAGATTAATGAGTTCTTTGGGACT	1502
Db	60	GTTAATATTTAAATAAGTCTTCAAAAGAAACATAAGAGATTAATGAGTTCTTTGGGACT	1

RESULT 11
US-10-450-763-22058
; Sequence 22058, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22058
; LENGTH: 1088
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1)..(687)
; OTHER INFORMATION: 98% homologous to Homo sapiens dJ30M3.3 (novel protein
; OTHER INFORMATION: similar to C. elegans Y63D3A.4), accession number AL031775, Smith-
; OTHER INFORMATION: Waterman Score=1199.
US-10-450-763-22058

Query Match 51.4%; Score 987.2; DB 9; Length 1088; Best Local Similarity 98.4%; Pred. No. 2.4e-238; Matches 1071; Conservative 0; Mismatches 8; Indels 9; Gaps 7;			
QY	416	GCTCGAGGGGTGCTTCTCTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGAA	475
Db	1	GCTCGAGGGGTGCTTCTCTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGAA	60
QY	476	GTTATTTCCCCCATATTATAGCTACCTAAAGAAGAGATCAAGTAATATGAGATTATTACA	535
Db	61	GTTATTTCCCCCATATTATAGCTACCTAAAGAAGAGATCAAGTAATATGAGATTATTACA	120
QY	536	GGTCATGAAGAAGATATTTTCAAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAA	595
Db	121	GGTCATGAAGAAGATATTTTCAAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAA	180
QY	596	AGCCAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAACCTTTTATGTGTGCAT	655
Db	181	AGCCAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAACCTTTTATGTGTGCAT	240
QY	656	GTGAATGTGTGAGAAATGAGCTTTTGCTTTATGACATCCCATTTTGGAGAGCACCAGAGGG	715
Db	241	GTGAATGTGTGAGAAATGAGCTTTTGCTTTATGACATCCCATTTTGGAGAGCACCAGAGGG	300
QY	716	CATGCTCGGAAACGAATGAATGAAATGTTTAAAGAAATGTTTAAAGAAATGCAAGAGGCTCCA	775
Db	301	CATGCTCGGAAACGAATGAATGAAATGTTTAAAGAAATGTTTAAAGAAATGCAAGAGGCTCCA	360
QY	776	GAGTCAGTACAGTTATTTTGCAGGAGATACAAATCTAAGGGATCGAGAGTTTACCAGA	835
Db	361	GAGTCAGTACAGTTATTTTGCAGGAGATACAAATCTAAGGGATCGAGAGTTTACCAGA	420
QY	836	TGTGGTGGTTTACCCAAACAACTTGTGGATGTCTGGGAGTTTGTGGGCAACCTTAAACAT	895
Db	421	TGTGGTGGTTTACCCAAACAACTTGTGGATGTCTGGGAGTTTGTGGGCAACCTTAAACAT	480
QY	896	TGCCAGTATATCATGGGATACAAAATGAATCTCTAAATCTTGGAAATACTGTCTGTGTAAA	955
Db	481	TGCCAGTATATCATGGGATACAAAATGAATCTCTAAATCTTGGAAATACTGTCTGTGTAAA	540
QY	956	CTTCGTTTTCGATCGAATATTTTTCAGAGCAGCAGGAGGACACATTATTTCCCGCA	1015

Qy	836	TGTGGTGGTTTATCCCAACAACATGTGGATGTCTGGAGTTTTTGGGCAAAACCTTAACAT	895
Db	452	TGTGGTGGTTTATCCCAACAACATGTGGATGTCTGGAGTTTTTGGGCAAAACCTTAACAT	511
Qy	896	TGCAGATATACATGGGATACACAAAATGAACTCTTAATCTTCGGAATAACTGCTGTTGTAAA	955
Db	512	TGCAGATATACATGGGATACACAAAATGAACTCTTAATCTTCGGAATAACTGCTGTTGTAAA	571
Qy	956	CTTCGTTTTGATCGAATATTTTTTCAGAGCAGCAGCAGAGAGGACACATTAATTCGCCGA	1015
Db	572	CTTCGTTTTGATCGAATATTTTTTCAGAGCAGCAGCAGAGAGGACACATTAATTCGCCGA	631
Qy	1016	AGTTTGACCTTC	1028
Db	632	AGTTTGACCTTC	644

```

RESULT 15
US-10-066-543-1084
; Sequence 1084, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuchu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indirias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR COLON CANCER
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1084
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3
; OTHER INFORMATION: n = A,T,C or G
; US-10-066-543-1084

```

Query Match	31.2%;	Score 600;	DB 5;	Length 633;
Best Local Similarity	100.0%;	Pred. NO. 1.1e-140;		
Matches 600;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0;			

QY	416	GCTCGAGGGGTGTGTTCTCTATTAGCTTTGTACGCCAGATGCTATATTTCTACAGAA	476
Db	34	GCTCGAGGGGTGTGTTCTCTACTTAGCTTTGTACGCCAGATGCTATATTTCTACAGAA	93
QY	476	GTATTTCCTCCCATATTTATAGCTTACCTAAAGAGAGATCAAGTAAATTTATGAGATTATTACA	535
Db	94	GTATTTCCTCCCATATTTATAGCTTACCTAAAGAGAGATCAAGTAAATTTATGAGATTATTACA	153
QY	536	GGTCATGAAGAAGGATATTTCA CAGCTATAATGTTGAAGAAATCAAGAGTGAAATTTAAA	595
Db	154	GGTCATGAAGAAGGATATTTCA CAGCTATAATGTTGAAGAAATCAAGAGTGAAATTTAAA	213
QY	596	AGCCGAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAA CCTTTATGTGTGCAT	655
Db	214	AGCCGAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAA CCTTTATGTGTGCAT	273
QY	656	GTGAATGTGTACAGGAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCAACCGAGGG	715
Db	274	GTGAATGTGTACAGGAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCAACCGAGGG	333

Qy	716	CATGCTGCGGAACGAATGAATCAGTTTAAATATGTTTTAAAGAAATATGCAAGAGGCTCCA	775
Db	334	CATGCTGCGGAACGAATGAATCAGTTTAAATATGTTTTAAAGAAATATGCAAGAGGCTCCA	393
Qy	776	GAGTCAGCTACAGTTTATATTTGCAAGAGATACAAATCTAAGGGATCGAGAGGTTACCAGA	835
Db	394	GAGTCAGCTACAGTTTATATTTGCAAGAGATACAAATCTAAGGGATCGAGAGGTTACCAGA	453
Qy	836	TGTGTGTGTTTTACCAACAACATTTGTGGATGCTGGAGTTTTTGGGCAAAACCTTAACAT	895
Db	454	TGTGTGTGTTTTACCAACAACATTTGTGGATGCTGGAGTTTTTGGGCAAAACCTTAACAT	513
Qy	896	TGCAGTATACATGGGATACACAAATGCAACTTAAATCTTGGAAATACTGCTGCTTGTAAA	955
Db	514	TGCAGTATACATGGGATACACAAATGCAACTTAAATCTTGGAAATACTGCTGCTTGTAAA	573
Qy	956	CTTCGTTTTGATCGAATATATTTTTTCAGACGACGACGAGAGGACACATTATTCGCCGA	1015
Db	574	CTTCGTTTTGATCGAATATATTTTTTCAGACGACGACGAGAGGACACATTATTCGCCGA	633

```

RESULT 16
US-10-066-543-548
; Sequence 548, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indirias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Sericist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 21021-563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 548
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 19, 71
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-548

```

Query Match 30.6%; Score 587; DB 5; Length 625;
Best Local Similarity 99.7%;
Pred. No. 2.2e-137;
Matches 598; Conservative 0; Mismatches 1; Indels 1; Gaps 1

416	GCTGAGGGGTGTGTTCTCTATTAGCTTTGTACAGCCAGATGTGATATTTCTACAGAA	475
26	GCTGAGGGGTGTGTTCTCTATTAGCTTTGTACAGCCAGATGTGNTATTTCTACAGAA	85
476	GTTATTCCCCCATATTATTAGCTACCTAAAGAAGAGATCAAGTAATTATTAGATTATTACA	535
86	GTTATTCCCCCATATTATTAGCTACCTAAAGAAGAGATCAAGTAATTATTAGATTATTACA	145
536	-GGTCATGAAGAAGAGATATTTTCAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAA	594
146	GGGTCAATGAAGAAGGATATTTTCAGAGTATAATGTTGAAGAAATCAAGAGTGAATTTAA	205
595	AAGCCAAGAGATTATTCCTTTTCAAGTACCAAATGATGAGAAACCTTTTATGTGTGCA	654

Db 206 AAGCCAAGAGATTATTCTCTTTCCAAAGTACCAAAATGATGAGAACCTTTTATGTGTGCA 265
Qy 655 TGTGAATGTGCAGAAATGAGCTTTGCTTTATGACATCCCATTTTGGAGAGCACCAGAGG 714
Db 266 TGTGAATGTGCAGAAATGAGCTTTGCTTTATGACATCCCATTTTGGAGAGCACCAGAGG 325
Qy 715 GCATCTCGGAAACCAATGAATCAGTTAAATGCTTTTAAAGAAATGCAAGAGGCTCC 774
Db 326 GCATCTCGGAAACCAATGAATCAGTTAAATGCTTTTAAAGAAATGCAAGAGGCTCC 385
Qy 775 AGAGTCAGCTACAGTTATATTTCAGAGAGATACAAATCTAAGGGATCGAGAGGTTACCAG 834
Db 386 AGAGTCAGCTACAGTTATATTTCAGAGAGATACAAATCTAAGGGATCGAGAGGTTACCAG 445
Qy 835 ATGTGGTGGTTTACCAACAACATTTGTGGATGCTCTGGAGTTTGGGCAACCTAAACA 894
Db 446 ATGTGGTGGTTTACCAACAACATTTGTGGATGCTCTGGAGTTTGGGCAACCTAAACA 505
Qy 895 TTGCCAGTATACATGGGATACACAATGAATCTTAATCTTGAATAAAGTCTGCTGTGTA 954
Db 506 TTGCCAGTATACATGGGATACACAATGAATCTTAATCTTGAATAAAGTCTGCTGTGTA 565
Qy 955 ACTTCGTTTTGATCGAATATTTTTCAGAGCAGCAGAGAGGAGACACATTTTCCCG 1014
Db 566 ACTTCGTTTTGATCGAATATTTTTCAGAGCAGCAGAGAGGAGACACATTTTCCCG 625

RESULT 17
US-10-066-543-1031
; Sequence 1031, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1031
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-1031

Query Match 30.4%; Score 584; DB 5; Length 625;
Best Local Similarity 100.0%; Pred. No. 1.2e-136;
Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 416 GCTCGAGGGGTGTGTTCTCTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAA 475
Db 42 GCTCGAGGGGTGTGTTCTCTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAA 101
Qy 476 GTTATTCCTCCCATATATATAGCTACTCTAAAGAGAGATCAAGTAATATGAGATATTACA 535
Db 102 GTTATTCCTCCCATATATATAGCTACTCTAAAGAGAGATCAAGTAATATGAGATATTACA 161
Qy 536 GGTCAATGAAGAAGGATATTTACAGCTATATATGTTGAAGAAATCAAGAGTGAATTTAA 595

Db 162 GGTCAATGAAGAAGGATATTTTCCAGCTATATGTTGAAGAAATCAAGAGTGAATTTAAA 221
Qy 596 AGCCAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCAT 655
Db 222 AGCCAAGAGATTATTCCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCAT 281
Qy 656 GTGAATGTGCAGAAATGAGCTTTGCTTTATGACATCCCATTTTGGAGAGCACCAGAGGG 715
Db 282 GTGAATGTGCAGAAATGAGCTTTGCTTTATGACATCCCATTTTGGAGAGCACCAGAGGG 341
Qy 716 CATCTCGGAAACCAATGAATCAGTTAAATGCTTTTAAAGAAATGCAAGAGGCTCCA 775
Db 342 CATCTCGGAAACCAATGAATCAGTTAAATGCTTTTAAAGAAATGCAAGAGGCTCCA 401
Qy 776 GAGTCAGCTACAGTTATATTTCAGAGGATACAAATCTAAGGGATCGAGAGGTTACCAG 835
Db 402 GAGTCAGCTACAGTTATATTTCAGAGGATACAAATCTAAGGGATCGAGAGGTTACCAG 461
Qy 836 TGTGGTGGTTTACCAACAACATTTGTGGATGCTCTGGAGTTTGGGCAACCTAAACAT 895
Db 462 TGTGGTGGTTTACCAACAACATTTGTGGATGCTCTGGAGTTTGGGCAACCTAAACAT 521
Qy 896 TGCCAGTATACATGGGATACACAATGAATCTTAATCTTGAATAAAGTCTGCTGTGTA 955
Db 522 TGCCAGTATACATGGGATACACAATGAATCTTAATCTTGAATAAAGTCTGCTGTGTA 581
Qy 956 CTTCGTTTTGATCGAATATTTTTCAGAGCAGCAGAGAGAGGG 999
Db 582 CTTCGTTTTGATCGAATATTTTTCAGAGCAGCAGAGAGAGGG 625

RESULT 18
US-10-066-543-983
; Sequence 983, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 983
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6, 35
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-983

Query Match 26.7%; Score 512; DB 5; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.8e-118;
Matches 512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 416 GCTCGAGGGGTGTGTTCTCTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAA 475
Db 42 GCTCGAGGGGTGTGTTCTCTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAA 101

QY 476 GTTATTTCCCCATATATATAGCTACCTAAAGAGAGATCAAGTAATATATCAGATATTACA 535
DB 102 GTTATTTCCCCATATATATAGCTACCTAAAGAGAGATCAAGTAATATATCAGATATTACA 161
QY 536 GGTCTATGAAGAGGATATTTTCAAGCTATATATGTTGAAGAAATCAAGAGTGAATTTAAAA 595
DB 162 GGTCTATGAAGAGGATATTTTCAAGCTATATATGTTGAAGAAATCAAGAGTGAATTTAAAA 221
QY 596 AGCCAGAGATTTATTCCTTTTCCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCAT 655
DB 222 AGCCAGAGATTTATTCCTTTTCCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCAT 281
QY 656 GTGAATGTCTCAGGAAATGAGCTTTTGCCTTTATGACATCCATTTTGGAGAGCACAGAGGG 715
DB 282 GTGAATGTCTCAGGAAATGAGCTTTTGCCTTTATGACATCCATTTTGGAGAGCACAGAGGG 341
QY 716 CATGCTGCGGAACGAATGAATCAGTTTAAAAATGGTTTAAAGAAATGCAAGAGGCTCCA 775
DB 342 CATGCTGCGGAACGAATGAATCAGTTTAAAAATGGTTTAAAGAAATGCAAGAGGCTCCA 401
QY 776 GAGTCAGCTACATTTATTTTTCAGGAGATACAAATCTTAAGGGATCGAGAGGTTACCAGA 835
DB 402 GAGTCAGCTACATTTATTTTTCAGGAGATACAAATCTTAAGGGATCGAGAGGTTACCAGA 461
QY 836 TGTGGTGGTTTACCCCAACAACTTGTGGATGTCTGGAGTCTTGGGCAAACTTAAACAT 895
DB 462 TGTGGTGGTTTACCCCAACAACTTGTGGATGTCTGGAGTCTTGGGCAAACTTAAACAT 521
QY 896 TGCCAGTATACATGGGATACACAAATGAACTC 927
DB 522 TGCCAGTATACATGGGATACACAAATGAACTC 553

RESULT 19

US-10-066-543-2173/c
; Sequence 2173, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2173
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 36, 69, 85, 193, 253, 380, 397, 421, 459, 491, 519, 546
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-2173

Query Match 25.78; Score 493; DB 5; Length 547;
Best Local Similarity 96.3%; Pred. No. 1.1e-113;
Matches 496; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 1406 GCTAATGTTTATATTTTTCATTCAGGCACCGAAATAGTTAATATTTAAATTAAGTCTTC 1465
DB 547 GNTAATGTTTATATTTTTCATTCAGGCACCGAAATAGTTAATATTTAAATTAAGTCTTC 488

QY 1466 AAAAGAAAAACATAAGAGATTATTGAGTTCTTTGGACTGGATCCTTTTATTTTATTAAGTTCA 1525
DB 487 AAAAGAAAAACATAAGAGATTATTGAGTTCTTTGGACTGGATCCTTTTATTTTATTAAGTTCA 428
QY 1526 GATCATCTTAAATGAAAATGCCATGATTATCTGCAGTTTAAGTAGTAGACAGCTATTCTAC 1585
DB 427 GATCATNTTAAATGAAAATGCCATGATTATNTGAGTTTAAGTAGTAGACAGCTATTCTTAC 368
QY 1586 ATCAGACTTGATTTTTTGTGACGTAATACATAAATGGTAAGNTATAAATGGAACCTTATG 1645
DB 367 ATCAGACTTGATTTTTTGTGACGTAATACATAAATGGTAAGCTATAATGGAACCTTATG 308
QY 1646 GCTTAAAAATCCTTTAACTCCTTTTGTGATTCATGTTTGTAGTCATGTTGTCAACAGAGGCA 1705
DB 307 GCTTAAAAATCCTTTAACTCCTTTTGTGATTCATGTTTGTAGTCATGTTGTCAACAGAGGCA 248
QY 1706 AAGTTAAGCTTGATGATGTTTAAAAATCGTTTGTATAGCACCATGGAGCATTTTTTTAAACA 1765
DB 247 AAGTTAAGCTTGATGATGTTTAAAAATCGTTTGTATAGCACCATGGAGCATTTTTTTAAACA 188
QY 1766 AAAATAAATCATGAAGAGACATAGCCCTTTTGTAGTTTGTGTAATGTGAAATGGAATGCT 1825
DB 187 AAAATAAATCATGAAGAGACATAGCCCTTTTGTAGTTTGTGTAATGTGGAATGGAATGCT 128
QY 1826 TTACAGGAAAGTAAATGCAAAATTTANTTTTAAAGTGTGCTTTTAAAGAAAAATATTTTCCCCAC 1885
DB 127 TTACAGGAAAGTAAATGCAAAATTTACTTTTAAAGTGTGCTTTTAAAGAAAAATATTTTCCCCNC 68
QY 1886 AGGAGAAATTTAAATAAAGAAATTTTATTTGGTAAA 1920
DB 67 AAGAGAAATTTAAATAAAGAAATTTTATTTGTNTAA 33

RESULT 20

US-10-066-543-442/c
; Sequence 442, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 442
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 13, 332, 499
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-442

Query Match 21.4%; Score 410.2; DB 5; Length 503;
Best Local Similarity 98.6%; Pred. No. 8.9e-93;
Matches 412; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1503 GGAATCCTTTTATTTTCAATTAAGTTCAGATCATCTTAAATGAAATGCCATGATTTCTCGAGT 1562

4 67	Db	GGATCCCTTTATTTCATCAAGTTTCAGATCATCTTAAATGAAAATGCCATGATTATCTCGCAGT	408
1563	Qy	TAAGTAGATGACAGCTATTCTACATCAGACTTGTGATTTTTGTGCAGCTAAATTACATAATTGG	1622
407	Db	TAAGTAGATGACAGCTATTCTACATCAGACTTGTGATTTTTGTGCAGCTAAATTACATAATTGG	348
1623	Qy	TAAGNTATAAATTGAAACCTTATGGCTTAAAAATCTCTTAACCTCTTTTGGATTCATGTTTG	1682
347	Db	TAAGCTATAAATTGAANCCTTATGGCTTAAAAATCTCTTAACCTCTTTTGGATTCATGTTTG	288
1683	Qy	TAGTCATGTTGTCACAGAGGCAAGTTAAGCTTGATGATGGTTAAAAATCGGTTTGATAG	1742
287	Db	TAGTCATGTTGTCACAGAGGCAAGTTAAGCTTGATGATGGTTAAAAATCGGTTTGATAG	228
1743	Qy	CACCATGGGACATTTTTTTTAAACAAAAATAATGCATGAAGGACATAGCCCTTTAGTTTT	1802
227	Db	CACCATGGGACATTTTTTTTAAACAAAAATAATGCATGAAGGACATAGCCCTTTAGTTTT	168
1803	Qy	GCTAAATTGCGAAATGGAATGCTTTACAGGAAGTAAATGCAAAATTANTTTTAAAGTGTGCT	1862
167	Db	GCTAAATTGCGAAATGGAATGCTTTACAGGAGTAAATGCAAAATTACTTTTTAGTGTGCT	108
1863	Qy	TTAAAGAAAAATATTTTTCCCAACAGGAGAAATTTAAATAAAGAAATTTATTTGGTAAA	1920
107	Db	TTAAAGAAAAATATTTTTCCCAACAGGAGAAATTTAAATAAAGAAATTTATTTGGTAAA	50

RESULT 21

US-10-066-543-438/c
; Sequence 438, Application US/10066543

; Publication No. US20

```

; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indirias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
;

```

OTHER INFORMATION: n = A, T, C or G
US-10-066-543-438

	Query Match	21.1%	Score 405.2	DB 5	Length 476
	Best Local Similarity	98.8%	Pred. No. 1.6e-91		
	Matches 407	Conservative 0	Mismatches 5	Indels 0	Gaps 0
QY	1509	TTTATTTCATAAGTTCAGATCATCTTAAATGAAAAATGCCATGATTTCTCGAGTTAAGTA	1568		
DB	476	TTTATTTCATAAGTTCAGATCATCTTAAATGAAAAATGCCATGATTTCTCGAGTTAAGTA	417		
QY	1569	GATGACAGCTATTCTACATCAGACTTGATTTTTGTGTAGCTAAATACATAATTTGGTAAAGNT	1628		
DB	416	GATGACAGCTATTCTACATCAGACTTGATTTTTGTGTAGCTAAATACATAATTTGGTAAAGCT	357		
QY	1629	ATAATTGAAACCTTATGGCTTAAAAATTCCTTAACTCCCTTTTTCGATTCATGTTGTAGTCA	1688		

US-10-066-543-878/c
; Sequence 878, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 878
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: 35, 231, 409
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-878

Query Match 21.0%; Score 403.2; DB 5; Length 482;
Best Local Similarity 98.3%; Pred. No. 5.1e-91;
Matches 405; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy	1509	TTTATTTTCATAGTTTCAGATCATCTTAATGAAATGCCATGATTTATCTGCAGTTAAGTA	1568
Db	482	TTTATTTTCATAGTTTCAGATCATCTTAATGAAATGCCATGATTTATCTGCAGTTAAGTA	423
Qy	1569	GATGACAGCTATTCTACATCAGACTTGATTTTGTGACGTAATTACATAAATGGTAAGNT	1628
Db	422	GATGACAGCTATTNTACATCAGACTTGATTTTGTGACGTAATTACATAAATGGTAAGCT	363
Qy	1629	ATAATTGAAACCTTATGGCTTAAATTCCTTAACCTCTTTTGTGATTCATGTTGTAGTCA	1688
Db	362	ATAATTGAAACCTTATGGCTTAAATTCCTTAACCTCTTTTGTGATTCATGTTGTAGTCA	303
Qy	1689	TGTTGTCAACAGAGGCAAGTTAAGCTTGATGATGGTTAAATCGGTTTGATAGCACCAT	1748
Db	302	TGTTGTCAACAGAGGCAAGTTAAGCTTGATGATGGTTAAATCGGTTTGATAGCACCAT	243
Qy	1749	GGGACATTTTTTTTAAACAAAAATAATGATGAAGACATAGCCCTTTTGTGTTTGTCTAAT	1808
Db	242	GGGACATTTTTTAAACAAAAATAATGATGAAGACATAGCCCTTTTGTGTTTGTCTAAT	183
Qy	1809	TGTGAATGGAATGCTTTACAGGAAGTAAATGCAAAATANTTTTAAAGTGCTTTTAAAG	1868
Db	182	TGTGAATGGAATGCTTTACAGGAAGTAAATGCAAAATANTTTTAAAGTGCTTTTAAAG	123
Qy	1869	AAAAATATTTTCCACAGGAGAAATTTTAAATAAGAAATTTTATTTGTTAA 1920	
Db	122	AAAAATATTTTCCACAGGAGAAATTTTAAATAAGAAATTTTATTTGTTAA 71	

RESULT 26
US-09-918-995-36673
; Sequence 36673, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES

; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36673
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(408)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-36673

Query Match 21.0%; Score 402.8; DB 3; Length 408;
Best Local Similarity 99.3%; Pred. No. 5.8e-91;
Matches 404; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1320	ATAAAAAGGGCACAAGCCTGTCTCAGAGTTCCTCAACGGTGTACAGCTGCCAGCTGGATT	1379
Db	1	ATAAAAAGGGCACAAGCCTGTCTCAGAGTTCCTCAACGGTGTCTTATAGCTGCCAGCTGGATT	60
Qy	1380	CCAAACAGGTACCCCATTTCTCTGAGCTAATGTTTATATTTTCCATTCAGGCACCGAA	1439
Db	61	CCAAACAGGTACCCCATTTCTCTGAGCTAATGTTTATATTTTCCATTCAGGCACCGAA	120
Qy	1440	ATAGTTAATATTTAAATAAGTCTTCAAAAGAAACATAAGAGATTATTGAGTTCCTTGGG	1499
Db	121	ATAGTTAATATTTAAATAAGTCTTCAAAAGAAACATAAGAGATTATTGAGTTCCTTGGG	180
Qy	1500	ACTGGATCCTTTATTTTCATAAGTTTCAGATCATCTTAAATGAAAATGCCATGATTATCTGC	1559
Db	181	ACTGGATCCTTTATTTTCATAAGTTTCAGATCATCTTAAATGAAAATGCCATGATTATCTGC	240
Qy	1560	AGTTAAGTAGATGACAGCTATTCTACATCAGACTTGATTTTGTGACGTAATTACATAAT	1619
Db	241	AGTTAAGTAGATGACAGCTATTCTACATCAGACTTGATTTTGTGACGTAATTACATAAT	300
Qy	1620	TGTTAAGNTAATTTGAAACCTTATGCTTAAATTCCTTAACCTCTTTTGTGATTCATGT	1679
Db	301	TGTTAAGNTAATTTGAAACCTTATGCTTAAATTCCTTAACCTCTTTTGTGATTCATGT	360
Qy	1680	TTGTAGTCATGTTGTCAACAGAGGCAAAAGTTAAGCTTTGATGATGGTT 1726	
Db	361	TTGTAGTCATGTTGTCAACAGAGGCAAAAGTTAAGCTTTGATGATGGTT 407	

RESULT 27
US-10-066-543-555/c
; Sequence 555, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 555
; LENGTH: 434
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 32, 33, 59, 183, 243, 361, 387, 411
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-555

Query Match      20.8%; Score 398.8; DB 5; Length 434;
Best Local Similarity 97.1%; Pred. No. 6.2e-90;
Matches 400; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1509 TTTATTTTCATAGTTTCAGATCATCTTAATGAAAATGCGCATGATTTATCTGCGAGTTAAGTA 1568
Db 434 TTTATTTTCATAGTTTCAGATCATCTTAATGAAAATGCGCATGATTTATCTGCGAGTTAAGTA 375

QY 1569 GATGACAGCTATCTACATCAGACTGATTTTGTGTCAGCTAATTTACATAATTTGGTAAGNT 1628
Db 374 GATGACAGCTATTTTACATCAGACTGATTTTGTGTCAGCTAATTTACATAATTTGGTAAGCT 315

QY 1629 ATAAATTTGAACTTTATGGCTTAAATTCCTTAATCTCTTTTTCATTCATGTTTGTAGTCA 1688
Db 314 ATAAATTTGAACTTTATGGCTTAAATTCCTTAATCTCTTTTTCATTCATGTTTGTAGTCA 255

QY 1689 TGTGTGTCACAGAGGCAAAAGTTAAGCTTCATGATGGTTAAATTCGGTTTGTAGTACACCAT 1748
Db 254 TGTGTGTCACAGAGGCAAAAGTTAAGCTTCATGATGGTTAAATTCGGTTTGTAGTACACCAT 195

QY 1749 GGGACATTTTTTTTAAACAAAATAAATGATGATGAGACATAGCCCTTTTAAAGTGTCTTAAT 1808
Db 194 GGGACATTTTTTTTAAACAAAATAAATGATGATGAGACATAGCCCTTTTAAAGTGTCTTAAT 135

QY 1809 TGTGAAATGGAATGCTTTTACAGAAAGTAAATGCAAAATTAATTTTAAAGTGTCTTAAAG 1868
Db 134 TGTGAAATGGAATGCTTTTACAGAAAGTAAATGCAAAATTAATTTTAAAGTGTCTTAAAG 75

QY 1869 AAAAAATTTTCCACAGAGAGAAATTTAAATAAGAAATTTTAAATTTGGTAAA 1920
Db 74 AAAAAATTTTCCACAGAGAGAAATTTAAATAAGAAATTTTAAATAAGAAATTTTAAATTTGGTAAA 23

RESULT 28
US-10-450-763-22059
; Sequence 22059, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22059
; LENGTH: 1227
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (84)..(203)
; OTHER INFORMATION: 85% homologous to Homo sapiens dJ30M3.3 (novel protein
; similar to C. elegans Y63D3A.4), accession number AL031775, Smith-
; OTHER INFORMATION: Waterman Score=164.
US-10-450-763-22059
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Query Match      20.7%; Score 397; DB 9; Length 1227;
Best Local Similarity 68.8%; Pred. No. 3.2e-89;
Matches 789; Conservative 0; Mismatches 115; Indels 243; Gaps 8;

QY 1 GTGCAGAGCGCGCAGGAAGATGGAGTTTGGGAGATGCTCTGG-AGGCGGGAGGGAGGGCG 59
Db 55 GTGCAGAGCGCGCAGGAATATGGAGTTTGGGAGTTGCTGTATGGCTTTAGGGAGGGCG 114

QY 60 CGGAGGAAGAGGGCGGAGCTCGAGGTGAAAAAGCGCGGACTTCTGTGTGTGGAGTTTGGCT 119
Db 115 CGGAGGAAGAGGGCGGAGCTCGAGGTGAAAAAGCGCGGACTTCTGTGTGTGGAGTTTGGCT 174

QY 120 CGGTCCGCAAGCTCGCATGCCGAGTG-GCTCAGTGTCTTCTGGCCGAGAACCACTGGGAG 178
Db 175 CGGTCCGCAAGCTCGCATGCCGAGTGAGTCCAGTGTCTTCTGGCCGAGAACCACTGGGAG 234

QY 179 ATGGAAGAGGGCTCTGAACTCTTACCTTCCAGCTCCGGGCGGAGGAGAGCGCTTGGACG 237
Db 235 ATGGAAGAGGGCTCTGAACTCTTACCTTCCAGCTCCGGGCGGAGGAGAGCGCTTGGACG 294

QY 238 CGGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAAACCAATGAAAGAAACAAC 297
Db 295 CGGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAAACCAATGAAAGAAACAAC 354

QY 298 TGATTTCCACCACTTCTTAAATCAGCCCATCTGAAGATCTCAGCAAGAAAAAT-GGCAGCA 356
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QY 357 TGTCTCTCTC-TGATTTACCTTGGAAATTT-----GATGGATTAGATCTTAAACAATCTGTTC 408
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QY 829 TACCAGATGTGGTGGTTTACCCCAACCAATTTGGATGTCTGGGAGTTTGGGCAAAACC 888
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Db 904 TCACGGGGTCTCTGTGCAACTTAGATATATATTTGTAATGTTTAAATGTTTCAAGTGTGGGT 963
Qy 1129 TTTGGCC 1135
Db 964 TTCGTC 970

RESULT 29
US-10-066-543-1363
; Sequence 1363, Application US/10066543
; Publication No. US20030087818A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margarita
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066.543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1363
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-066-543-1363

Query Match 19.9%; Score 383; DB 5; Length 401;
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Matches 383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 79 GTTATTCCTCCCATATATATAGTACCTAAAGAGAGATCAAGTAATATGAGATTATACA 138
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Qy 656 GTGAATGTGTCAGGAATAGCTTTTCCCTTTTCCAGTACCTAAAGAGAGATCAAGTAATATGAGATTATACA 715
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Qy 716 CATGCTCGGACGAATCAATCAAGTAAATGTTTAAAGAAATCAAGAGAGCTCCA 775
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Db 379 GAGTCAGCTACAGTTATATTTGC 401

RESULT 30
US-10-242-535A-39507
; Sequence 39507, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242.535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39507
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (24)-(24)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (365)..(365)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-39507

Query Match 19.5%; Score 374.4; DB 7; Length 379;
Best Local Similarity 98.9%; Pred. No. 8.3e-84;
Matches 375; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 1 AGCTGGATTCCAAACAGGTACCTNATTTCTCTGAGCTAAATGTTTATATTTTCCATTCA 60
Qy 1431 GGCACCGAAATAGTAAATATTTTAAATAAGTCTTCAAAAGAAACATAAGAGATTATTGA 1490
Db 61 GGCACCGAAATAGTAAATATTTTAAATAAGTCTTCAAAAGAAACATAAGAGATTATTGA 120
Qy 1491 GTTCTTGGGACTGGATCTTTTATTTTCAATAGTTTCTAGTATCATCTTAAATGAAATGCCATG 1550
Db 121 GTTCTTGGGACTGGATCTTTTATTTTCAATAGTTTCTAGTATCATCTTAAATGAAATGCCATG 180
Qy 1551 ATTATCTGCAGTTAAGTAGATGACAGCTATTCTACATCAGACTTGATTTTGTGAGCTAA 1610
Db 181 ATTATCTGCAGTTAAGTAGATGACAGCTATTCTACATCAGACTTGATTTTGTGAGCTAA 240
Qy 1611 TTACATAATTGGTAAGNTAATTAATGAAACCTTATGGCTTAAATTCCTTAACCTCTTTT 1670
Db 241 TTACATAATTGGTAAGCTATTAATGAAACCTTATGGCTTAAATTCCTTAACCTCTTTT 300
Qy 1671 GATTTCATGTTTGTAGTCAATGTTTGTCAACAGAGGCAAGTTAAGCTTGTGATGTTTAA 1730
Db 301 GATTTCATGTTTGTAGTCAATGTTTGTCAACAGAGGCAAGTTAAGCTTGTGATGTTTAA 360
Qy 1731 TCGGTTTGTAGTACCATG 1749
Db 361 TCGGTTTGTAGTACCATG 379

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99	38.8	2.0	66219	3	US-09-949-016-12038	Sequence 12038, A	C 172	1.9	14000	3	US-09-817-762-10	Sequence 10, Appl
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c 109	38.6	2.0	4164	3	US-09-902-540-4661	Sequence 4661, Ap	C 182	1.9	32392	3	US-09-662-254B-27	Sequence 27, Appl
c 110	38.6	2.0	29384	3	US-09-902-540-1229	Sequence 1229, Ap	C 183	1.9	123463	3	US-09-949-016-17078	Sequence 17078, A
c 111	38.6	2.0	100877	3	US-09-949-016-13276	Sequence 13276, A	C 184	1.9	193555	3	US-09-949-016-15553	Sequence 15553, A
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c 117	38.2	2.0	25067	3	US-09-949-016-11794	Sequence 11794, A	C 190	1.9	1963	3	US-09-813-356-3	Sequence 3, Appl
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c 119	38.2	2.0	32392	3	US-09-662-254B-27	Sequence 27, Appl	C 192	1.9	678533	3	US-09-949-016-14577	Sequence 14577, A
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c 126	37.8	2.0	601	3	US-09-949-016-91175	Sequence 91175, A	C 199	1.9	107140	3	US-09-949-016-14834	Sequence 14834, A
c 127	37.8	2.0	31820	3	US-09-949-016-13356	Sequence 13356, A	C 200	1.9	601	3	US-09-949-016-13807	Sequence 13807, A
c 128	37.8	2.0	175236	3	US-09-949-016-14353	Sequence 14353, A	C 201	1.9	601	3	US-09-949-016-31808	Sequence 31808, A
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c 154	37.2	1.9	31407	3	US-09-949-016-17359	Sequence 17359, A	C 227	1.9	69924	3	US-09-949-016-15367	Sequence 15367, A
c 155	37.2	1.9	33519	3	US-09-949-016-17165	Sequence 17165, A	C 228	1.9	106418	3	US-09-949-016-13974	Sequence 13974, A
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c 161	37	1.9	661	3	US-09-814-915A-104	Sequence 104, App	C 234	1.9	261	3	US-09-913-514-23	Sequence 23, Appl
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c 164	37	1.9	6107	3	US-09-976-594-557	Sequence 557, App	C 237	1.9	6996	2	US-09-573-080A-29	Sequence 29, Appl
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c 166	37	1.9	36457	3	US-09-949-016-13031	Sequence 13031, A	C 239	1.9	9046	6	PCT-US95-0468A-2-1	Sequence 1, Appl
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c 168	37	1.9	55806	3	US-09-949-016-15605	Sequence 15605, A	C 241	1.9	23210	3	US-09-596-002-17	Sequence 17, Appl
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C 431 34.4 1.8 633 3 US-09-134-001C-834 Sequence 834, App
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ALIGNMENTS

RESULT 1

US-09-697-863A-1
; Sequence 1, Application US/09697863A
; Patent No. 6812203

GENERAL INFORMATION:

; APPLICANT: Vlaams Interuniversitair Instituut Voor Biotechnologie VZW
; TITLE OF INVENTION: CD-40 INTERACTING AND TRAF-INTERACTING PROTEINS

; FILE REFERENCE: 2676-4555US
; CURRENT APPLICATION NUMBER: US/09/697,863A

; CURRENT FILING DATE: 2000-10-27

; PRIOR APPLICATION NUMBER: PCT/EP99/03025

; PRIOR FILING DATE: 1999-04-28

; PRIOR APPLICATION NUMBER: EPO 98201392.2

; PRIOR FILING DATE: 1998-04-29

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 1920

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1627)..(1627)

; OTHER INFORMATION: N stands for any nucleotide.

; FEATURE: CDS

; NAME/KEY: CDS

; LOCATION: (20)..(1108)

; OTHER INFORMATION:

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1849)...(1849)
; OTHER INFORMATION: N stands for any nucleotide.
US-09-697-863A-1

Query Match 99.9%; Score 1918; DB 3; Length 1920;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GTGCGAGCGCGCAGGAGATGGAGTTGGGAGTTGCCCTGGAGGCGGAGGAGCGGC	60
Db	1	GTGCGAGCGCGCAGGAGATGGAGTTGGGAGTTGCCCTGGAGGCGGAGGAGCGGC	60
Qy	61	GGAGGAAGGCGCGAGCTGAGCTGAAAGCGGCGACTTCTGTGTGGAGTTGGCTC	120
Db	61	GGAGGAAGGCGCGAGCTGAGCTGAAAGCGGCGACTTCTGTGTGGAGTTGGCTC	120
Qy	121	GGTGCAGAGCTCGATGCGCGAGTGGCTCAGTGTCTTGGCGGAGAACGACTGGAGAT	180
Db	121	GGTGCAGAGCTCGATGCGCGAGTGGCTCAGTGTCTTGGCGGAGAACGACTGGAGAT	180
Qy	181	GGAAAGGGCTCTGAACCTCTACTTCGAGCTCGGTGGAGGAGCGCTTGGAGCGCG	240
Db	181	GGAAAGGGCTCTGAACCTCTACTTCGAGCTCGGTGGAGGAGCGCTTGGAGCGCG	240
Qy	241	ACCTGAAACCATCTCTGAGCCCAAGACCTATGTGACCTAAACCAATGAAGAAACAAC	300
Db	241	ACCTGAAACCATCTCTGAGCCCAAGACCTATGTGACCTAAACCAATGAAGAAACAAC	300
Qy	301	TTCCACCACTTCTAAATCAGCCCACTCTGAAGATCTCAGCAAGAAATGGCAGCATGT	360
Db	301	TTCCACCACTTCTAAATCAGCCCACTCTGAAGATCTCAGCAAGAAATGGCAGCATGT	360
Qy	361	CTCTCTCATCTGAGATTTAGATGGATAGATCTAAACAATCTCTCAGAGGCGCTCG	420
Db	361	CTCTCTCATCTGAGATTTAGATGGATAGATCTAAACAATCTCTCAGAGGCGCTCG	420
Qy	421	AGGGGTGCTCTCTACTTGTGACCCAGATGTGATTTCTCAGCAAGCTTAT	480
Db	421	AGGGGTGCTCTCTACTTGTGACCCAGATGTGATTTCTCAGCAAGCTTAT	480
Qy	481	TCCCCCATATTTAGCTACCTAAAGAGAGATCAAGTAAATTTAGATTTATCAGGTCA	540
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Qy	601	AGAGATTTATCTCTTCCAGTACCAAAATGATGAGAACTTTTATGTGTCATGTGAA	660
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Db	661	TGTGTCAAGGAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCACCAGAGGCGATGC	720
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Qy	781	AGCTACAGTTATTTTTCAGGAGATCAAAATCTAAGGGATCGAGAGTTACCAAGATGTGG	840
Db	781	AGCTACAGTTATTTTTCAGGAGATCAAAATCTAAGGGATCGAGAGTTACCAAGATGTGG	840
Qy	841	TGGTTTACCACCAACCAATCTGTGGAGTTTGGGCAAACTTAAACATTTGCCA	900
Db	841	TGGTTTACCACCAACCAATCTGTGGAGTTTGGGCAAACTTAAACATTTGCCA	900
Qy	901	GTATACATGGGATACACAAATGAATCTTAATCTTGGAAATCACTGCTGTTGTAACCTTCG	960
Db	901	GTATACATGGGATACACAAATGAATCTTAATCTTGGAAATCACTGCTGTTGTAACCTTCG	960
Qy	961	TTTTGATCGAATATTTTTCAGAGCAGCAGAGGAGGACACATTTATTTCCCGAGTTT	1020

Db	961	TTTTGATCGAATATTTTTCAGAGCAGCAGCAGAGAGGAGCACAATTTATTTCCCGAAGTTT	1020
Qy	1021	GGACCTTCTTGGATTAGAAAACTGGACTGTGGTAGATTCTCTAGTAGATCACTGGGGTCT	1080
Db	1021	GGACCTTCTTGGATTAGAAAACTGGACTGTGGTAGATTCTCTAGTAGATCACTGGGGTCT	1080
Qy	1081	TCTGTGCAACTTAGATATAATTTGTAAAAATGCTTTTCAAGTGTGGGTTTGGCCCTGATT	1140
Db	1081	TCTGTGCAACTTAGATATAATTTGTAAAAATGCTTTTCAAGTGTGGGTTTGGCCCTGATT	1140
Qy	1141	GTGCAAAATACAAATTTCCACCTTCTGNAAGTAGTTTCTGTGGAGGAATAATGTAC	1200
Db	1141	GTGCAAAATACAAATTTCCACCTTCTGNAAGTAGTTTCTGTGGAGGAATAATGTAC	1200
Qy	1201	TAGATCATTTGTACAGAAAAACCAACTATGATTTATGTTTGTGTTTTCAGAAATTCACAAT	1260
Db	1201	TAGATCATTTGTACAGAAAAACCAACTATGATTTATGTTTGTGTTTTCAGAAATTCACAAT	1260
Qy	1261	TAAAGATTAATGTTTTTAAACGAAACATTTCTGCAATTCAGGATGTGAGGCCATTTAA	1320
Db	1261	TAAAGATTAATGTTTTTAAACGAAACATTTCTGCAATTCAGGATGTGAGGCCATTTAA	1320
Qy	1321	TAAAGAGGCGACAAAGCCTGTGAGGTTTCAACGGTCTTACAGCTGCCAGCTGGATTTC	1380
Db	1321	TAAAGAGGCGACAAAGCCTGTGAGGTTTCAACGGTCTTACAGCTGCCAGCTGGATTTC	1380
Qy	1381	CAACAGAGTACCCCATTTCTCTGAGCTAATGTTTATATTTTCCATTCAGCAGCCGAAA	1440
Db	1381	CAACAGAGTACCCCATTTCTCTGAGCTAATGTTTATATTTTCCATTCAGCAGCCGAAA	1440
Qy	1441	TAGTTAAATTTAAATAAGTCTTCAAAAGAAAAACATAAGAGATTTATGAGTCTTTGGGA	1500
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Db	1501	CTGGATCCTTTATTTTCATAAGTTTCAGATCATCTTAAATGAANAATGCCATGATTCTGCA	1560
Qy	1561	GTTAAGTAGATGACAGCTATTCTACATCAGACTTCGATTTTCTCAGCTAATTTACATAAT	1620
Db	1561	GTTAAGTAGATGACAGCTATTCTACATCAGACTTCGATTTTCTCAGCTAATTTACATAAT	1620
Qy	1621	GTTAAGTAGATGACAGCTATTCTACATCAGACTTCGATTTTCTCAGCTAATTTACATAAT	1680
Db	1621	GTTAAGTAGATGACAGCTATTCTACATCAGACTTCGATTTTCTCAGCTAATTTACATAAT	1680
Qy	1681	TGTAGTCATGTTGTCAACAGAGGCAAAAGTTAAGCTTTGATGATGTTTAAATCGGTTTGT	1740
Db	1681	TGTAGTCATGTTGTCAACAGAGGCAAAAGTTAAGCTTTGATGATGTTTAAATCGGTTTGT	1740
Qy	1741	AGCACCATGGGACATTTTAAACAAATTAATGTCATCAAGAGACATAGCCCTTTTAGTT	1800
Db	1741	AGCACCATGGGACATTTTAAACAAATTAATGTCATCAAGAGACATAGCCCTTTTAGTT	1800
Qy	1801	TTGCTAATGTCGAATGGAATGCTTTTACAGGAAGTAAATGCAAAATTTTAAAGTGTG	1860
Db	1801	TTGCTAATGTCGAATGGAATGCTTTTACAGGAAGTAAATGCAAAATTTTAAAGTGTG	1860
Qy	1861	CTTTTAAAGAAAAATATTTTCCCAAGGAGAAATTTAAATTAAGAAATTTTATTTGGTAAA	1920
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RESULT 2
US-09-620-312D-889
; Sequence 899, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chinghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie

```
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Xue, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 889_
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(1127)
US-09-620-312D-889

Query Match 98.8%; Score 1897.6; DB 3; Length 1948;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1900; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 34 GGAAGATGGAGTGGGGAGTTGCTTGGAGGGCGGGAGGGCGGGAGGAGGCGGGAGGAGGCGG 93

Qy 75 AGCCTGAGTGAAGGCGGAGCTTCTGTGTGGAGTTTGGCTCGGTCCGACAGCTGCG 134
Db 94 AGCCTGAGTGAAGGCGGAGCTTCTGTGTGGAGTTTGGCTCGGTCCGACAGCTGCG 153

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; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Xue, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 889_
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(1127)
US-09-620-312D-889

555 TCACAGCTATAATGTTTGAAGAAATCAAGAGTGAATTTAAAGCCAGAGGATTTATTCCTT 614
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675 AGCTTTGCCCTTATGACATCCCATTTTGGAGACACAGAGGGCATGTGCGGAAACGAATGA 734
694 AGCTTTGCCCTTATGACATCCCATTTTGGAGACACAGAGGGCATGTGCGGAAACGAATGA 753
735 ATCAGTTAAAAATGGTTTTTAAAGAAATGCAAGAGGCTCCAGAGTCAGCTACAGTTTAT 794
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814 TTGCAGGAGATACAAATCTAAGGGATCGAGAGGTTTACAGATGTGTGGTGTTCACCAACA 873
855 ACATTTGGATGTCTGGAGTTTTTGGGCAAACTTAAACATTTGCCAGTATACATGGGATA 914
874 ACATTTGGATGTCTGGAGTTTTTGGGCAAACTTAAACATTTGCCAGTATACATGGGATA 933
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1575 AGCTATTCTACATCAGACTTGTATTTTTTGTGAGCTTAATTAATAATTTGGTAAAGTATTAAT 1634
1594 AGCTATTCTACATCAGACTTGTATTTTTTGTGAGCTTAATTAATAATTTGGTAAAGTATTAAT 1653
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Db 1654 GAAACCTTATGCTTAAATTCCTTAACTCCTTTTGTATTCATGTTTGTAGTCATGTTGT 1713
Qy 1695 CAACAGAGCGAAAGTTAAGCTTGATGATGTTTAAATCGGTTTGATACACCATGGGACA 1754
Db 1714 CAACAGAGCGAAAGTTAAGCTTGATGATGTTTAAATCGGTTTGATACACCATGGGACA 1773
Qy 1755 TTTTCTTAAACAAAATAAATGATCAAGACATAGCCTTTTGTAGTTTGTCTAAATGTGAA 1814
Db 1774 TTTTCTTAAACAAAATAAATGATCAAGACATAGCCTTTTGTAGTTTGTCTAAATGTGAA 1833
Qy 1815 ATGGAATGCTTTTACAGGAAGTAAATGCAAAATTANTTTTAAAGTGTGCTTTTAAAGAAAAT 1874
Db 1834 ATGGAATGCTTTTACAGGAAGTAAATGCAAAATTACTTTTAAAGTGTGCTTTTAAAGAAAAT 1893
Qy 1875 ATTTTCCCAAGAGGAATTTAAATTAAGAAATTTTATTTGTGTA 1920
Db 1894 ATTTTCCCAAGAGGAATTTAAATTAAGAAATTTTATTTGTGTA 1939

RESULT 3

US-09-118-554-63/c

; Sequence 63, Application US/09118554A

; Patent No. 6365348

; GENERAL INFORMATION: ☒

; APPLICANT: Reed, Steven G.

; APPLICANT: Xu, Jiangchun

; TITLE OF INVENTION: COMPOUNDS FOR DIAGNOSIS OF BREAST CANCER AND

; TITLE OF INVENTION: METHODS FOR THEIR USE

; FILE REFERENCE: 210121.450C1

; CURRENT APPLICATION NUMBER: US/09/118,554A

; CURRENT FILING DATE: 1998-07-17

; EARLIER APPLICATION NUMBER: 08/988,255

; EARLIER FILING DATE: 1997-12-24

; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 63

; LENGTH: 1079

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-118-554-63

Query Match 55.5%; Score 1066.4; DB 3; Length 1079;

Best Local Similarity 99.8%; Pred. No. 3.5e-290;

Matches 1078; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 423 GGGTGTGTTCCCTACTTACTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTC 482
Db 1079 GGGTGTGTTCCCTACTTACTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTC 1020
Qy 483 CCCATATTATAGCTACCTAAAGAGAGATCAAGTAATTTATGAGATTTATACAGGTCATG 542
Db 1019 CCCATATTATAGCTACCTAAAGAGAGATCAAGTAATTTATGAGATTTATACAGGTCATG 960
Qy 543 AAGAAGATATTTACAGCTATATGTTGAGAAATCAAGAGTGAATTTAAAGCCAAAG 602
Db 959 AAGAAGATATTTACAGCTATATGTTGAGAAATCAAGAGTGAATTTAAAGCCAAAG 900
Qy 603 AGATTATTCCTTTTCAAGTACCATAATGATGAGAAACCTTTTATGTCATGTGAATG 662
Db 899 AGATTATTCCTTTTCAAGTACCATAATGATGAGAAACCTTTTATGTCATGTGAATG 840
Qy 663 TGTACAGGAATGAGCTTTGCTTTATGATCCATTTGGAGAGACACAGAGGCGATGCTG 722
Db 839 TGTACAGGAATGAGCTTTGCTTTATGATCCATTTGGAGAGACACAGAGGCGATGCTG 780
Qy 723 CGGAAACGAATGATCAGTTAAATGTTTTAAAGAAATGCAAGAGGCTCCAGAGTCAG 782
Db 779 CGGAAACGAATGATCAGTTAAATGTTTTAAAGAAATGCAAGAGGCTCCAGAGTCAG 720
Qy 783 CTACAGTTATTTGACAGGAGATACAAATCTAAGGGATCGAGAGGTTTACAGATGTGGTG 842
Db 719 CTACAGTTATTTGACAGGAGATACAAATCTAAGGGATCGAGAGGTTTACAGATGTGGTG 660

Qy 843 GTTTACCCAAACAATTTGATGCTCTGGGAGTTTGTGGGCAAAACCTTAAACAATTCGCCAGT 902
Db 659 GTTTACCCAAACAATTTGATGCTCTGGGAGTTTGTGGGCAAAACCTTAAACAATTCGCCAGT 600
Qy 903 ATACATGGGATACACAATGAACTCTAATCTTGGAAATCACTGCTGTGTAACCTTCGTT 962
Db 599 ATACATGGGATACACAATGAACTCTAATCTTGGAAATCACTGCTGTGTAACCTTCGTT 540
Qy 963 TTGATCGAATATTTTTCAGAGCAGCAGAGAGGAGGACACATTTATTTCCCGAAGTTTGG 1022
Db 539 TTGATCGAATATTTTTCAGAGCAGCAGAGAGGAGGACACATTTATTTCCCGAAGTTT-G 481
Qy 1023 ACCTTTCTTGGATTAGAAAACTGGACTGTGTAGATTTCTTAGTATCACTGGGGTCTTC 1082
Db 480 ACCTTTCTTGGATTAGAAAACTGGACTGTGTAGATTTCTTAGTATCACTGGGGTCTTC 421
Qy 1083 TGTGCAACTTAGATATATATTTGTAATGCTTTTCAAGTGTGGGTTTGGCCCTGATGTT 1142
Db 420 TGTGCAACTTAGATATATATTTGTAATGCTTTTCAAGTGTGGGTTTGGCCCTGATGTT 361
Qy 1143 TGCAAATACAATTTCCACCTTCTGGAAGGTAGGTTTCTGTGGAGGAAATAATGTACTTA 1202
Db 360 TGCAAATACAATTTCCACCTTCTGGAAGGTAGGTTTCTGTGGAGGAAATAATGTACTTA 301
Qy 1203 GATCATTTGTACAGAAAAACCAACTATGATTTATGTTGTGTTTTCAGAAATTCACATTA 1262
Db 300 GATCATTTGTACAGAAAAACCAACTATGATTTATGTTGTGTTTTCAGAAATTCACATTA 241
Qy 1263 AAGATTAATGTTTATTTAAAGAAACACATTCCTGCTGATTCAGGATGTAGGCCATTAATA 1322
Db 240 AAGATTAATGTTTATTTAAAGAAACACATTCCTGCTGATTCAGGATGTAGGCCATTAATA 181
Qy 1323 AAAAGGGCACAAGGCTGTACAGATTTTCAAGGTCCTTACAGCTGCCAGCTGGATTCCA 1382
Db 180 AAAAGGGCACAAGGCTGTACAGATTTTCAAGGTCCTTACAGCTGCCAGCTGGATTCCA 121
Qy 1383 AACAGGTATACCCCATTTGCTCTGAGCTAATGTTTATATTTTCCATTCAGGCAACCGAAATA 1442
Db 120 AACAGGTATACCCCATTTGCTCTGAGCTAATGTTTATATTTTCCATTCAGGCAACCGAAATA 61
Qy 1443 GTTAATATTTAAATAAAGTCTTTCAAAAGAAACATAGAAGATTTAGTTCTTGGGACT 1502
Db 60 GTTAATATTTAAATAAAGTCTTTCAAAAGAAACATAGAAGATTTAGTTCTTGGGACT 1

RESULT 4

US-09-118-627-63/c

; Sequence 63, Application US/09118627A

; Patent No. 6379951

; GENERAL INFORMATION: ☒

; APPLICANT: Reed, Steven G.

; APPLICANT: Xu, Jiangchun

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF BREAST CANCER

; TITLE OF INVENTION: AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.446C1

; CURRENT APPLICATION NUMBER: US/09/118,627A

; CURRENT FILING DATE: 1998-07-17

; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 63

; LENGTH: 1079

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-118-627-63

Query Match 55.5%; Score 1066.4; DB 3; Length 1079;

Best Local Similarity 99.8%; Pred. No. 3.5e-290;

Matches 1078; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 423 GGGTGTGTTCCCTACTTACTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTC 482
Db 1079 GGGTGTGTTCCCTACTTACTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTC 1020


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QY 483 CCCATATTATAGCTACCTAAGAAGAGATCAAGTAATTATGAGATTATTACAGGTCATG 542
Db 1019 CCCCATATTATAGCTACCTAAGAAGAGATCAAGTAATTATGAGATTATTACAGGTCATG 960
QY 543 AAGAAGGATATTTCACAGCTAATAATGTTGAAGAAATCAAGAGTCAAAATTAAGAAAGCCAAAG 602
Db 959 AAGAAGGATATTTCACAGCTAATAATGTTGAAGAAATCAAGAGTCAAAATTAAGAAAGCCAAAG 900
QY 603 AGATTATTCCTTTCCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCATGTGAATG 662
Db 899 AGATTATTCCTTTCCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCATGTGAATG 840
QY 663 TGTCAAGGAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCACAGAGGGCATGCTG 722
Db 839 TGTCAAGGAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCACAGAGGGCATGCTG 780
QY 723 CGGAACGAATGAATCAGTTAAATAATGTTTAAAGAAATCAAGAGGCTCCAGAGTCAG 782
Db 779 CGGAACGAATGAATCAGTTAAATAATGTTTAAAGAAATCAAGAGGCTCCAGAGTCAG 720
QY 783 CTACAGTTATATTTCAGAGGATACAAATCTAAGGGATCGAGAGTTACCCAGATGTGGTG 842
Db 719 CTACAGTTATATTTCAGAGGATACAAATCTAAGGGATCGAGAGTTACCCAGATGTGGTG 660
QY 843 GTTTACCCAAACAATGTGTGATGCTGGGAGTTTGGGCAAACTTAAACATTTGCCAGT 902
Db 659 GTTTACCCAAACAATGTGTGATGCTGGGAGTTTGGGCAAACTTAAACATTTGCCAGT 600
QY 903 ATACATGGGATACAAATGAACCTTAATCTTGAATAAATGCTGCTTGTAAACCTTCGTT 962
Db 599 ATACATGGGATACAAATGAACCTTAATCTTGAATAAATGCTGCTTGTAAACCTTCGTT 540
QY 963 TTGATCGAATATTTTCAGAGCAGCAGAGAGGACACATTAATTTCCCGAAGTTTGG 1022
Db 539 TTGATCGAATATTTTCAGAGCAGCAGAGAGGACACATTAATTTCCCGAAGTTT-G 481
QY 1023 ACCCTTCTGGATTAGAATAATCTGACTGTGTGATATTCCTAGTGATCACTGGGGTCTTC 1082
Db 480 ACCCTTCTGGATTAGAATAATCTGACTGTGTGATATTCCTAGTGATCACTGGGGTCTTC 421
QY 1083 TGTCAACTTAGATATATATTGTAATAATGCTTTTCAAGTGTGGGTTTGGCCCTGATTGT 1142
Db 420 TGTCAACTTAGATATATATTGTAATAATGCTTTTCAAGTGTGGGTTTGGCCCTGATTGT 361
QY 1143 TGCAAAATACAATTTCCACCTTCTGGAAGGTAGGTTGCTGTGGAGGAAATAATGTACTA 1202
Db 360 TGCAAAATACAATTTCCACCTTCTGGAAGGTAGGTTGCTGTGGAGGAAATAATGTACTA 301
QY 1203 GATCATTTGTACAGAAAACCAACTATGATTTATGTTGTTGTTTTCAGAAATCAACATTA 1262
Db 300 GATCATTTGTACAGAAAACCAACTATGATTTATGTTGTTGTTTTCAGAAATCAACATTA 241
QY 1263 AAGATTATGTTTATTTAAACGAACACATCTGCTGATTCAGAGTGTGAGGCCATTTAATA 1322
Db 240 AAGATTATGTTTATTTAAACGAACACATCTGCTGATTCAGAGTGTGAGGCCATTTAATA 181
QY 1323 AAAAGGGCACAAGGCTGTGAGAGTTTTCACCGGTGCTTACAGCTGCCAGCTGGAATCCA 1382
Db 180 AAAAGGGCACAAGGCTGTGAGAGTTTTCACCGGTGCTTATAGCTGCCAGCTGGAATCCA 121
QY 1383 AACAGGTACCCCATGCTGCTGAGCTAATGTTTATATTTTTCATTCAGGACCCGAATA 1442
Db 120 AACAGGTACCCCATGCTGCTGAGCTAATGTTTATATTTTTCATTCAGGACCCGAATA 61
QY 1443 GTTAATATTTAAATAAGCTTTCAAAAGAAACATAAGAGATTAATGAGTTCTTTGGGACT 1502
Db 60 GTTAATATTTAAATAAGCTTTCAAAAGAAACATAAGAGATTAATGAGTTCTTTGGGACT 1
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RESULT 5

US-09-602-877A-63/c

; Sequence 63, Application US/09602877A

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; Patent No. 6432707
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.446C5
; CURRENT APPLICATION NUMBER: US/09/602,877A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 63
; LENGTH: 1079
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-602-877A-63
```

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Query Match 55.5%; Score 1066.4; DB 3; Length 1079;
Best Local Similarity 99.8%; Pred.No. 3.5e-290;
Matches 1078; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 423 GGGTGTGTTCTCTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGAAATTTATC 482
Db 1079 GGGTGTGTTCTCTACTTAGCTTTGTACAGCCAGATGTGATATTTCTACAGAAATTTATC 1020
QY 483 CCCCATATTATAGCTACCTAAGAAGAGATCAAGTAATTATGAGATTATTACAGGTCATG 542
Db 1019 CCCCATATTATAGCTACCTAAGAAGAGATCAAGTAATTATGAGATTATTACAGGTCATG 960
QY 543 AAGAAGGATATTTCACAGCTAATAATGTTGAAGAAATCAAGAGTCAAAATTAAGAAAGCCAAAG 602
Db 959 AAGAAGGATATTTCACAGCTAATAATGTTGAAGAAATCAAGAGTCAAAATTAAGAAAGCCAAAG 900
QY 603 AGATTATTCCTTTCCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCATGTGAATG 662
Db 899 AGATTATTCCTTTCCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGCATGTGAATG 840
QY 663 TGTCAAGGAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCACAGAGGGCATGCTG 722
Db 839 TGTCAAGGAATGAGCTTTGCCCTTATGACATCCCATTTGGAGAGCACAGAGGGCATGCTG 780
QY 723 CGGAACGAATGAATCAGTTAAATAATGCTTTTAAAGAAATGCAAGAGGCTCCAGAGTCAG 782
Db 779 CGGAACGAATGAATCAGTTAAATAATGCTTTTAAAGAAATGCAAGAGGCTCCAGAGTCAG 720
QY 783 CTACAGTTATATTTCAGAGGATACAAATCTAAGGGATCGAGAGTTTACAGATGTGGTG 842
Db 719 CTACAGTTATATTTCAGAGGATACAAATCTAAGGGATCGAGAGTTTACAGATGTGGTG 660
QY 843 GTTTACCCAAACAATGTGTGATGCTGGGAGTTTGGGCAAACTTAAACATTTGCCAGT 902
Db 659 GTTTACCCAAACAATGTGTGATGCTGGGAGTTTGGGCAAACTTAAACATTTGCCAGT 600
QY 903 ATACATGGGATACAAATGAACCTTAATCTTGAATAAATGCTGCTTGTAAACCTTCGTT 962
Db 599 ATACATGGGATACAAATGAACCTTAATCTTGAATAAATGCTGCTTGTAAACCTTCGTT 540
QY 963 TTGATCGAATATTTTCAGAGCAGCAGAGAGGACACATTAATTTCCCGAAGTTTGG 1022
Db 539 TTGATCGAATATTTTCAGAGCAGCAGAGAGGACACATTAATTTCCCGAAGTTT-G 481
QY 1023 ACCCTTCTGGATTAGAATAATCTGACTGTGTGATATTCCTAGTGATCACTGGGGTCTTC 1082
Db 480 ACCCTTCTGGATTAGAATAATCTGACTGTGTGATATTCCTAGTGATCACTGGGGTCTTC 421
QY 1083 TGTCAACTTAGATATATATTGTAATAATGCTTTTCAAGTGTGGGTTTGGCCCTGATTGT 1142
Db 420 TGTCAACTTAGATATATATTGTAATAATGCTTTTCAAGTGTGGGTTTGGCCCTGATTGT 361
QY 1143 TGCAAAATACAATTTCCACCTTCTGGAAGGTAGGTTTGTGCTGTGGAGGAAATAATGTACTA 1202
Db 360 TGCAAAATACAATTTCCACCTTCTGGAAGGTAGGTTTGTGCTGTGGAGGAAATAATGTACTA 301
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; LENGTH: 268
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-397-787-312

Query Match      14.0%; Score 268; DB 3; Length 268;
Best Local Similarity 100.0%; Pred. No. 2.3e-65; Mismatches 0; Indels 0; Gaps 0;
Matches 268; Conservative 0;

Qy 982 AGCAGCAGCAGAGAGGAGGACACATTATTCGCCGAAGTTTGGACCTTCTTGATTTAGAAAA 1041
Db 268 AGCAGCAGCAGAGAGGAGGACACATTATTCGCCGAAGTTTGGACCTTCTTGATTTAGAAAA 209

Qy 1042 ACTGCATGTGGTAGATTCTCTAGTAGATCACTGGGGTCTTCTGTGCAACTTAGATATAAT 1101
Db 208 ACTGCATGTGGTAGATTCTCTAGTAGATCACTGGGGTCTTCTGTGCAACTTAGATATAAT 149

Qy 1102 ATTGTAAATGCTTTTCAAGTGTGGGTTTTCGCCCTGATTGTTGCAAAATACAAATTTCCACC 1161
Db 148 ATTGTAAATGCTTTTCAAGTGTGGGTTTTCGCCCTGATTGTTGCAAAATACAAATTTCCACC 89

Qy 1162 TTCTGGAAGGTAGGTTTGTCTGTGGAGGAAATAATGTACTAGATCATTTGTCCACAGAAAA 1221
Db 88 TTCTGGAAGGTAGGTTTGTCTGTGGAGGAAATAATGTACTAGATCATTTGTCCACAGAAAA 29

Qy 1222 CCAACTATGATTATGTTGTTGTTTCA 1249
Db 28 CCAACTATGATTATGTTGTTGTTTCA 1

RESULT 8
US-09-621-976-8403
; Sequence 8403, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8403
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8403

Query Match      4.5%; Score 86.6; DB 3; Length 379;
Best Local Similarity 91.1%; Pred. No. 4e-14;
Matches 92; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 170 GACTGGGAGATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCCGGTGGAGGAGCGCC 229
Db 7 GCCTTTGTTTTCAGAGGGGCTCTGAACCTCTACTTCGAGCCTCCGGTGGAGGAGCGCC 66

Qy 230 TTGGAACGCCGACCTGAAACCATCTCTGAGCCCAAGACCTA 270
Db 67 TTGGAACGCCGACCTGAAACCATCTCTGAGCCCAAGACCTA 107

RESULT 9
US-09-806-708B-22
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806.708B
; CURRENT FILING DATE: 2001-04-03

; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. PAEL promoters
US-09-806-708B-22

Query Match      3.0%; Score 58; DB 3; Length 1141;
Best Local Similarity 11.5%; Pred. No. 8.9e-06;
Matches 89; Conservative 296; Mismatches 379; Indels 7; Gaps 2;

Qy 1123 GTGGGTTTCCCTGATTGTTGCAATACAAATTCACCTTCTGGAAGGTAGGTTTGCT 1182
Db 54 SKSRKWTWARMYCKYREYNNKGRWKGWYKKBWYBCANNNTSBRYHARRKMDKTA YBMT 113

Qy 1183 GTGGAGGAAATAATGTACTAGATCATTTGTCCACAGAAAAACAA--CTATGATTTATGTT 1240
Db 114 MTNKGKGTGRHRYWRWRAMEDTVDHHYVTAMNNATTTTCMDKDKDKRTRWWWKNNAT 173

Qy 1241 GTGTTTTCAGAAATTCACATTAAGATTAATGTTTATTTAAACGAAACACATTCCTGCAATT 1300
Db 174 GWDDDTKYHMMNNNGCBTVTMVRYKTDROWSBKRMNYGMWKNWSYDVTVYYVWVDDM 233

Qy 1301 CAGGATGTGAGGCCATTTAATAAAAGGSCACAAAGCCTGTCCAGAGTTTTCACGGTGCT 1360
Db 234 CKRVREWVTRGRMRNMYMAWBTFAHRRRTNNGWBTBAMAYRRWTTMNNNNNNNAKAMCKRAK 293

Qy 1361 TACAGCTGCCAGCTGGGATTCACAAACAGGTACCCCATTTCTCTGAGCTAATGTTTATATT 1420
Db 294 YWGNRABVNSTCTTWKSKTTKVRTSWANNCRAGDANKDKHKWKWSAAMGVYNNNNNN 353

Qy 1421 TTTCATTCAGGCACCGAAATAGTTAATATTTAAATAAGTCTTTCACAAAGAAACACATAAG 1480
Db 354 NWTYKARHBARDWVWWSAWKWHANAHAHYSRKWTBYKRKTVMVNNNGGTTTMMKRWAW 413

Qy 1481 AGATTATTGAGTCTCTGGGACTCGATCCTTATTTCATAGTTCCAGATCATCTTAAATGA 1540
Db 414 YWKMDMDVBGTYYNNNNNGGRTYYGWTNKKKMTYYKWKANNCKWRADWDKCTCHNNTTW 473

Qy 1541 AAATGCCATGATTATCTGCAGTTAAGTAGATGACAGCTATTTCTACATCAGACTTGATTTT 1600
Db 474 KMKTYNNCYWKSMTNGSKSHRBAAAVTYTWMMWRRYAHANNNNNDYWWKACTWYKYBVC 533

Qy 1601 TGTGAGTAATTCATAAATTTGGTAAAGNTATAAATTTGAAACCTTATGGCTTAAATTCCTTA 1660
Db 534 SKWNNYAAWYTKSSWNTSYRYRWKTNNSWRWSDTRSMGRANNYARABHYGKWNTRW 593

Qy 1661 ACTCCTTTTGTATCATGTTTGTAGTCATGTTGTCAACAGAGGCAAGATTAAAGCTTGATG 1720
Db 594 WBWSHTWBHRA-----GAHYWMBMYBAKCHCMKAWYKAKKYAGAGGNNNNNNNNNN 648

Qy 1721 ATGGTTAAATTCGGTTTGTATAGCACCATGGGACATTTTTTTAAACAAAAATAAATGCGATGA 1780
Db 649 NNNNNNATCARDYYAASRWYMANAKWYYKYBAANNAYYTHANNWGCWNNATDTRTM 708

Qy 1781 AGAGACATAGCCTTTTGTAGTTTGTGTAATGTGAAATGGAATGCTTTTACAGGAAGTAAT 1840
Db 709 WKNNNNNAGTWKNNNNNNAKNSAAKVAAYAAAAKAAKCHWRWANKWAMRGWHAADAABT 768

Qy 1841 GCAAAATTANTTTAAGTGTGCTTTTAAAGAAAAATATTTTCCCCACAGAGA 1891
Db 769 TDKRNNGATKYTTTTNNNTTYRGVVTNTAARDGWANNNNNNNNNNNNNNNGW 819

RESULT 10
US-10-131-827-787
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D6
1106 RRRRRRRRRRRRRRRRRRRRRRRRRRRR 1075

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RESULT 13
US-09-949-002-592
; Sequence 592, Application US/09949002
; Patent No. 690016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN
; TITLE OF INVENTION: WITH INFLAMMATORY AUTO
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10923
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 592
; LENGTH: 18651
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-592

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Query Match	2.5%	Score	47.6	DB	3	Length	18651
Best Local Similarity	44.5%	Pred. No.	0.039				
Matches	185	Conservative	0	Mismatches	231	Indels	0
Qy	1505	ATCCTTTATTTTCATAGTTCAGATCATCTTAAATGAAATGCCATGATTCATGCAGTTA	1564				
Db	9966	ATTTTAAATTTTAAATAAATTTTAAATTAATAAAATTTAAATTTTAAATTAATAATAATTA	10025				
Qy	1565	AGTAGATGACAGAGCTATCTACATCAGACACTTGAATTTTGTGACAGCTAAATTCATAATTCGTA	1624				
Db	10026	AAATTTTAAATTTTAAATTTTAAATAAATAATTAATAATTTAAATTTTAAATTTTAAATTT	10085				
Qy	1625	AGNTATTAATTTGAAACCTTATGGCTTAAAAATTCCTTAATCCTTTTGTGAATTCATGTTTGTGA	1684				
Db	10086	TAAATTTAAATTTTAAATTAATAAATAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT	10145				
Qy	1685	GTCAATGTTGTCAACAGAGGCAAGTTTAAGCTTCATGATGTTAAATTCGGTTCGTGATAGCA	1744				
Db	10146	AAATTTAAATTTAACTTAATTTTAAATTTTAAATTTTAACTTAATTTTAAATTTTAAATTTTAAATTT	10205				
Qy	1745	CCATGGGACATTTTTTTTAAACAAAAATAAATGCAATGAAGAGACATAGCCTTTTATGTTTTGTC	1804				
Db	10206	TTAAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA	10265				
Qy	1805	TAATTTGGAATGGAATGCTTTTACAGGAAGTAAATGCAAAATTAATTTTAAAGTGTCCTTTT	1864				
Db	10266	TATTTTAAATTTTAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT	10325				
Qy	1865	AAAGAAAAATATTTTCCCCACAGAGAAAAATTTAAATAAAGAAATTTTATTTTGGTAAA	1920				
Db	10326	AAATTTTAAATTTGCTTCAATATAAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA	10381				

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RESULT 14
US-09-949-002-786
; Sequence 786, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08

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; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 786
; LENGTH: 18682
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-786

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Query Match	2.5%;	Score 47.6;	DB 3;	Length 18682;
Best Local Similarity	44.5%;	Pred. No. 0.039;		
Matches 185;	Conservative 0;	Mismatches 231;	Indels 0;	Gaps 0;
Qy	1505	ATCCTTTATTTTCATAGTTTCAGATCATCTTAAATGAAAATGCCATGATTATCTGCAGTTA	1564	
Db	9986	ATTTTTTAATTAATAAATTTTAATTTATTAATAATTAATAATTTTAATTTAAATATTAATAA	10045	
Qy	1565	AGTAGATGACAGCTATTTACATTCAGACTTGATTTTTTGTCTAGCTAATTTACATAAATGGTA	1624	
Db	10046	AAATTTTTTAATTTTAAATTTTAAATAATAATTTAAATTTAAATTTTAAATTTTAAATTT	10105	
Qy	1625	AGNTATAAATGAAACCTTATGCTTAAAAATTCCTTAACTCCTTTTTTGTATTCATGTTTCTGA	1684	
Db	10106	TAAATTTAAATTTTAAATAAACATTTTAAATTTTTTAAATTTTAAATTTAAATTTAAATTTT	10165	
Qy	1685	GTCAATGTCGCAACGAGAGCAAGTTAAAGCTTTGATGATGGTTTAAATCGGTTTGTATAGCA	1744	
Db	10166	AATATTAAATTTAACTTTTAAATTTTAAATTTAAATTTAACTTTAAATTTAAATTTAAATA	10225	
Qy	1745	CNATGGGACATTTTTTTTAAACAAAAATAAATGCAATGCAATGAGAGACATAGCCTTTTACGTTTGC	1804	
Db	10226	TTAAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA	10285	
Qy	1805	TAAATGCGAAATGGAATGCTTTTACAGGAAGTAAATGCAAAATTAATTTTAAAGTGTGCTTT	1864	
Db	10286	TATTTTTTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT	10345	
Qy	1865	AAAGAAAAATTTTTCCCAACAGGAGAAATTTTAAATAAAGAAATTTTATTTGGTAAA	1920	
Db	10346	AATTTTAAATGCTTCAATATTAATAATTAATAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA	10401	

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RESULT 15
US/08-916-421B-1/c
  Sequence 1, Application US/08916421B
  Patent No. 6503729
  GENERAL INFORMATION:
  APPLICANT: Bult et al.
  TITLE OF INVENTION: Complete Genome Sequence
  Patent No. 6503729
  TITLE OF INVENTION: jannaschii
  FILE REFERENCE: FB275
  CURRENT APPLICATION NUMBER: US/08/916,421B
  CURRENT FILING DATE: 1997-08-22
  PRIOR APPLICATION NUMBER: US 60/024,428
  PRIOR FILING DATE: 1996-08-22
  NUMBER OF SEQ ID NOS: 3
  SOFTWARE: PatentIn version 3.1
  SEQ ID NO 1
  LENGTH: 1664976
  TYPE: DNA
  ORGANISM: Methanococcus jannaschii
  FEATURE:
  NAME/KEY: misc feature
  LOCATION: (28222)..(28222)
  OTHER INFORMATION: n equals a, t, c, or g
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  NAME/KEY: misc feature
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  OTHER INFORMATION: n equals a, t, c, or g
  NAME/KEY: misc feature
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;; OTHER INFORMATION: n equals a, t, c, or g
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;; OTHER INFORMATION: n equals a, t, c, or g
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;; LOCATION: (682442)..(682442)
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;; OTHER INFORMATION: n equals a, t, c, or g
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;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc feature
;; LOCATION: (871619)..(871619)
;; OTHER INFORMATION: n equals a, t, c, or g
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;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc feature
;; LOCATION: (1096846)..(1096846)
;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc feature
;; LOCATION: (1119881)..(1119881)
;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc feature
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;; OTHER INFORMATION: n equals a, t, c, or g
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;; LOCATION: (1310988)..(1310988)
;; OTHER INFORMATION: n equals a, t, c, or g
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;; LOCATION: (1313224)..(1313224)
;; OTHER INFORMATION: n equals a, t, c, or g
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;; LOCATION: (1349473)..(1349473)
;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc feature
;; LOCATION: (1349491)..(1349491)
;; OTHER INFORMATION: n equals a, t, c, or g
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;; LOCATION: (1602912)..(1602912)
;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc feature
;; LOCATION: (1603734)..(1603734)
;; OTHER INFORMATION: n equals a, t, c, or g
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;; LOCATION: (1637998)..(1637998)
;; OTHER INFORMATION: n equals a, t, c, or g
;; NAME/KEY: misc feature
;; LOCATION: (1664854)..(1664854)
;; OTHER INFORMATION: n equals a, t, c, or g
;; US-08-916-421B-1
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LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
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NAME/KEY: misc feature
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FEATURE:
NAME/KEY: misc feature
LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc feature
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OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
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OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g
Query Match 2.4%; Score 47; DB 3; Length 1664976;
Best Local Similarity 52.9%; Pred. No. 0.78;
Matches 101; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 457 TGTGATATTTCTACAGGAGTTATTTCCCCATATATATAGTACCTAAAGAGAGATCAAG 516
Db 685950 TGCTATATAACTTTTGTGAATTTTAAATAACAAATTAATAAATAGACACATTATAAAAAAGT 685891
QY 517 TAAATTATGAGATTATTACAGGTCTATGAAGAAGGATATTTTCACAGCTATAATGTTTGAAGAA 576
Db 685890 TAGTATTGACTTTTATCAAAATATATAAAGAAATAAATAAATAATATGATAATAAA 685831
QY 577 ATCAAGAGTGAATTTAAAGCCAGAGATATTTCCTTTTCCAAAGTACCAAAATGATGAG 636
Db 685830 AAAATATTTAAATATAAAATGCTAATGTTTATTTCTATTCCTCAATTTCTTTAAAACTGGG 685771
QY 637 AAACCTTTTAT 647
Db 685770 TCAACTGGGAT 685760
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```
RESULT 17
US-09-422-978-2947/c
Sequence 2947, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ilya
FILE OF INVENTION: Biallelic markers for use in constructing a high density...
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 2947
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 99-20228-290 : polymorphic base T or C
US-09-422-978-2947
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Query Match 2.4%; Score 46.6; DB 3; Length 47;
Best Local Similarity 97.9%; Pred. No. 0.0023;
Matches 46; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1430 AGGCACCGAAATAGTTAATATTTAAATAAAGTCTTCAAAAGAAACA 1476
Db 47 AGGCACCGAAATAGTTAATATTTTAAATAAAGTCTTCAAAAGAAACA 1
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RESULT 18
US-09-248-796A-6470
Sequence 6470, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
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Db 86583 TGTAATATATTACTATGTAATATATTACATAGTAAATATATGTAATATTAATGTAATTAATA 86524
Qy 1744 ACCATGGGACATTTTTTTTAAACAAATAAATGCGATGAAGACATAGCCTTTTATAGTTTG 1803
Db 86523 ATGTAGATTATATATATATATATATATATATATATATATATATATATATATATATATATAT 86464
Qy 1804 CTAATTGGAATGGAATGCTTTTACAGGAAGTAATGCAATTAATTTTAAAGTGT 1859
Db 86463 TATACCTTATATATAGTATCTGTTATATATAGTATATATATATATATATATATATATAT 86408

RESULT 23
US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATTORI, WASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match 2.2%; Score 42.8; DB 3; Length 640681;
Best Local Similarity 47.0%; Pred. No. 6.9;
Matches 131; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

Qy 1570 ATGACAGCTATTCTACATCAGACTTGATTTTGTGACGTAATATACATAATTTGGTAAGNTA 1629
Db 35588 ATTATCCCTTTTATTATATATGTAATAAATTAATAATTTATTAGATATTTTGTAAATAT 35647
Qy 1630 TAATTGAACTTATGCTTAAATCTTAACTCTTTTGAATCATGTTTGTAGTCAT 1689
Db 35648 AATTTGAAAAAATTTATTTTGAATAATATATTTTGTGATGATAAATTTTATTACTTAT 35707
Qy 1690 GTTGTCACAGAGCAAGTAAAGCTTGATGATGTTTAAATCGGTTTGTAGCACCATG 1749
Db 35708 TTGATATAAAGAAAAATATATTTTTCATATTAATAATCTATATTAATTAACATG 35767
Qy 1750 GGACATTTTTTAAACAAAAATAATGCGATGAAGACATAGCCTTTTATAGTTTGTCTAAT 1809
Db 35768 TTAATTTTGAANAATAATATAAANAAGATCAGATTTCAAAATTTCAAAATTTGAATAAAA 35827
Qy 1810 GTGAATGGAATGCTTTTACAGGAGTAATGCAATTA 1848
Db 35828 TTAAATATATATATATATCTAAAAATCATCAAAAAATA 35866

RESULT 24
US-09-990-613A-33
; Sequence 33, Application US/09990613A
; Patent No. 6818446
; GENERAL INFORMATION:
; APPLICANT: Wu, Reen
; APPLICANT: Chen, Yin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: ANALYSIS OF MUCIN GENE EXPRESSION AND IDENTIFICATION OF
; TITLE OF INVENTION: DRUGS HAVING THE ABILITY TO INHIBIT MUCIN GENE EXPRESSION
; FILE REFERENCE: 39754-0721A
; CURRENT APPLICATION NUMBER: US/09/990,613A
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 36
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2751
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-990-613A-33

Query Match 2.2%; Score 42.6; DB 3; Length 2751;
Best Local Similarity 55.9%; Pred. No. 0.33;
Matches 81; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 9 GCGGCAGGAAGATGGAGTTGGGGAGTTGCTTGGAGGCGGGAGGCGGCGGAGGAAG 68
Db 1449 GGGGCTGTCTGGGCGAGGAGAGCTGCTTGGGCGGGGAGGGGCTGTAGGCCACAGG 1508
Qy 69 AGGCGAGCCTGAGGTGAAAAAGCGCGACTTCTGTGTGTGGAGTTTGCCTCGGTCCCAA 128
Db 1509 AGGGCTGCTTGGGCTGGGAGGGGCTGCTGGGGTGGGAGGGGCTGCTGCGCGCGGA 1568
Qy 129 GCTCGATGCCGCGAGTGGCTCAGTG 153
Db 1569 GCCGGGCGTGGGAGTGGCTGGTTG 1593

RESULT 25
US-09-990-613A-6
; Sequence 6, Application US/09990613A
; Patent No. 6818446
; GENERAL INFORMATION:
; APPLICANT: Wu, Reen
; APPLICANT: Chen, Yin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: ANALYSIS OF MUCIN GENE EXPRESSION AND IDENTIFICATION OF
; TITLE OF INVENTION: DRUGS HAVING THE ABILITY TO INHIBIT MUCIN GENE EXPRESSION
; FILE REFERENCE: 39754-0721A
; CURRENT APPLICATION NUMBER: US/09/990,613A
; CURRENT FILING DATE: 2001-11-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22773
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-990-613A-6

Query Match 2.2%; Score 42.6; DB 3; Length 22773;
Best Local Similarity 55.9%; Pred. No. 1.1;
Matches 81; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 9 GCGGCAGGAAGATGGAGTTGGGGAGTTGCTTGGAGGCGGGAGGCGGCGGAGGAAG 68
Db 5611 GGGGCTGTCTGGGCGAGGAGAGCTGCTTGGGCGGGGAGGGGCTGTAGGCCACAGG 5670
Qy 69 AGGCGAGCCTGAGTGAATAAAGCGCGACTTCTGTGTGTGGAGTTTGCCTCGGTCCCAA 128
Db 5671 AGGGCTGCTTGGGCTGGGAGGGGCTGCTGGGGTGGGAGGGGCTGCTGCGCGCGGA 5730
Qy 129 GCTCGATGCCGCGAGTGGCTCAGTG 153
Db 5731 GCCGGGCGTGGGAGTGGCTGGTTG 5755

RESULT 26
US-09-949-016-12923/c
; Sequence 12923, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
;
US-08-724-394A-21

Query Match 2.2%; Score 42.4; DB 2; Length 246240;
Best Local Similarity 48.2%; Pred. No. 5.1;
Matches 150; Conservative 0; Mismatches 157; Indels 4; Gaps 1;

Qy 1512 ATTTCATAAGTTCAGATCATCTTAAATGAAATGCCATGATATCTGCGATTAAGTAGAT 1571
Db 234314 ATTTCAAATTCGTAATAATCTTGTAAACACACATGCATTATATTCACACAGGAATATATA 234255

Qy 1572 GACAGCTATCTACATCAGACTTGATTTTTCGACGTAATACATAATTCGTAAGNTATA 1631
Db 234254 ATTTATAATTATAATTTAGGATCAACAGATGACAAACCTTTAGAGGTTTGATTATTAACC 234195

Qy 1632 ATTGAACCTTATGGCTTAAATTCCTTAACCTCTTTTGATTCATGTTTGTAGTCATGT 1691
Db 234194 TTAATAATATAATTTTAAATTTGGTTATAAAAATTTCTAATCTTCTT---TTTGT 234139

Qy 1692 TGTCAACAGAGCGAAAGTTAGCTTGATGGTTAAATCGGTTTGATACACCATGGG 1751
Db 234138 GACCTCAAGGGGAAAATATAATCTTATAAAAGTTCAAATGATTACAGATACAAAAAG 234079

Qy 1752 ACATTTTTTTTAAACAAAATAATGCATCAAGAGACATAGCCTTTTAGTTTTGCTAATGT 1811
Db 234078 TGAATAGAGATGATGAATGAATTAAGGAAAGGATATTGCTACATAGATTTGGAAATTTTA 234019

Qy 1812 GAAATGGAAT 1822
Db 234018 AAAAGGGAAT 234008

RESULT 29
US-08-724-394A-22/c
; Sequence 22, Application US/08724394A
; Patent No. 587237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Krommal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
;
US-08-724-394A-22

Query Match 2.2%; Score 42.4; DB 2; Length 246240;
Best Local Similarity 48.2%; Pred. No. 5.1;
Matches 150; Conservative 0; Mismatches 157; Indels 4; Gaps 1;

Qy 1512 ATTTCATAAGTTCAGATCATCTTAAATGAAATGCCATGATATCTGCGATTAAGTAGAT 1571
Db 234314 ATTTCAAATTCGTAATAATCTTGTAAACACACATGCATTATATTCACACAGGAATATATA 234255

Qy 1572 GACAGCTATCTACATCAGACTTGATTTTTCGACGTAATACATAATTCGTAAGNTATA 1631
Db 234254 ATTTATAATTATAATTTAGGATCAACAGATGACAAACCTTTAGAGGTTTGATTATTAACC 234195

Qy 1632 ATTGAACCTTATGGCTTAAATTCCTTAACCTCTTTTGATTCATGTTTGTAGTCATGT 1691
Db 234194 TTAATAATATAATTTTAAATTTGGTTATAAAAATTTCTAATCTTCTT---TTTGT 234139

Qy 1692 TGTCAACAGAGCGAAAGTTAGCTTGATGGTTAAATCGGTTTGATACACCATGGG 1751
Db 234138 GACCTCAAGGGGAAAATATAATCTTATAAAAGTTCAAATGATTACAGATACAAAAAG 234079

Qy 1752 ACATTTTTTTTAAACAAAATAATGCATCAAGAGACATAGCCTTTTAGTTTTGCTAATGT 1811
Db 234078 TGAATAGAGATGATGAATGAATTAAGGAAAGGATATTGCTACATAGATTTGGAAATTTTA 234019

Qy 1812 GAAATGGAAT 1822
Db 234018 AAAAGGGAAT 234008

RESULT 30
US-09-949-016-1751/c
; Sequence 1751, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1751
; LENGTH: 3025
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1751

Query Match          2.2%; Score 41.8; DB 3; Length 3025;
Best Local Similarity 52.7%; Pred. No. 0.58;
Matches 307; Conservative 0; Mismatches 249; Indels 27; Gaps 9;

Qy 1294 CTGCATTTCAGGATGTGAGGCCATTTAATAAAAGGGCACAAGCCCTG--TCAGAGTTTTC 1351
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2791 CTGGGTGCAGATGCAAGCCTCTAAAGGAGAGGATACAAAGTCAGGTGAGTAGGGGCC 2732

Qy 1352 AACGGTGTCTACAGCTGCCAGCTGGATCCAAACAGGTACCCCA-----TTGTCTCTGA 1405
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2731 ATTGGCAATGCTCAGAGCCAGCCAGACTCCAAACAGGGAGCCCAAGTGGTGTTCCTGG 2672

Qy 1406 GCTAATGTTTATATATTTTCCATTTCAGGCACCGAAATAGTTAATATTTTAAATAAAGTCTTC 1465
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2671 GACACTCTACTTGAATATTGTTTAAATTAGTCAACCATAGATCTTCAAAAGAGACAATT 2612

Qy 1466 AAAAGAAAACATAAGAGATTATTAGTTCCTGGGACTGGATCCTTTATTTCATAAG----- 1521
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2611 AGTTAAACATGATAAAAGTGACTGCAATCTTTGGACTGTATCATTAATTATAGTAAGCAA 2552

Qy 1522 TTCAGATCATCTTAATGAAATGCCATGATTA-TCTGCAGTTAAGTAGATGACAGCTAT 1580
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2551 TTCTGACAGTTTTTAATGAAAAATAGCCTCCACCATTTCAGGTATGAAGATAACTTTAATT 2492

Qy 1581 TCTACATCAGACTTGTATTTTGTGACGTAATTACATAAATGGTAAGNTATAATTGAAA-- 1638
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2491 ATCCACAGGGCTTTTAAATGCTGCTGGACAATACATGAATGATAGTATTAATGACATT 2432

Qy 1639 -CCTTATGGCTTAAAAATCCTTAACTCCTTTTGTGATTCATGTTGTAGTCATGTGTCAA 1697
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2431 GTTTTATGATATAAAAAATACTAGTTTTTTTTCATTTTATTATTTCTATAGGCAT-TCAC 2373

Qy 1698 CAGAGCAAAGTTAAGCTTGATGA-TGGTTAAATCGGTTTGTATAGCACCATGGGACATT 1756
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2372 TTGAGTCAAGGTTAGGCTTGTAAAGTGATTAAGGCAATTTTATTACAGCAGCATGTACT 2313

Qy 1757 T-----TTTTAAACAAAATAAATGATGATGAAGACATAGCCCTTT---TAGTTTTGCTAA 1807
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2312 TATTCTATTCTAAAGAAATAATTTCTATAACAGAAACAGGTTTTTATATTGTTTGCAC 2253

Qy 1808 TTGTGAAATGGAATGCTTTACAGGAAGTAAATGCAAAATTANT 1850
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2252 CTGCAAAATTTGAATTATTGCTGTATATAAAATACTAAGAACT 2210
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Search completed: December 3, 2005, 23:32:55
Job time : 414.114 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 09:21:06 ; Search time 8019.87 Seconds
(without alignments)
11201.085 Million cell updates/sec

Title: US-10-757-745-1
Perfect score: 1920
Sequence: 1 ggcagagcgcgagga.....aaagaatttttggtaaa 1920

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 41078325 seqs, 23393541228 residues 82156650
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1892.4	98.6	1909	4	CR595644 full-leng
2	1882.4	98.0	1894	4	CR597293 full-leng
3	1698	88.4	1743	4	CR602029 full-leng
4	1414	73.6	1620	4	CR592636 full-leng
5	1160.4	60.4	1168	4	CR601303 full-leng
6	1087.4	56.6	1089	11	DQ049205 Homo sapi
7	1067.4	55.6	1089	11	DQ049206 Pan trogl
8	994.8	51.8	1081	5	BX444691 BX444691
9	961.2	50.1	1087	7	CR642527 ILLUMIGEN
10	939.4	48.9	981	5	CR642527 ILLUMIGEN
11	936.4	48.8	1018	5	CR642527 ILLUMIGEN
12	935	48.7	994	5	CR642527 ILLUMIGEN
13	935	48.7	1067	5	CR642527 ILLUMIGEN
14	926.4	48.2	1072	5	CR642527 ILLUMIGEN
15	912.4	47.5	1004	1	AL577861 AL577861
16	888.2	46.8	965	7	CR642527 ILLUMIGEN
17	884.8	46.6	904	5	CR642527 ILLUMIGEN
18	888.6	46.3	952	3	CR642527 ILLUMIGEN
19	878.8	45.8	972	3	CR642527 ILLUMIGEN
20	878.4	45.7	1046	3	CR642527 ILLUMIGEN
21	870.4	45.3	948	1	AL555333 AL555333
22	858.2	44.7	954	5	CR642527 ILLUMIGEN

96	636.4	33.1	908	2	BG391213	BG391213	602417244	169	544	28.3	583	3	BP195721	BP195721
97	634	33.0	634	6	CB157906	CB157906	K-EST0217	170	542.8	28.3	546	2	BG541031	BG541031
c 98	631.6	32.9	715	6	CA424213	CA424213	UI-H-FE1-	171	541	28.0	889	2	BG537046	BG537046
c 99	630.2	32.8	650	5	BUT83858	BUT83858	in10f06.x	172	538.4	28.0	917	2	BG285455	BG285455
c 100	629.8	32.8	659	8	CB243068	CB243068	UI-CF-FNO	c 173	536.2	27.9	574	3	AW025475	AW025475
c 101	629.8	32.8	799	8	CK756424	CK756424	AGENCOURT	174	535.8	27.9	774	3	B1833367	B1833367
c 102	625.6	32.6	649	6	CA315043	CA315043	UI-CF-FNO	175	535.4	27.9	581	3	BP262638	BP262638
c 103	625	32.6	1289	4	AK009089	AK009089	Mus muscu	176	535.2	27.9	749	3	BP130513	BP130513
c 104	624.6	32.5	995	2	B892886	B892886	601435730	177	534.6	27.8	683	7	CN789157	CN789157
c 105	624.4	32.5	798	8	DN122208	DN122208	1123297 M	178	534.4	27.8	580	3	BP261787	BP261787
c 106	619.4	32.3	650	2	BG431303	BG431303	602499879	179	534.2	27.8	563	2	BG496889	BG496889
c 107	615.4	32.1	748	2	B1224035	B1224035	602942947	180	532.4	27.7	534	7	CN298921	CN298921
c 108	611.4	31.8	826	5	BU943127	BU943127	AGENCOURT	181	529	27.6	530	3	BM846221	BM846221
c 109	609.4	31.7	621	6	CB069952	CB069952	is31e10.y	c 182	528.4	27.5	540	1	AI720834	AI720834
c 110	605.8	31.6	634	7	CV023369	CV023369	288 Full	183	526.8	27.4	610	2	BF978004	BF978004
c 111	604.2	31.5	649	1	AV706840	AV706840	AV706840	184	526.2	27.4	533	1	AW027358	AW027358
c 112	604	31.5	641	3	BM978066	BM978066	UI-CF-EC1	185	525.4	27.4	527	1	AA145487	AA145487
c 113	604	31.5	879	2	BF678894	BF678894	602153515	186	525.2	27.4	750	2	B1181461	B1181461
c 114	600.4	31.3	603	3	B1517642	B1517642	603042252	187	524.4	27.3	584	3	BP274942	BP274942
c 115	599	31.2	602	2	AL703449	AL703449	DKZP686G	188	520.4	27.1	554	2	BE967376	BE967376
c 116	597	31.1	597	2	BG285530	BG285530	602380521	189	518.4	27.0	644	3	B1333830	B1333830
c 117	595.8	31.0	710	1	AV706680	AV706680	AV706680	c 190	513	26.7	579	1	AU157899	AU157899
c 118	594	30.9	652	7	CR753214	CR753214	DKFZP469I	c 191	507	26.4	528	1	AI819345	AI819345
c 119	594	30.9	887	2	BG616987	BG616987	602615670	192	506.6	26.4	875	2	BF790756	BF790756
c 120	592	30.8	614	7	CV572431	CV572431	o324f09.y	193	504.4	26.3	506	6	CB133935	CB133935
c 121	592	30.8	793	2	BG533717	BG533717	602562373	194	502.8	26.2	648	6	CF764797	CF764797
c 122	585.2	30.5	924	2	B8548823	B8548823	601071834	195	501.8	26.1	523	7	CN791432	CN791432
c 123	585	30.5	715	3	B1915865	B1915865	603184527	196	500.6	26.1	523	3	BM068730	BM068730
c 124	584	30.4	680	7	CK952220	CK952220	4091710 B	c 197	499	26.0	859	2	BE857301	BE857301
c 125	583.8	30.4	601	5	BQ581727	BQ581727	i112c11.x	198	498.4	26.0	852	2	BF028675	BF028675
c 126	582	30.3	582	3	BP219740	BP219740	BP219740	c 199	487.8	25.9	520	1	AM380605	AM380605
c 127	582	30.3	582	3	BP261141	BP261141	BP261141	200	487.2	25.9	582	3	BM507091	BM507091
c 128	582	30.3	582	3	BP270415	BP270415	BP270415	201	486.6	25.9	556	3	BP243301	BP243301
c 129	582	30.3	582	3	BP275810	BP275810	BP275810	c 202	495.8	25.8	513	1	AI460313	AI460313
c 130	582	30.3	583	3	BP262741	BP262741	BP262741	203	493.2	25.7	635	3	BM539358	BM539358
c 131	581	30.3	581	3	BP262101	BP262101	BP262101	204	491.2	25.6	497	3	BP418588	BP418588
c 132	581	30.2	581	3	BP207751	BP207751	BP207751	205	480.4	25.5	578	1	AV602300	AV602300
c 133	580	30.2	581	3	BP270744	BP270744	BP270744	206	489.8	25.5	764	2	BF029501	BF029501
c 134	580	30.2	581	3	BP349936	BP349936	BP349936	c 207	487.4	25.4	502	1	BP393589	BP393589
c 135	579.8	30.2	583	3	BP262103	BP262103	BP262103	c 208	487	25.4	506	1	AA714544	AA714544
c 136	579.4	30.2	581	1	AV717253	AV717253	AV717253	c 209	484.8	25.2	539	1	AA527087	AA527087
c 137	579.4	30.2	581	3	BP379659	BP379659	BP379659	c 210	484.6	25.2	512	1	AM380606	AM380606
c 138	579	30.2	581	3	BP225088	BP225088	BP225088	211	484.2	25.2	1021	5	BQ960570	BQ960570
c 139	578.8	30.1	582	3	BP261789	BP261789	BP261789	212	481.4	25.1	493	7	CK904588	CK904588
c 140	578.2	30.1	584	3	BP263059	BP263059	BP263059	c 213	480.6	25.0	489	1	AA512951	AA512951
c 141	577	30.1	577	7	CN298919	CN298919	170006001	c 214	480.2	25.0	485	1	AA486032	AA486032
c 142	577	30.1	583	5	BU783229	BU783229	in01a08.y	c 215	479.2	25.0	487	1	AA918983	AA918983
c 143	577	30.1	811	8	DN122554	DN122554	1122781 M	216	478.8	24.9	827	8	CV805216	CV805216
c 144	576	30.0	576	3	BP263642	BP263642	BP263642	217	477.8	24.9	547	2	BP130236	BP130236
c 145	574.2	29.9	580	3	BP274368	BP274368	BP274368	218	476.6	24.8	652	8	W02878	W02878
c 146	574.2	29.9	959	2	BP161201	BP161201	602865659	c 219	476	24.8	490	6	CB068689	CB068689
c 147	573.6	29.9	582	3	BP233592	BP233592	BP233592	220	475.4	24.8	581	6	CB286391	CB286391
c 148	571.4	29.8	583	3	BP234218	BP234218	BP234218	221	474.2	24.7	770	2	BG391295	BG391295
c 149	571	29.7	571	6	CB125492	CB125492	K-EST0174	c 222	473.4	24.7	477	1	AA488650	AA488650
c 150	568.8	29.6	626	2	BF977971	BF977971	602148451	223	473.2	24.6	608	7	CK966606	CK966606
c 151	568.2	29.6	573	3	BP261500	BP261500	BP261500	224	473	24.6	480	1	AI750554	AI750554
c 152	567.2	29.5	573	3	BP221260	BP221260	BP221260	c 225	472.6	24.6	670	2	BG896990	BG896990
c 153	566.6	29.5	584	3	BP348623	BP348623	BP348623	226	472.4	24.6	734	2	BF246577	BF246577
c 154	565.4	29.4	588	3	BP348796	BP348796	BP348796	227	472	24.6	473	6	CB120234	CB120234
c 155	565.2	29.4	588	3	BP236074	BP236074	BP236074	228	471.4	24.5	486	1	AA259166	AA259166
c 156	565	29.4	565	3	BP226620	BP226620	BP226620	c 229	470.8	24.5	477	1	AI342418	AI342418
c 157	562.2	29.3	568	3	BP257211	BP257211	BP257211	230	470.2	24.5	815	5	B0936308	B0936308
c 158	562	29.3	565	3	BP226464	BP226464	BP226464	231	470	24.5	470	3	BP417720	BP417720
c 159	560.2	29.2	566	3	BP220508	BP220508	BP220508	c 232	466.8	24.3	688	6	CF789017	CF789017
c 160	556.8	29.0	577	1	AW964871	AW964871	ESTJ376839	c 233	466.4	24.3	788	3	B1830384	B1830384
c 161	555	28.9	573	1	AU279894	AU279894	AU279894	c 234	465.6	24.3	798	1	AI830384	AI830384
c 162	552.6	28.8	570	3	BP258309	BP258309	BP258309	c 235	464	24.2	499	3	BM054720	BM054720
c 163	552	28.7	583	3	BP319548	BP319548	BP319548	236	462.2	24.1	482	5	BU072078	BU072078
c 164	550.8	28.7	554	3	BP220985	BP220985	BP220985	237	460.8	24.0	617	7	CN694288	CN694288
c 165	550.6	28.7	559	2	BE162174	BE162174	ILA-HT044	c 238	460.4	24.0	599	3	BM506743	BM506743
c 166	547.6	28.5	581	3	BP199948	BP199948	BP199948	c 239	459.8	23.9	471	7	CR543841	CR543841
c 167	545.2	28.4	570	3	BM172060	BM172060	imageqc_3	240	458.2	23.9	793	2	BF696251	BF696251
c 168	544.4	28.4	570	3	BP221518	BP221518	BP221518	241	451.6	23.5	463	3	BP389218	BP389218

BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195721	BP195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242	451.6	23.5	572	3	BP262485	BP262485	BP262485	315	367.8	19.2	517	9	C248786	CK529 Bay
243	449	23.4	582	3	BP263516	BP263516	BP263516	C 316	367.6	19.1	394	1	A1362474	QV166005.x
244	448.4	23.4	724	6	CB443087	693950 MA	CB443087	317	367.4	19.1	391	3	BM784919	K-EST0063
245	443.6	23.1	452	1	A1912676	we12e02 .x	A1912676	C 318	366.2	18.9	467	3	BQ329405	MR3-EN008
246	443	23.1	587	1	AM608908	RC3-PT002	AM608908	319	363.6	18.9	623	3	BP045278	BP250008A
247	443	23.1	587	1	AM608952	RC3-PT002	AM608952	C 320	362.6	18.9	639	6	CB545297	AMGNNUC.N
248	442.2	23.0	450	1	A1373266	qz48611.x	A1373266	C 321	362.2	18.9	369	1	A1434664	t135e08.x
249	441.8	23.0	447	1	A1803163	tc36908.x	A1803163	C 322	362.2	18.9	448	1	A1750553	CN04801.x
250	439.6	22.9	456	2	BP996980	QV3-GN020	BP996980	323	361.4	18.8	548	3	BP375391	BP375391
251	439.4	22.9	734	7	CV119018	AGENCYCOURT	CV119018	324	358.4	18.7	581	3	BP270589	BP270589
252	437.8	22.8	614	7	CN788690	4123052.B	CN788690	C 325	357.6	18.6	367	1	AA857279	CH96601.8
253	436.4	22.7	440	2	BP982036	MR3-CN014	BP982036	C 326	354.4	18.5	737	3	BJ639656	BJ639656
254	435.6	22.7	463	2	BF852284	MR3-EN008	BF852284	327	353.6	18.4	355	8	T35414	EST84519.Hu
255	435.4	22.7	440	2	BF893925	PM1-MT014	BF893925	C 328	353.4	18.4	373	1	A1206401	GG21907.x
256	434.6	22.7	440	2	BF893167	H3085C02-	BF893167	329	351.8	18.3	390	2	BG654943	1b43g11.y
257	433.2	22.6	443	1	A1445723	t109b11.x	A1445723	330	348	18.1	365	7	CR767008	DKF2p469G
258	431.6	22.5	450	3	BQ315535	PM0-IT001	BQ315535	C 331	347.6	18.1	390	2	BG54943	1b43g11.y
259	430.2	22.4	491	1	AJ681912	uA681912	AJ681912	332	347.4	18.1	435	5	BQ332331	MR4-ET014
260	429.8	22.4	441	2	BF992415	PM1-MT014	BF992415	333	347.2	18.1	645	5	BY737520	BY737520
261	429.8	22.4	441	2	BF893925	PM1-MT014	BF893925	C 334	347.2	18.1	435	5	BY737520	BY737520
262	429.4	22.4	644	2	BG083167	H3085C02-	BG083167	335	346	18.0	352	5	BQ787387	im09c09.x
263	425.2	22.1	714	2	BG070243	H3085C02-	BG070243	336	345.8	18.0	760	5	BU204728	im09c09.y
264	425	22.1	614	2	BG695251	N1SC iv14	BG695251	C 337	344.6	17.9	942	2	BF773259	PM0-IT001
265	423.2	22.0	431	1	A1636852	ts60f08.x	A1636852	C 338	344.2	17.9	452	2	BG298330	PM0-IT001
266	423	22.0	429	5	BQ582059	1112c11.y	BQ582059	C 339	342	17.8	347	5	BU070378	im09c09.x
267	422.8	22.0	840	2	BF676881	602086559	BF676881	340	341.4	17.8	471	1	AA681654	VR43d12.s
268	420.4	21.9	444	2	BF893187	PM1-MT014	BF893187	C 342	338	17.6	468	1	AA636415	VQ86d01.8
269	419.8	21.9	647	1	AA536734	v188b09.r	AA536734	343	337.6	17.6	531	3	AA824213	VY20h08.r
270	419.2	21.8	503	3	BQ323527	RC1-CL011	BQ323527	344	337.2	17.6	984	5	BA846715	BA846715
271	418	21.8	463	3	BF852788	MR3-EN008	BF852788	345	337	17.6	493	1	AA163045	AA163045
272	417.4	21.7	458	3	BQ366782	QV3-GN020	BQ366782	346	335.4	17.5	524	3	BP263000	BP263000
273	415.6	21.6	436	1	AA725768	a122h03.8	AA725768	347	333.6	17.3	919	6	CA973696	AGENCYCOURT
274	415.4	21.6	453	2	BF893919	PM1-MT014	BF893919	348	331.6	17.3	900	6	CA980929	AGENCYCOURT
275	414.2	21.5	421	1	AA653453	ag66c04.8	AA653453	349	330.4	17.2	896	6	CA971409	AGENCYCOURT
276	413.6	21.5	580	3	BM503555	ih13e07.y	BM503555	C 350	329.6	17.1	950	6	CF378639	AGENCYCOURT
277	413.2	21.5	454	2	BG982031	MR3-CN014	BG982031	C 351	328.6	17.1	396	1	A1524416	A1524416
278	413.4	21.5	744	7	CN155540	942844 MA	CN155540	352	327.4	17.1	368	2	BE694706	BE694706
279	412.8	21.5	622	5	BX372531	BX372531	BX372531	C 353	326.8	17.0	520	6	CB220518	CB220518
280	409	21.3	666	7	CN789130	4123550.B	CN789130	354	326.8	17.0	326	1	AA366358	AA366358
281	408.8	21.3	1078	2	BE546098	601072630	BE546098	355	326	17.0	326	1	AA366358	AA366358
282	408	21.2	534	7	CK838233	4063591.B	CK838233	356	325	16.9	544	1	AA308842	AA308842
283	407.8	21.2	460	2	BF893150	PM1-MT014	BF893150	C 357	324.2	16.9	695	6	CB443534	CB443534
284	407.8	21.2	460	2	BF893150	PM1-MT014	BF893150	358	324.2	16.9	388	1	AA659558	AA659558
285	405.6	21.1	467	1	AW371042	PM4-BT027	AW371042	C 359	321.6	16.8	343	1	AA639790	AA639790
286	404.5	21.1	413	3	BP931115	Om87f03.8	BP931115	C 360	320.6	16.7	961	2	B1150788	B1150788
287	402.2	20.9	573	3	BP379251	BP379251	BP379251	C 361	320	16.7	749	5	BR753763	BR753763
288	402	20.9	413	3	BQ323232	MR4-ET014	BQ323232	C 362	318.8	16.6	835	2	DR867245	DR867245
289	400.6	20.9	408	2	BE004233	CM0-EN010	BE004233	C 363	316.4	16.5	409	2	BG900023	BG900023
290	400.6	20.9	459	2	BE004233	MR3-CN014	BE004233	364	316.4	16.5	467	6	CF788416	CF788416
291	400.2	20.8	408	1	A1636151	t206a07.x	A1636151	365	315.8	16.4	946	5	BU468774	BU468774
292	400	20.8	437	2	BF082663	PM2-BT072	BF082663	366	314.6	16.4	321	8	DN097147	DN097147
293	400	20.8	437	2	BG949509	PM2-BT072	BG949509	367	313.8	16.3	827	1	AA243535	AA243535
294	400	20.8	437	2	BG949509	PM2-BT072	BG949509	368	313.2	16.3	525	2	BE290901	BE290901
295	399.8	20.8	407	6	CB118797	K-EST0165	CB118797	369	311.4	16.2	841	2	BF784792	BF784792
296	398.2	20.7	420	3	BM980338	UI-CF-EN1	BM980338	370	311.8	16.2	892	5	BU309561	BU309561
297	396.6	20.7	406	1	AA857277	Oh96C02.8	AA857277	C 371	310.6	16.2	491	2	BI016235	BI016235
298	395.8	20.6	456	3	BQ323231	MR4-ET014	BQ323231	C 372	310.6	16.2	441	9	AQ452054	AQ452054
299	395.8	20.6	751	2	BF243927	601877278	BF243927	373	309.6	16.1	310	8	T26956	T26956
300	395.2	20.6	402	1	AA622205	no43a01.8	AA622205	374	308.8	16.1	325	8	T31666	T31666
301	393.4	20.5	471	2	BF893924	PM1-MT014	BF893924	C 375	306.4	16.0	310	1	AA259127	AA259127
302	390.8	20.5	394	1	AV661333	AV661333	AV661333	C 376	305.4	15.9	341	6	CA444867	CA444867
303	388.8	20.2	419	2	BF853399	MR3-EN008	BF853399	C 377	305.2	15.9	341	1	AA748451	AA748451
304	383.4	20.0	405	1	AA514276	nf61a11.8	AA514276	C 378	301.6	15.7	1077	5	BU131072	BU131072
305	382.2	19.9	447	2	BF891509	PM1-MT014	BF891509	379	300.2	15.6	437	2	BF768820	BF768820
306	381.4	19.9	383	7	CN389327	170006001	CN389327	C 380	300	15.6	422	2	BG982044	BG982044
307	379.4	19.8	767	8	CK226137	MBM01355	CK226137	C 381	299.4	15.6	579	2	BF997052	BF997052
308	374.8	19.5	860	8	CK958090	JGI_CAA09	CK958090	382	298	15.5	802	8	BN100293	BN100293
309	374.2	19.5	407	8	N49017	YY77G10.r	N49017	383	297.2	15.5	558	5	BK258258	BK258258
310	374	19.5	911	2	BF101875	601753033	BF101875	384	294.8	15.4	648	1	AW321603	AW321603
311	373.6	19.5	392	8	T30014	EST10355.Hu	T30014	385	294.2	15.3	782	5	BU406549	BU406549
312	371.6	19.4	891	1	AL879624	AL879624	AL879624	386	292.8	15.2	909	6	CA982823	CA982823
313	371.6	19.4	894	5	BX776016	BX776016	BX776016	387	292.6	15.2	691	7	CK798310	CK798310
314	371.6	19.4	894	5	BX780455	BX780455	BX780455	388	292.6	15.2				

into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

Location/Qualifiers
 1..1909
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI052YNI3"
 /tissue_type="Placenta Cot 25-normalized"
 /plasmid="pCMVSPORT_6"

ORIGIN

Query Match	98.6%;	Score	1892.4;	DB 4;	Length	1909;			
Best Local Similarity	99.6%;	Pred. No.	0;	Mismatches	8;	Indels	0;	Gaps	0;
Matches	1896;	Conservative	0;						

QY	1	GTGCAGAGCGG	CAGGAAGATGGAGTTGGGGAGTTGCCCTGGAGGGCGGGAGGGAGCGGC	60
DB	6	GTGCAGAGCGG	CAGGAAGATGGAGTTGGGGAGTTGCCCTGGAGGGCGGGAGGGAGCGGC	65
QY	61	GGAGGAAGAGCGG	CGCCTGAGGTGAAAAAGCGGGACCTTCTGTGTGTGGAGTTTGCCTTC	120
DB	66	GGAGGAAGAGCGG	CGCCTGAGGTGAAAAAGCGGGACCTTCTGTGTGTGGAGTTTGCCTTC	125
QY	121	GGTGGCAAGCTGCGATGCGCGAGTGGCTCAGTGTCTTCCGCGGAGAACGACTGGGAGAT	180	
DB	126	GGTGGCAAGCTGCGATGCGCGAGTGGCTCAGTGTCTTCCGCGGAGAACGACTGGGAGAT	185	
QY	181	GGAAAGGGCTGTAACCTCTACTTTCGAGCTCCGGTGGAGGAGAGCGCCTTGGAAACGCG	240	
DB	186	GGAAAGGGCTGTAACCTCTACTTTCGAGCTCCGGTGGAGGAGAGCGCCTTGGAAACGCG	245	
QY	241	ACCTGAAACCATCTCTGAGCCCAAGACCTATGTGTGACCTAAACCAATGAAAGAAACAACCTGA	300	
DB	246	ACCTGAAACCATCTCTGAGCCCAAGACCTATGTGTGACCTAAACCAATGAAAGAAACAACCTGA	305	
QY	301	TTCCACACATCTTAAATACGCCCATCTGAGATCTCAGCAGAAATGGCAGCATGTT	360	
DB	306	TTCCACACATCTTAAATACGCCCATCTGAGATCTCAGCAGAAATGGCAGCATGTT	365	
QY	361	CTCTCTCATTTACCTGGAAATATTCATGATTTAGATCTAAACCAATCTGTACAGAGGCGCTCG	420	
DB	366	CTCTCTCATTTACCTGGAAATATTCATGATTTAGATCTAAACCAATCTGTACAGAGGCGCTCG	425	
QY	421	AGGGGTGTGTTCTTACTTGTACAGCCCGAGATGTGATATTTCTACAGGAAGTTAT	480	
DB	426	AGGGGTGTGTTCTTACTTGTACAGCCCGAGATGTGATATTTCTACAGGAAGTTAT	485	
QY	481	TCCCCCATATTTAGCTTACCTAAAGAGAGATCAAGTAATTTAGATTTATTTACAGGTCA	540	
DB	486	TCCCCCATATTTAGCTTACCTAAAGAGAGATCAAGTAATTTAGATTTATTTACAGGTCA	545	
QY	541	TGAAGAGGATATTTACAGCTAATGTTGAAGAAATCAAGAGTGAATTTAAAAAGCCCA	600	
DB	546	TGAAGAGGATATTTACAGCTAATGTTGAAGAAATCAAGAGTGAATTTAAAAAGCCCA	605	
QY	601	AGAGATTATTTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAA	660	
DB	606	AGAGATTATTTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAA	665	
QY	661	TGTGTACGAAATAGCTTTTCCCTTATGACATCCCATTTGGAGAGCACCGAGGGCATGC	720	
DB	666	CGTGTACGAAATAGCTTTTCCCTTATGACATCCCATTTGGAGAGCACCGAGGGCATGC	725	
QY	721	TGCGGAACGATGATCAGTTTAAATGTTTTTAAAGAAATCAAGAGGCTCCAGAGTC	780	
DB	726	TGCGGAACGATGATCAGTTTAAATGTTTTTAAAGAAATCAAGAGGCTCCAGAGTC	785	
QY	781	AGCTACAGTTTATATTTTCAGGAGATACAAATCTAAGGGATCGAGAGTTTACCAGATGTGG	840	
DB	786	AGCTACAGTTTATATTTTCAGGAGATACAAATCTAAGGGATCGAGAGTTTACCAGATGTGG	845	

QY	841	TGTTTTACCCCAACACATTTGTGGATGCTGGAGTTTGGGCAAACTTAAACATTTGCCA	900
DB	846	TGTTTTACCCCAACACATTTGTGGATGCTGGAGTTTGGGCAAACTTAAACATTTGCCA	905
QY	901	GTATACATGGGATACACAAATGAACTTAATCTTGGAAATACCTGCTGTGTAACCTTCG	960
DB	906	GTATACATGGGATACACAAATGAACTTAATCTTGGAAATACCTGCTGTGTAACCTTCG	965
QY	961	TTTTGATCGAAATATTTTTCAGAGCAGCAGCAGAGAGGAGCACATATTTCCCGAAGTTT	1020
DB	966	TTTTGATCGAAATATTTTTCAGAGCAGCAGCAGAGAGGAGCACATATTTCCCGAAGTTT	1025
QY	1021	GGACCTTCTTGGATTAGAAAACTGGAATGTTGGTATGATTTCTAGTATGATCACTGGGCTCT	1080
DB	1026	GGACCTTCTTGGATTAGAAAACTGGAATGTTGGTATGATTTCTAGTATGATCACTGGGCTCT	1085
QY	1081	TCTGTGCAACTTAGATATATTTTGAATGCTTTTCAAGTGTGGTTTTCGCCCTGATTT	1140
DB	1086	TCTGTGCAACTTAGATATATTTTGAATGCTTTTCAAGTGTGGTTTTCGCCCTGATTT	1145
QY	1141	GTTCGCAAAATACAAATTTCCACCTTCTGGAAAGGTAGGTTTGTCTGTGGAGGAAATAATGTAC	1200
DB	1146	GTTCGCAAAATACAAATTTCCACCTTCTGGAAAGGTAGGTTTGTCTGTGGAGGAAATAATGTAC	1205
QY	1201	TAGATCATTTGTCAAGAAAAACCAACTATGATTTATGTTTGTGTTTTCAGAAATTCACAT	1260
DB	1206	TAGATCATTTGTCAAGAAAAACCAACTATGATTTATGTTTGTGTTTTCAGAAATTCACAT	1265
QY	1261	TAAAGATTAAATGTTTATTTAAACGAAACATTTCTGTCATTTCCAGGATGTCAGGCGCATTTAA	1320
DB	1266	TAAAGATTAAATGTTTATTTAAACGAAACATTTCTGTCATTTCCAGGATGTCAGGCGCATTTAA	1325
QY	1321	TAAAGAGGCGCAAAAGCCTGTCCAGAGTTTTCACCGTGTCTTACAGCTGCCAGCTGATTC	1380
DB	1326	TAAAGAGGCGCAAAAGCCTGTCCAGAGTTTTCACCGTGTCTTACAGCTGCCAGCTGATTC	1385
QY	1381	CAAAACAGGTACCCCATTTGCTCTGAGCTAATGTTTATATTTTTCATTCAGGCACCGAAA	1440
DB	1386	CAAAACAGGTACCCCATTTGCTCTGAGCTAATGTTTATATTTTTCATTCAGGCACCGAAA	1445
QY	1441	TAGTTAAATATTTAAATAAGTCTTCAAGAAAAACATAAGAGATTATTTGAGTTCTTTGGGA	1500
DB	1446	TAGTTAAATATTTCAATAAGTCTTCAAGAAAAACATAAGAGATTATTTGAGTTCTTTGGGA	1505
QY	1501	CTGGATCTTTTATTTTATTAAGTTTCAGATCATCTTAAATGAAATGCGCATGATTATCTGCA	1560
DB	1506	CTGGATCTTTTATTTTATTAAGTTTCAGATCATCTTAAATGAAATGCGCATGATTATCTGCA	1565
QY	1561	GTAAAGTAGATGACAGCTATTCTACATCAGACTTGAATTTTGTGTCAGCTAATTTACATAAT	1620
DB	1566	GTAAAGTAGATGACAGCTATTCTACATCAGACTTGAATTTTGTGTCAGCTAATTTACATAAT	1625
QY	1621	GGTAAGNTAATATTTGAAACCTTTATGGCTTAAATTTCTTAACTCTTTTGTGATTCATGTT	1680
DB	1626	GGTAAGNTAATATTTGAAACCTTTATGGCTTAAATTTCTTAACTCTTTTGTGATTCATGTT	1685
QY	1681	TGTAGTCATGTTGTCAACAGAGCGAAAGTTTAAAGCTTGTATGATGTTTAAAAATCGGTTTGTAT	1740
DB	1686	TGTAGTCATGTTGTCAACAGAGCGAAAGTTTAAAGCTTGTATGATGTTTAAAAATCGGTTTGTAT	1745
QY	1741	AGCACCATGGGACATTTTAAAAATAAATGCAATGAAGAGACATACGCTTTTATGTT	1800
DB	1746	AGCACCATGGGACATTTTCTAACAAAAATAAATGCAATGAAGAGACATACGCTTTTATGTT	1805
QY	1801	TTCTAATTGTGAAATGGAAATGCTTTACAGGAAGTAAATGCAAAATTTTAAAGTGTG	1860
DB	1806	TTCTAATTGTGAAATGGAAATGCTTTACAGGAAGTAAATGCAAAATTTTAAAGTGTG	1865
QY	1861	CTTTAAAGAAAAATATTTTCCCAAGGAGAAATTTTAAATAAAG	1904
DB	1866	CTTTAAAGAAAAATATTTTCCCAAGGAGAAATTTTAAATAAAG	1909

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RESULT 2
CRS97293      1894 bp      mRNA      linear      HTC 21-JUL-2004
LOCUS         full-length cDNA clone CSODK007YK05 of HeLa cells Cot 25-normalized
DEFINITION   of Homo sapiens (human).
ACCESSION    CRS97293
VERSION      CRS97293.1 GI:50478100
KEYWORDS     HTC; CNSLT.cDNA
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Homnidae; Homo.
REFERENCE    1. (bases 1 to 1894)
AUTHORS     Li.W.B., Gruber.C., Jesse.J. and Polayes.D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished
REMARK      Contact : Feng Liang Email : fliang@lifetech.com URL :
             http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
             Faraday Avenue
             2. (bases 1 to 1894)
             Genoscope.
             Direct Submission
             Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
             BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
             - Web : www.genoscope.cns.fr)
COMMENT      1st strand cDNA was primed with a NotI-oligo(dn) primer. Five prime
             end enriched, double-strand cDNA was digested with Not I and cloned
             into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
             was normalized. Library v was constructed by Life Technologies, a
             division of Invitrogen.
FEATURES     Location/Qualifiers
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             /clone="CSODK007YK05"
             /tissue_type="HeLa cells Cot 25-normalized"
             /plasmid="pCMVSPORT_6"
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Query Match      98.0%; Score 1882.4; DB 4; Length 1894;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1886; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY      2   TGCAGAGCGCGCAGGAAGATGGAGTTGGGGAGTTGCCTTGGAGGGCGGAGGGAGGCGCGC 61
DB      1   TGCAGAGCGCGCAGGAAGATGGAGTTGGGGAGTTGCCTTGGAGGGCGGAGGGAGGCGCGC 60
QY      62   GAGGAAGAGGCGGAGCGCTGAGGTGAAAGCGGCGACTTCTGTGTGGAGTTTGCCTCG 121
DB      61   GAGGAAGAGGCGGAGCGCTGAGGTGAAAGCGGCGACTTCTGTGTGGAGTTTGCCTCG 120
QY      122   GTCCGACGTCGGATGCCGCGAGTGGCTCAGTGTCTCGGCGGAGAGCGCTTGGAAACGCCGA 181
DB      121   GTCCGACGTCGGATGCCGCGAGTGGCTCAGTGTCTCGGCGGAGAGCGCTTGGAAACGCCGA 180
QY      182   GAAAGGGGCTCTGAACTCTACTTTCAGAGCTCCGGTGGAGGAGCGCGCTTGGAAACGCCGA 241
DB      181   GAAAGGGGCTCTGAACTCTACTTTCAGAGCTCCGGTGGAGGAGCGCGCTTGGAAACGCCGA 240
QY      242   CCTGAACCACTCTGTAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACCACTGAT 301
DB      241   CCTGAACCACTCTGTAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACCACTGAT 300
QY      302   TCCACCACTCTTAAATCAGCCCACTCTCAAGACTCTAGCAAGAAATGGCAGCATGTTTC 361
DB      301   TCCACCACTCTTAAATCAGCCCACTCTCAAGACTCTAGCAAGAAATGGCAGCATGTTTC 360
QY      362   TCTCTCATTACCTGGAATATTGATGGATTAGATCTTAAACAATCTGTCTAGAGAGGGCTCGA 421
DB      361   TCTCTCATTACCTGGAATATTGATGGATTAGATCTTAAACAATCTGTCTAGAGAGGGCTCGA 420
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QY      422   GGGGTGTGTTCTTACTTAGCTTTGTACAGCCAGATGCTGATATTTCTACAGGAAGTTATT 481
DB      421   GGGGTGTGTTCTTACTTAGCTTTGTACAGCCAGATGCTGATATTTCTACAGGAAGTTATT 480
QY      482   CCCCCTATTATAGTACTACCTAAAGAAGAGATCAAGTAATATATGAGATTATTACAGGTGAT 541
DB      481   CCCCCTATTATAGTACTACCTAAAGAAGAGATCAAGTAATATATGAGATTATTACAGGTGAT 540
QY      542   GAAGAAGGATATTTTACAGCTATATATGTTGAAGAAATCAAGAGTGAATATTAAGGCCAA 601
DB      541   GAAGAAGGATATTTTACAGCTATATATGTTGAAGAAATCAAGAGTGAATATTAAGGCCAA 600
QY      602   GAGATTATTCCTTTTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTGAT 661
DB      601   GAGATTATTCCTTTTCCAAGTACCAAAATGATGAGAAACCTTTTATGTGTCATGTGAT 660
QY      662   GTGTGAGAAATGAGCTTTTGCCTTATGACATCCCATTTGGAGAGCACACAGAGGGCATGCT 721
DB      661   GTGTGAGAAATGAGCTTTTGCCTTATGACATCCCATTTGGAGAGCACACAGAGGGCATGCT 720
QY      722   GCGGAACGAATGAATCAGTTTAAATAATGGTTTAAAGAAATGCAAGAGGCTCCAGAGTCA 781
DB      721   GCGGAACGAATGAATCAGTTTAAATAATGGTTTAAAGAAATGCAAGAGGCTCCAGAGTCA 780
QY      782   GCTACAGTTATATTTGAGGAGATACAAATCTAAGGATCGAGAGTTTACAGATGTGCT 841
DB      781   GCTACAGTTATATTTGAGGAGATACAAATCTAAGGATCGAGAGTTTACAGATGTGCT 840
QY      842   GGTTTACCCCAACAACATTTGGAGTGTCTGGAGTGTCTGGAGTGTCTGGCAACCTTAAACAT 901
DB      841   GGTTTACCCCAACAACATTTGGAGTGTCTGGAGTGTCTGGAGTGTCTGGCAACCTTAAACAT 900
QY      902   TATACATGGGATACACAAATGAATCTAAATCTTGAATAAATGCTGTGTGTAATCTTCGT 961
DB      901   TATACATGGGATACACAAATGAATCTAAATCTTGAATAAATGCTGTGTGTAATCTTCGT 960
QY      962   TTTGATCGAATATTTTTCAGAGCAGCAGAGGAGGACACATATTTCCCGGAGTTTG 1021
DB      961   TTTGATCGAATATTTTTCAGAGCAGCAGAGGAGGACACATATTTCCCGGAGTTTG 1020
QY      1022   GACCTCTCTGGATTAGAAAAAATCGACTGTGGTGTAGATTTCTCTAGTGTACCTGGGGTCTT 1081
DB      1021   GACCTCTCTGGATTAGAAAAAATCGACTGTGGTGTAGATTTCTCTAGTGTACCTGGGGTCTT 1080
QY      1082   CTGTGCAACTTAGATATAATATTTGTAATGCTTTTCAAGTGTGGGTTTGGCCCTGATTTG 1141
DB      1081   CTGTGCAACTTAGATATAATATTTGTAATGCTTTTCAAGTGTGGGTTTGGCCCTGATTTG 1140
QY      1142   TTGCAAAATACAAATTTCCACCTTCTGGAAGGTAGGTTTGTCTGGAGGAAATATATGTACT 1201
DB      1141   TTGCAAAATACAAATTTCCACCTTCTGGAAGGTAGGTTTGTCTGGAGGAAATATATGTACT 1200
QY      1202   AGATCATTTGTACAGAAAAACCAACTATGATTTATGTTGTGTTTTCAGAAATTCACAAAT 1261
DB      1201   AGATCATTTGTACAGAAAAACCAACTATGATTTATGTTGTGTTTTCAGAAATTCACAAAT 1260
QY      1262   AAAGATTAAATGTTTATTTAAACGAAACATTTCTGCAATTCAGGATGTGAGGCCATTTAAT 1321
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QY      1322   AAAAAGGCGCAAGAGCCGTGTCAGAGTTTTCAGCGTGTCTACAGCTGCAGCTCGATTC 1381
DB      1321   AAAAAGGCGCAAGAGCCGTGTCAGAGTTTTCAGCGTGTCTACAGCTGCAGCTCGATTC 1380
QY      1382   AAACAGGTACCCCATTTCTCTGAGCTAAATGTTTATATTTTCCATTCAGGCAACCGAAAT 1441
DB      1381   AAACAGGTACCAATTTCTCTGAGCTAAATGTTTATATTTTCCATTCAGGCAACCGAAAT 1440
QY      1442   AGTTAAATTTTAAATTAAGTCTTCAAAGAAAAATTAAGAGATTTATGAGTTCTTGGAC 1501
DB      1441   AGTTAAATTTTAAATTAAGTCTTCAAAGAAAAATTAAGAGATTTATGAGTTCTTGGAC 1500
QY      1502   TGGATCCTTTATTTTCATAAGTTTCAGATCATCTTAAATGAAAAATGCCATGATTTATCTGCAG 1561
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Db 1100 GAATTCACATTAAGATTAAATGTTATTTAAACGACACACATTCCTGCAATTCAGATGTG 1159
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Qy 1610 ATTACATAATTGGTAAGNTATAATTGAAACCTTATGGCTTAAATTCCTTAACTCCTTTT 1669
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Qy 1670 TGATTCAATGTTGTAGTCATGTCTGCAACAGAGCAAGTTAAGCTTGATGATGTTTAA 1729
Db 1520 TGATTCAATGTTGTAGTCATGTCTGCAACAGAGCAAGTTAAGCTTGATGATGTTTAA 1579
Qy 1730 ATCGGTTGATGACACCATGGGACATTTTAAACAAATAAATGCAATGAAGACATA 1789
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Qy 1790 GCCTTTTGTAGTTTGTCTAATTCGAAATGGAATGCTTTTACAGGAAGTAAATGCAAAATTAN 1849
Db 1640 GCCTTTTGTAGTTTGTCTAATTCGAAATGGAATGCTTTTACAGGAAGTAAATGCAAAATTAC 1699
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Db 1700 TTTTAAAGTGTCTTTAAAGAAATAATTTTCCACAGGAGAAA 1743
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RESULT 4
CR592636
LOCUS
DEFINITION CR592636 1620 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CSODM007YB11 of Fetal liver of Homo sapiens
(human).
ACCESSION CR592636
VERSION CR592636.1 GI:50473443
KEYWORDS HTC; cDNA; cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1620)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
JOURNAL
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1620)
Genoscope.
Direct Submission
JOURNAL
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
```

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was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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Best Local Similarity 89.3%; Pred. No. 0;
Matches 1613; Conservative 0; Mismatches 7; Indels 186; Gaps 1;
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Db 1 CCTGAGGTGAAAAAGCGCGACATTCCTGTGTGTGAGTTCCTCGTTCGCAAGCTGGAT 60
Qy 137 GCGCAGTGGCTCAGTCTTCCTGGCCGAGAAACGATGCGGAGATGGAAGGGCTCTGAAC 196
Db 61 GCGCAGTGGCTCAGTCTTCCTGGCCGAGAAACGATGCGGAGATGGAAGGGCTCTGAAC 120
Qy 197 TCCTACTTCGAGCTCCGGTGGAGGAGCGCTTGGAAACGCGACCTGAAACCATCTCT 256
Db 121 TCCTACTTCGAGCTCCGGTGGAGGAGCGCTTGGAAACGCGACCTGAAACCATCTCT 180
Qy 257 GAGCCCAAGACCTATGTTGACCTTAAACCAATGAAGAAACAACTGATCCACCATCTTCAA 316
Db 181 GAGCCCAAGACCTATGTTGACCTTAAACCAATGAAGAAACAACTGATCCACCATCTTCAA 240
Qy 317 ATCAGCCCATCTGAAGATATCTCAGCAAGAAATGCGAGCATGTTCTCTCATTTACCTGG 376
Db 241 ATCAGCCCATCTGAAGATATCTCAGCAAGAAATGCGAGCATGTTCTCTCATTTACCTGG 300
Qy 377 AATATTGATGGATTAGATCTTAAACAACTCTCAGAGAGGGCTCGAGGGGTGTGTTCTTAC 436
Db 301 AATATTGATGGATTAGATCTTAAACAACTCTCAGAGAGGGCTCGAGGGGTGTGTTCTTAC 360
Qy 437 TTAGCTTTGTACAGCCCGAGATGTGATATTTCTACAGGAAGTTATTTCCCCCATATATTAGC 496
Db 361 TTAGCTTTGTACAGCCCGAGATGTGATATTTCTACAGGAAGTTATTTCCCCCATATATTAGC 420
Qy 497 TACCTAAAGAGAGATCAAGTAATATTAGATTTATTAAGTCTATGAAGAGGATATTTTC 556
Db 421 TACCTAAAGAGAGATCAAGTAATATTAGATTTATTAAGTCTATGAAGAGGATATTTTC 480
Qy 557 ACAGCTATATGTTGAAGAAATCAAGAGTGAATTTAAAGCCCAAGAGATTTATTCCTTTT 616
Db 481 ACAGCTATATGTTGAAGAAATCAAGAGTGAATTTAAAGCCCAAGAGATTTATTCCTTTT 540
Qy 617 CCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAATGTCTCAGGAAATGAG 676
Db 541 CCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAACGTGTCAAGAAATGAG 600
Qy 677 CTTTGCCTTATGACATCCCATTTGGAGAGCACCAGAGGGCATGTGCGGAAACGAATGAAT 736
Db 601 CTTTGCCTTATGACATCCCATTTGGAGAGCACCAGAGGGCATGTGCGGAAACGAATGAAT 660
Qy 737 CAGTTAAAAATGGTTTAAAGAAATCAAGAGGCTCCAGAGTCCAGAGTCAAGTTATATTT 796
Db 661 CAGTTAAAAATGGTTTAAAGAAATCAAGAGGCTCCAGAGTCCAGAGTCAAGTTATATTT 720
Qy 797 GCAGGAGATCAAAATCTAAGGGATCGAGAGGTTACCAAGATGTGGTGGTTTACCAACAAC 856
Db 721 GCAGGAGATCAAAATCTAAGGGATCGAGAGGTTACCAAGATGTGGTGGTTTACCAACAAC 780
Qy 857 ATTGTGAGTGTGGGAGTGTGGGCAAAACCTTAAACATTTGCCAGTATACATGGGATACA 916
Db 781 ATTGTGAGTGTGGGAGTGTGGGCAAAACCTTAAACATTTGCCAGTATACATGGGATACA 840
Qy 917 CAAATGAACCTAATCTTGGAAATAACTGCTGCTTGTAAACTTTCGTTTTGTGATCGAATATTT 976
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Db 841 CAAATGAATCTTAATCTTGGATAACTGCTGCTTGTAAACTTCGTTTGGATGAATATTT 900
Qy 977 TTCAGAGCAGCAGCAGAGAGGAGCACAATATTTCCCGAAGTTTGGACCTTCTTGATTA 1036
Db 901 TTCAGAGCAGCAGCAGAGAGGAGCACAATATTTCCCGAAGTTTGGACCTTCTTGATTA 960
Qy 1037 GAAAACTGACCTGTTGGTAGATTTCTCTAGTGATCACTGGGGTCTTCTGTGCAACTTAGAT 1096
Db 961 GAAAACTGACCTGTTGGTAGATTTCTCTA 988
Qy 1097 ATAATATTGAAATGCTTTTCAAGTGTGGGTTTTTGGCCCTGATTTGTGCAATACAATTT 1156
Db 989 ----- 988
Qy 1157 CCACCTTCTGGAAAGTAGGTTTGTGTGGAGGAAATAATGTAAGTATGTCACAG 1216
Db 989 ----- 988
Qy 1217 AAAAACCAACTATGATTTATGTTGTTTTCAGAAATTCACATTAAGATTAAATGTTTA 1276
Db 989 -----AATTCACATTAAGATTAAATGTTTA 1014
Qy 1277 TTTAAACGAACATTTCTGCAATTCAGGATGTGAGGCCATTTAATAAAAGGCGCAAAAG 1336
Db 1015 TTTAAACGAACATTTCTGCAATTCAGGATGTGAGGCCATTTAATAAAAGGCGCAAAAG 1074
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Db 1075 CCGTGTGAGAGTTTCAACGGTGTGTTATAGTGCAGCTGGATTCGAAACAGGTACCCAT 1134
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Db 1255 ATAAGTTTCAGATCATCTTAAATGAAATGCAATGATTAATTCGAGTTAAGTAGATGACAG 1314
Qy 1577 CTATTTCTACATCAGACTTGTATTTTGTGCTAATTAATTAATTAATTTGTAATTTGTA 1636
Db 1315 CTATTTCTACATCAGACTTGTATTTTGTGCTAATTAATTAATTAATTTGTAATTTGTA 1374
Qy 1637 AACCTTATGGCTTAAATTCCTTAACTCCTTTTGTGATTCATGTTTGTAGTCAATGTTGTCA 1696
Db 1375 AACCTTATGGCTTAAATTCCTTAACTCCTTTTGTGATTCATGTTTGTAGTCAATGTTGTCA 1434
Qy 1697 ACAGAGCAAAGTTAAGCTTTGATGATGGTTTAAATCGGTTTGTAGCACAATGGGACATT 1756
Db 1435 ACAGAGCAAAGTTAAGCTTTGATGATGGTTTAAATCGGTTTGTAGCACAATGGGACATT 1494
Qy 1757 TTTTAAACAAAATAAATGATGATGAGACATAGCCCTTTTGTAGTTTGTCTAATTTGTAAT 1816
Db 1495 TTTTAAACAAAATAAATGATGATGAGACATAGCCCTTTTGTAGTTTGTCTAATTTGTAAT 1554
Qy 1817 GGAATCTTTTACAGGAAGTAAATGCAAAATTAATTTTAAAGTGTCTTTAAAGAAAATAT 1876
Db 1555 GGAATCTTTTACAGGAAGTAAATGCAAAATTAATTTTAAAGTGTCTTTAAAGAAAATAT 1614
Qy 1877 TTTCCC 1882
Db 1615 TTTCCC 1620

RESULT 5
CR601303
LOCUS
DEFINITION full-length cDNA clone CSODN005YN02 of Adult brain of Homo sapiens (human).

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CR601303
CR601303.1 GI:50482110
HTC; CNSLT cDNA.
Homo sapiens (human)

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
1 (bases 1 to 1168)

AUTHORS
Li W.B., Gruber C., Jessee J. and Polayes D.

TITLE
Full-length cDNA libraries and normalization

JOURNAL
Unpublished

REMARK
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue

REFERENCE
2 (bases 1 to 1168)

AUTHORS
Genoscope.

JOURNAL
Direct Submission

COMMENT
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr

FEATURES
Location/Qualifiers
1..1168
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODN005YN02"
/tissue_type="Adult brain"
/plasmid="PCMVSPORT_6"

ORIGIN

Query Match 60.4%; Score 1160.4; DB 4; Length 1168;

Best Local Similarity 99.9%; Pred. No. 1.9e-276;

Matches 1161; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTGCGAGGCGGCGAGGAGATCGAGTTGGGGAGTTCCCTGGAGGGCGGAGGAGCGGC 60

Db 7 GTGCGAGGCGGCGAGGAGATCGAGTTGGGGAGTTCCCTGGAGGGCGGAGGAGCGGC 66

Qy 61 GGAGGAAGAGGCGAGCGCTGAGGTGAAAAAGCGGCGACTTCTGTGTGGAGTTTGCTC 120

Db 67 GGAGGAAGAGGCGAGCGCTGAGGTGAAAAAGCGGCGACTTCTGTGTGGAGTTTGCTC 126

Qy 121 GGTGCGAAGCTGCGATGCGCGAGTGGCTCAGTGTCTTCTGGCCGAGAACGACTGGGAGAT 180

Db 127 GGTGCGAAGCTGCGATGCGCGAGTGGCTCAGTGTCTTCTGGCCGAGAACGACTGGGAGAT 186

Qy 181 GGAAAGGCTCTGAATCTCTACTTTCAGCTCCGGTGGAGGAGCGCCTTGGAAACGCCG 240

Db 187 GGAAAGGCTCTGAATCTCTACTTTCAGCTCCGGTGGAGGAGCGCCTTGGAAACGCCG 246

Qy 241 ACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAAACCAATGAAGAAACAACCTGA 300

Db 247 ACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAAACCAATGAAGAAACAACCTGA 306

Qy 301 TTCACCACTTCTAAATCAGCCCATCTGAAGATACTCAGCAAGAAATGGCAGCATGTT 360

Db 307 TTCACCACTTCTAAATCAGCCCATCTGAAGATACTCAGCAAGAAATGGCAGCATGTT 366

Qy 361 CTCTCTCATCTTGAATATTCATGATAGTATTAACAATCTGTACAGAGGCGCTCG 420

Db 367 CTCTCTCATCTTGAATATTCATGATAGTATTAACAATCTGTACAGAGGCGCTCG 426

Qy 421 AGGGGTGTCTCTACTTGTACAGCCCGAGATGTGATATTTCTACAGGAAGTTAT 480

Db 427 AGGGGTGTCTCTACTTGTACAGCCCGAGATGTGATATTTCTACAGGAAGTTAT 486

Qy 481 TCCCCCATATATTATAGCTACCTAAAGAGAGATCAAGTAATTTATGAGATTTATTACAGGTCA 540

Db	487	TCCCCCATATTAGCTACCTAAAGAGAGATCAAGTAATTATGAGATTATACAGGTCA	546
Qy	541	TGAAGAAGGATATTTACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAGGCCA	600
Db	547	TGAAGAAGGATATTTACAGCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAGGCCA	606
Qy	601	AGAGATTATCTTTTCCAACTACCAAAATGATGAGAACTTTTATGTGTCATGTGAA	660
Db	607	AGAGATTATCTTTTCCAACTACCAAAATGATGAGAACTTTTATGTGTCATGTGAA	666
Qy	661	TGTGTCCAGAAATGAGCTTTGCTTTATGACATCCCAATTTGAGAGCACCAAGGGCATGC	720
Db	667	CGTGTCCAGAAATGAGCTTTGCTTTATGACATCCCAATTTGAGAGCACCAAGGGCATGC	726
Qy	721	TGCGGAACGAATGAATCAAGTTAAATAGTTTAAAGAAATGCAAGAGGCTCCAGAGTC	780
Db	727	TGCGGAACGAATGAATCAAGTTAAATAGTTTAAAGAAATGCAAGAGGCTCCAGAGTC	786
Qy	781	AGCTACAGTTATATTTGACAGGATACAAATCTAAGGGATCGAGAGTTACCAAGTGG	840
Db	787	AGCTACAGTTATATTTGACAGGATACAAATCTAAGGGATCGAGAGTTACCAAGTGG	846
Qy	841	TGGTTTACCACCAACATTTGTGGATGCTCTGGAGTTTTTGGGCAACCTAAACATTTGCCA	900
Db	847	TGGTTTACCACCAACATTTGTGGATGCTCTGGAGTTTTTGGGCAACCTAAACATTTGCCA	906
Qy	901	GTATACATGGGATACACAAATGAACTCTAAATCTTTGGAAATACTGCTGCTGTAAACTTCG	960
Db	907	GTATACATGGGATACACAAATGAACTCTAAATCTTTGGAAATACTGCTGCTGTAAACTTCG	966
Qy	961	TTTTGATCGAATATTTTTCAGAGCAGCAGAGAGAGGGACACATATTATCCCCGAAGTTT	1020
Db	967	TTTTGATCGAATATTTTTCAGAGCAGCAGAGAGAGGGACACATATTATCCCCGAAGTTT	1026
Qy	1021	GGACCTCTCTGGATTAGAAAAAATGGAGCTGTGGTAGATTTCTCTAGTAGTCACTGGGGTCT	1080
Db	1027	GGACCTCTCTGGATTAGAAAAAATGGAGCTGTGGTAGATTTCTCTAGTAGTCACTGGGGTCT	1086
Qy	1081	TCTGTGCAACTTAGATATAATTTGTAAAAATGCTTTTCAAGTGTGGGTTTTGCCCTGATT	1140
Db	1087	TCTGTGCAACTTAGATATAATTTGTAAAAATGCTTTTCAAGTGTGGGTTTTGCCCTGATT	1146
Qy	1141	GTTCGAATACATTTCCACCT	1162
Db	1147	GTTCGAATACATTTCCACCT	1168

RESULT 6	
DQ049205	
LOCUS	DQ049205 1089 bp DNA linear GSS 02-JUN-2005
DEFINITION	Homo sapiens TTRAP gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION	DQ049205
VERSION	DQ049205.1 GI:66902404
KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1 (bases 1 to 1089) Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civallo,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees (ex) PLoS Biol. 3 (6), E170 (2005)
AUTHORS	15869325
TITLE	2 (bases 1 to 1089) Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civallo,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
JOURNAL	
PUBMED	
REFERENCE	
AUTHORS	

TITLE	Direct Submission
JOURNAL	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
FEATURES	Location/Qualifiers
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Query Match	56.6%; Score 1087.4; DB 11; Length 1089;
Best Local Similarity	99.9%; Pred. No. 2.4e-258;
Matches 1088; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
Qy	20 ATGAGATTGGGAGTTCCCTGGAGGGCGGAGGAGCGCGGAGGAGGAGGCGAGGCT 79
Db	1 ATGAGATTGGGAGTTCCCTGGAGGGCGGAGGAGGCGCGGAGGAGGCGAGGCT 60
Qy	80 GAGGTGAAGGCGGCGACCTCTGTGTGGAGTTTCCTCGTCCGTCGCAAGCTCGATGCC 139
Db	61 GAGGTGAAGGCGGCGACCTCTGTGTGGAGTTTCCTCGTCCGTCGCAAGCTCGATGCC 120
Qy	140 GCAGTGGCTCAGTCTCTTCGGCCGAGAACGACCTGGGAGATGGAAGGGCTCTCAACTCC 199
Db	121 GCAGTGGCTCAGTCTCTTCGGCCGAGAACGACCTGGGAGATGGAAGGGCTCTCAACTCC 180
Qy	200 TACTTCGAGCTCCGTTGGAGGAGGCGCTTGGAAACCGGACCTGAAACCATCTCTGAG 259
Db	181 TACTTCGAGCTCCGTTGGAGGAGGCGCTTGGAAACCGGACCTGAAACCATCTCTGAG 240
Qy	260 CCCAAGACCTATGTTGACCTAAACCAATGAAGAAACAATGTTCCACCACTTCTAAATC 319
Db	241 CCCAAGACCTATGTTGACCTAAACCAATGAAGAAACAATGTTCCACCACTTCTAAATC 300
Qy	320 AGCCCATCTGAAGATACCTCAGCAAGAAAATGGCAGCATGTTCTCTCTCATTTACCTGGAAT 379
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Qy	380 ATTGATCGATTAGATCTAAACAATCTGTCAAGAGGCTCGAGGGGTGTGTTCTTACTTA 439
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Qy	440 GCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTTCCCCCATATATAGCTAC 499
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Qy	500 CTAAGAAGAGAGATCAAGTAATTATGAGATTATTACAGTCAATGAAGAGGATATTTTACA 559
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Qy	560 GCTATAATGTTGAAGAAATCAAGAGTGAATTTAAAAAGCCCAAGAGATATTTCTTTTCCA 619
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Qy	620 AGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGATGTCTCAGGAATGAGCTT 679
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Qy	680 TGCCTTATGATCATCCCATTTGGAGAGCACCAAGGGCATGCTGCGGAACGAATGAATCAG 739
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Qy	740 TTAATAATGTTTAAAGAAAAATGCAAGAGGCTCCAGAGTCCAGTACAGTTATATTGCA 799
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RESULT 8
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LOCUS      BX444691 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone  EST 04-MAY-2004
DEFINITION CSODN005YN02 5-PRIME, mRNA sequence.
ACCESSION  BX444691
VERSION     BX444691.2  GI:47009162
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homidae; Homo.
REFERENCE   1 (bases 1 to 1081)
AUTHORS     Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     On May 15, 2003 this sequence version replaced gi:30780264.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            This sequence belongs to sequence cluster 3474.r
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?e=CSODN005DG01QP1&c=3474.r.

FEATURES             source
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                    /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                    was primed with a NotI-oligo(dT) primer. Five prime end
                    enriched, double-strand cDNA was digested with Not I and
                    cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                    vector. Library was not normalized."

ORIGIN
Query Match      51.8%; Score 994.8; DB 5; Length 1081;
Best Local Similarity 98.7%; Pred. No. 2.3e-235;
Matches 1048; Conservative 6; Mismatches 3; Indels 5; Gaps 5;

Qy 1 GTGCAGAGCGCGCAGGAGATGGAGTTGGGAGTTGCTGGAGGCGC-GGAGGAGGCGG 59
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Qy 7 GTGCAGAGCGCGCAGGAGATGGAGTTGGGAGTTGCTGGAGGCGC-GGAGGAGGCGG 66
Db 7 |||||
Qy 60 CGGAGGAGAGCGCGCAGGCTGAGTGAAGGCGGCGACTTCTGTGTGAGATTGCGCT 119
Db 60 |||||
Qy 67 CGGAGGAGAGCGCGGAGCGCTGAGTGAAGGCGGCGACTTCTGTGTGAGATTGCGCT 126
Db 67 |||||
Qy 120 CGGTGCGAAGCTGCGATGCCGCGAGTGGCTCAGTGTCTCTGCGCGAGAACACTGGGAGA 179
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Qy 127 CGGTGCGAAGCTGCGATGCCGCGAGTGGCTCAGTGTCTCTGCGCGAGAACACTGGGAGA 186
Db 127 |||||
Qy 180 TGGAAAGGGCTCTGAACCTCTTACTTCGAGCTCCGGTGGAGGAGCGCCCTTGAACGCC 239
Db 180 |||||
Qy 187 TGGAAAGGGCTCTGAACCTCTTACTTCGAGCTCCGGTGGAGGAGCGCCCTTGAACGCC 246
Db 187 |||||
Qy 240 GACCTGAACCACTCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAAGAAACAACCTG 299
Db 240 |||||
Qy 247 GACCTGAACCACTCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAAGAAACAACCTG 306
Db 247 |||||
Qy 300 ATTCACCACTTCTAAATACGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGCATGT 359
Db 300 |||||
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Db 307 ATTCACCACTTCTAAATACGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGCATGT 366
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Db 367 TCTCTCTCAATTA CTTGGAATATTGATGGATTTAGATCTTAAACAATCTGTTCAGAGAGGGCTC 426
Qy 420 GAGGGGTGTGTTCTACTTCTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTA 479
Db 427 GAGGGGTGTGTTCTACTTCTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTA 486
Qy 480 TTCCCCCATATTA TAGCTACCTAAAGAGAGATCAAGTAATATATGAGATTTATACAGGTC 539
Db 487 TTCCCCCATATTA TAGCTACCTAAAGAGAGATCAAGTAATATATGAGATTTATACAGGTC 546
Qy 540 ATGAAGAAGGATATTTACAGCTATTAATGTTTGAAGAAATCAAGAGTGAATATAAAGGCC 599
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Qy 660 ATGTGTGAGGAAATGAGCTTTTGCCTTATGACATCCCATTTGGAGAGCACCAGAGGGCATG 719
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Qy 840 GTGGTTTACCACAAACAATTTGTGGATCTCTGGAGTTTGGGCAAACTTAAACAATTTGCC 899
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Qy 1020 TGACCTTTCTGGATTAGAAAACTGGACTGTGTAGATTTC 1061
Db 1024 TGGACCTTTCTGGATTAG-AAAACCTGGACTGTGTAGATTTC 1064

RESULT 9
CN642527
LOCUS      CN642527
DEFINITION ILLUMINEN MQO_6530 Katze MWPL2 Macaca mulatta cDNA clone IBIUM:4699
            5' similar to Bases 1 to 1084 highly similar to human TTRAP
            (Hs.210628), mRNA sequence.
ACCESSION  CN642527
VERSION     CN642527
KEYWORDS    EST.
SOURCE      Macaca mulatta (rhesus monkey)
ORGANISM    Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Cercopithecoidea; Cercopithecinae; Macaca.
            1 (bases 1 to 1087)
REFERENCE   1 (bases 1 to 1087)
AUTHORS     Magnus, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agv, M.B.,
            Prohl, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
            Iadonato, S.P.
TITLE       Analysis of the Macaca mulatta transcriptome and the sequence
            divergence between Macaca and human
JOURNAL     Genome Biol. 6 (7), R60 (2005)
PUBMED     15998449
```

COMMENT

Contact: C. Magnus
 Illumigen Biosciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagnus@illumigen.com
 Sequenced on 2003.12.24. 840 Q20 bases.
 PCR Primers
 FORWARD: CCTCACTAAAGGGACAAAA
 BACKWARD: CACTATAGGGGAATTGGGTA
 Insert Length: 1087 Std Error: 0.00
 Plate: CL000066 row: D column: 10
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 POLyA-No.

FEATURES

source

Location/Qualifiers
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 /mol_type="mRNA"
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 /clone_lib="Katze_MWPL2"
 /note="Organ: placenta; Vector: Uni-ZAP XR; Site 1: Ecor
 I; Site 2: Xho I; Created from Stratagene ZAP-cDNA
 Synthesis kit (catalog #200400) and ZAP-cDNA Gigapack III
 Gold Cloning Kit (Catalog #200450)"

ORIGIN

Query Match 50.1%; Score 961.2; DB 7; Length 1087;
 Best Local Similarity 95.2%; Pred. No. 4.9e-227;
 Matches 1001; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

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QY 301 TTCCACACCTTCTAAATCAGCCCATCTGAAGATACCTCAGCAGAGAAAATGGCAGCATGTT 360
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QY 361 CTCTCTCATTTACCTGGAATATGATGATAGATCTAAACAATCTGTCTGAGAGGGCTCG 420
DB 61 CTGCTTTCATTTACCTGGAATATGATGATAGATCTAAACAATCTGTCTGAGAGGGCTCG 120
QY 421 AGGGGTGTCTTCTACTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTAT 480
DB 121 AGGGGTGTCTTCTACTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTAT 180
QY 481 TCCCCCATATTATAGCTTACCTAAAGAGAGATCAAGTAATTATGAGATTATTACAGGTCA 540
DB 181 TCCCCCATATTATAGCTTACCTAAAGAGAGAGATCAAGTAATTATGAGATTATTACAGGTCA 240
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QY 661 TGTGTCAAGAAATGAGCTTTTGCCTTATGACATCCCATTTGAGAGACCAAGAGGGCATGC 720
DB 361 TGTGTCAAGAAATGAGCTTTTGCCTTATGACATCCCATTTGAGAGACCAAGAGGGCATGC 420
QY 721 TGGGGACGAATGAATCAGTTAAATAATGTTTAAAGAAAATCAAGAGGCTCCAGATC 780
DB 421 TGGGGACGAATGAATCAGTTAAATAATGTTTAAAGAAAATCAAGAGGCTCCAGATC 480
QY 781 AGCTACAGTTATATTTCAGAGAGATCAAAATCTAAGGATCGAGAGTTACAGATGTC 840
DB 481 AGCTACAGTTATATTTCAGAGAGATCAAAATCTAAGGATCGAGAGTTACCAAAATGTC 540
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DB 541 TGGTTTACCAACCAACATTTGTGGATGCTGGAGTTTTTGGGCAAACTTAAACATTTGCCA 600
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DB 601 GTATACATGGGATACACAAATGAACCTCTAATCTTGGAAATAACTGCTGCTGTGTAACTTCG 660
QY 961 TTTTGATCGAATATTTTTCAGAGCAGCAGAGAGAGGACACATTTATTTCCCGAAGTTT 1020
DB 661 TTTTGATCGAATATTTTTCAGAGCAGCAGAGAGAGGACACATTTATTTCCCGAAGTTT 720
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DB 721 GGACCTTCTTGGATTGGAAAACTCGACTGTGGTAGATTTCCTAGTGATCACTGGGGTCT 780
QY 1081 TCTGTGCAACTTAGATATAATATTCTAAAAATGCTTTTCAAGTGTGGGTTTTTGCCTTGATT 1140
DB 781 TCTGTGCAACTTAGATATAATATTCTAAAAATGCTTTTCAAGTGTGGGTTTTTGCCTTGATT 840
QY 1141 GTTGCAAAATACAAATTTCCACCTTCTGGAAAGGTAGTTTGTCTGTGGAGGAAATAATGTAC 1200
DB 841 TTTTGCAAAATACAGTTTCCACCTTCTGGAAAGGTAGTTTGTCTGTGGAGGAAATAATGTAC 900
QY 1201 TAGATCATGTGTACAGAAAACCAACTATGATTTATGTTGTGTTTTCAGAATTCAACAT 1260
DB 901 TAGATCATGTGTACAGAAAACCAACTATGATTTATGTTGTGTTTTCAGAATTCAACAT 960
QY 1261 TAAAGATTAAATGTTTTTAAACGAAACACATTCCTGCATTCAGGATGTGAGGCCATTTAA 1320
DB 961 TAAAGATTAAATGTTTTTAAATGAACCCCTTCCCTGTTTTCAGATGTGAGGCCCTTTA 1020
QY 1321 TAA-AAAGGGCACAAAGCCTGTACAGATTTT 1350
DB 1021 TAAATTAAGGGCACAAAGCCTGTTTAAAGTTT 1051

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RESULT 10

BX338160
 LOCUS BX338160
 DEFINITION BX338160 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
 clone CS0D1056YC23 5-PRIME, mRNA sequence.
 ACCESSION BX338160
 VERSION BX338160.2 GI:46283046
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 981)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 2, 2003 this sequence version replaced gi:30345671.
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE
 Email: seqrefgenoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 3474.r

FEATURES

source

Location/Qualifiers
 1..981
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1056YC23"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?se=CS0D1056AB12QP1sc=3474.r.


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330 AAGATACCTCAGCAAGAAATGCGCAGCATGTTCTCTCTATACCTGGGAATATTGATGAT 389
301 AAGATACCTCAGCAAGAAATGCGCAGCATGTTCTCTCTATACCTGGGAATATTGATGAT 360
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361 TAGATCTAAACAATCTGTCAGAGAGGGCTCGAGGGGTGTTCTCTACTTACCTTGTGTACA 420
450 GCCCAGATGTGATATTCTTACAGGAAGTTATTCCCCATATTATATAGTACCTTAAAGAAGA 509
421 GCCCAGATGTGATATTCTTACAGGAAGTTATTCCCCATATTATATAGTACCTTAAAGAAGA 480
510 GATCAAGTAATTATGAGATTATACAGGTCATGAGAGAGGATATTTCACAGCTATAATGT 569
481 GATCAAGTAATTATGAGATTATACAGGTCATGAGAGAGGATATTTCACAGCTATAATGT 540
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541 TGAAGAAATCAAGAGTGAATTTAAAGGCAAGAGATATTCTCTTCCAACTACCAAAA 600
630 TGATCAGAAACCTTTTATGTGTCATGTCGAATGTGTCAGGAATAGAGCTTTGCCCTTATGA 689
601 TGATCAGAAACCTTTTATGTGTCATGTCGAATGTGTCAGGAATAGAGCTTTGCCCTTATGA 660
690 CATCCCATTTGGAGACACAGAGGCTGCTGCGGAAGCAATGATCATGTTAAAATGG 749
661 CATCCCATTTGGAGACACAGAGGCTGCTGCGGAAGCAATGATCATGTTAAAATGG 720
750 TTTTAAAGAAATGCAAGAGGCTCCAGAGTCAGTACAGTATATTTTGCAGGAGATACAA 809
721 TTTTAAAGAAATGCAAGAGGCTCCAGAGTCAGTACAGTATATTTTGCAGGAGATACAA 780
810 ATCTAAGGATCGAGAGGTTTACAGATGTGGTGGTTTACCACAAATTTGGATGCT 869
781 ATCTAAGGATCGAGAGGTTTACCAGATGTGGTGGTTTAMMAAAAMATTTGGATGAT 840
870 GGGAGTTTGGGCAACCTTAAACATGTCAGTATACATGCGGATACAGAAATGAACTCTA 929
841 GGGAGTTTGGGCAACCTTAAACATGTCAGTATACATGCGGATACAGAAATGAACTCTA 900
930 ATCTCGAATACTGCTGCTGTAAACCTGTTTGCATCGAATATTCTTGGATAGAAA 1041
901 ATCTCGAATACTGCTGCTGTAAACCTGTTTGCATCGAATATTCTTGGATAGAAA 956
990 CAGAGAGGGACATATTATCCCCGAGTTTGGACCTTCTTGGATAGAAA 1041
957 MGVAAGAAGGGRCAATTTTMMCSGAGTTTGGMCTCTTGGATWRAAAA 1008
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RESULT 12
BX358706/c
LOCUS
DEFINITION
BX358706 Homo sapiens PLACENTA COT 25-NORMALIZED EST 08-APR-2004
clone CSOD1042YL19 3-PRIME, mRNA sequence.
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ACCESSION
BX358706
VERSION
BX358706.2 GI:46305664
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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REFERENCE
1 (bases 1 to 994)
Li, W.-B., Gruber, C., Jesse, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
```

```
On May 5, 2003 this sequence version replaced gi:30376263.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
```

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3474.1

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CSOD1042CF10NP1&c=3474.1.

FEATURES

source

Location/Qualifiers

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/organism="Homo sapiens"

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/db_xref="taxon:9606"

/clone="CSOD1042YL19"

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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 48.7%; Score 935; DB 5; Length 994;
Best Local Similarity 98.5%; Pred. No. 1.5e-220; Indels 2;
Matches 960; Conservative 2; Mismatches 11; Gaps 2;

QY 919 AATGAACCTCTATCTTTGGAATAAATCTGCTGCTTGTAAACTTCGTTTGTGATCGAATATTTT 978

Db 973 AATGAACCTCTATCTK-GNATTAACCTGCTGCTTGTAAAC-TCGTTTGTGATCGAATATTTT 916

QY 979 CAGACGACGACGAGAAGAGGGACACATTAATCCCGAAGTTGGACCTTCCTGGATTAGA 1038

Db 915 CAGACGACGACGAGAAGAGGGACACATTAATCCCGAAGTTGGACCTTCCTGGATTAGA 856

QY 1039 AAAACCTGGACTGTGTAGATTTTCTAGTAGATCACTGGGGCTTCTGTCGAACCTAGATAT 1098

Db 855 AAAACCTGGACTGTGTAGATTTTCTAGTAGATCACTGGGGCTTCTGTCGAACCTAGATAT 796

QY 1099 AATATTGTAAAAATGCTTTTCAAGTGTGGGTTTGGCCCTGATTTGTCGCAATACAAATTTTC 1158

Db 795 AATATTGTAAAAATGCTTTTCAAGTGTGGGTTTGGCCCTGATTTGTCGCAATACAAATTTTC 736

QY 1159 ACCTTCTGAAAAGGTAGGTTTCTGTGGAGGAAATAATGTACTAGATCAATGTGCACAGAA 1218

Db 735 ACCTTCTGAAAAGGTAGGTTTCTGTGGAGGAAATAATGTACTAGATCAATGTGCACAGAA 676

QY 1219 AAACCAACTATGATTTATGTTGTTTTCAGAAATTCACATTAAGATTAATGTTTATT 1278

Db 675 AAACCAACTATGATTTATGTTGTTTTCAGAAATTCACATTAAGATTAATGTTTATT 616

QY 1279 TAAACGACACATTCCTGCAATTCAGGATGTGAGGCCATTTAATAAAAAGGCGACAAAGCC 1338

Db 615 TAAACGACACATTCCTGCAATTCAGGATGTGAGGCCATTTAATAAAAAGGCGACAAAGCC 556

QY 1339 TGTACAGATTTTCAACGGTGTCTTACAGCTGCCAGCTGGATTCGCAACAGATACCCCATTTG 1398

Db 555 TGTACAGATTTTCAACGGTGTCTTACAGCTGCCAGCTGGATTCGCAACAGATACCCCATTTG 496

QY 1399 TCTCTGAGCTAATGTTTATATTTTCCATTCAGGACCCGAAATAGTTAATTTTAAATA 1458

Db 495 TCTCTGAGCTAATGTTTATATTTTCCATTCAGGACCCGAAATAGTTAATTTTAAATA 436

QY 1459 AGTCTTCAAAAGAAAAACATAAGAGATTAATGAGTTCTTGGGACTGGATCCTTTATTTTTCAT 1518

Db 435 AGTCTTCAAAAGAAAAACATAAGAGATTAATGAGTTCTTGGGACTGGATCCTTTATTTTCAT 376

QY 1519 AAGTTCCAGATCACTTTTAAATGAAAAATGCCATGATTAATCTGACGTTAAGTAGATGACAGCT 1578

Db 375 AAGTTCCAGATCACTTTTAAATGAAAAATGCCATGATTAATCTGACGTTAAGTAGATGACAGCT 316

QY 1579 ATTCTACATCAGACTTTGATTTTGTGACGCTTAATTTACATTAATTCGTAAGTATTAATTCAAA 1638

Db 315 ATTCTACATCAGACTTTGATTTTGTGACGCTTAATTTACATTAATTCGTAAGTATTAATTCAAA 256

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1072)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 2, 2003 this sequence version replaced gi:30337654.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DI052CG07NP1&c=3474.r.
FEATURES
Location/Qualifiers
1..1072
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="CS0DI052YN13"
/tissue_type="PLACENTA COT 25-NORMALIZED"
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 48.2%; Score 926.4; DB 5; Length 1072;
Best Local Similarity 91.4%; Pred. No. 2.1e-218;
Matches 969; Conservative 35; Mismatches 52; Indels 4; Gaps 4;
QY 845 TTACCCACCAACATCTGGATGCTGGGAGATTTTGGGCAAACTTAAACATGCCAGTAT 904
DB 1056 TTACCCANAMMTTKGGATGACTGGGNG-FTTGGACAACTTAAACATAKCCWRTAT 998
QY 905 ACATGGGATACAAATGAATCTTAATCTTGGAAATACCTGCTGCTTGTAAATCTCGTTT 964
DB 997 ACTT-GGATASACAAATKRACTCTAATCTTGGAAATKCKGTGCTTGTAA-ATCGTTT 940
QY 965 GATCGAATATTTTCAGACGACGACGAGGAGGACACATTTATCCCGAGTTTGGAC 1024
DB 939 GAGCGAATATTTTGCAGRGCRDCATYAKWGWGKACACTTTATCCCGAAGTTTGGAC 880
QY 1025 CTTCCTGGATTGAAACAACTGGAGTGGTGGATTTTCTAGTGATCACTGGGGTCTTCTG 1084
DB 879 CTTCCTGGATTGAAACAACTGGAGTGGTGGATTTTCTAGTGATCACTGGGGTCTTCTG 820
QY 1085 TGCAACTTAGATATAATATTGTAATATGCTTTTCAAGTGTGGTGTTCGCCCTGATTTG 1144
DB 819 TGCAACTTAGATATAATATTGTAATATGCTTTTCAAGTGTGGTGTTCGCCCTGATTTG 760
QY 1145 CAATACAAATTCACCTCTCGAAGAGTAGTTTGTGTGGAGGAATTAATGCTACTAGA 1204
DB 759 CAATACAAATTCACCTCTCGAAGAGTAGTTTGTGTGGAGGAATTAATGCTACTAGA 700
QY 1205 TCATTTGTCAGAAAAACCAACTATGATTTATGTTGTGTTTTCAGAAATTCACATTTAA 1264
DB 699 NCATTTGTCAGAAAAACCAACNANGANNANGNNGNNGTTTCAGAAATTCACANNAA 640
QY 1265 GATTAAATGTTTATTTAAACGAACACATTCCTGCAATTCAGGATGTGGCCCATTTAAATA 1324
DB 639 GANNAANGTTTATNTAAACGAACACATTCCTGCAATTCAGGATGTGGCCCATTTAAATA 580
QY 1325 AAGGGCACAAAGCCTGTGACAGTGTTCACAGCGTGTCTTACAGCTGCCAGCTGGATTCCAA 1384

Db 579 AAGGGCACAAAGCCTGTGACAGATTTTCAACGGTGCTTATAGCTGCCAGCTGGATKCCAAA 520
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Db 519 CAGGTACCCCATCTCTGAGCTAAATGTTTATATTTTCCACACAGCGMCCGAATAGT 460
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QY 1505 ATCCTTTATTTATTAAGTTCAGATCATCTTAAATGAAAATGCCATGATTTATCTGCAGTTA 1564
Db 399 AYCCTTTATTTATTAAGTTCAGATCATCTTAAATGAAAATGCCATGATTTATCTGCAGTTA 340
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QY 1625 AGNTATTAATGAAACCTTATGGCTTAAATTTCCCTTAACCTCTTTTGAATTCATGTTGTA 1684
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QY 1685 GTCATGTTTGTCAACAGAGGCAAGTAAAGCTTGTGATGATGTTTAAATCGGTTTGTAGCA 1744
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Db 159 CCATGGGACATTTTCTTAAACAAAATTAATGATGATGATGATGATGATGATGATGATGATGAT 100
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Db 99 KAATTTGKAATTTGGAATGCTTTTACAGGAAGTAAATGTAATTAATTTTAAAGTGTCTTT 40
QY 1865 AAGGAAAAATATTTTCCACAGGAGAAATTTTAAATAAAG 1904
Db 39 AAGGAAAAATA-TTTCCACAGAGAGNCTDTAAATAAAG 1
RESULT 15
AL577861/c
LOCUS
DEFINITION AL577861 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DK007YK05 3-PRIME, mRNA sequence.
ACCESSION AL577861
VERSION AL577861.3 GI:46256847
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1004)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 16, 2001 this sequence version replaced gi:31316108.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DK007AF03NP1&c=3474.r.
FEATURES
Location/Qualifiers
1..1004
/organism="Homo sapiens"


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/clone="CSODK007YK05"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match          47.5%; Score 912.4; DB 1; Length 1004;
Best Local Similarity 96.1%; Pred. No. 6.2e-215;
Matches 954; Conservative 18; Mismatches 17; Indels 4; Gaps 4;

Qy 891 AACATTGCGAGTATACATGGGATACACAAATCTAAATCTTGGAAATACTGCTGCTT 950
Db 1004 AACATKCCAGTATACAT-GGATACACAAAR-ACTCTAATCTTGGCATACTGCTGCTT 947

Qy 951 GTAAACCTGCTTTGATCGAATATTTT-TCAGAGCAGCAGCAGAGAGGGACACATTAT 1009
Db 946 GTAAATGCGTTTGAATCGAATATTTTTCAGAGCAGCAGCAGAGAGGGACACATTAT 887

Qy 1010 -CCCCGAAGTTGGACCTTCTGGATTAGAAAACCTGACTGTGGTAGATTCCTAGTGA 1068
Db 886 CCCCCGAATTTGGACCTTCTTGTATTAKAAAAACCTGGACTGTGGTAGATTCCTAGTGA 827

Qy 1069 TCACCTGGGCTCTCTGTGCAACTTAGATATATATTGTAATAATGCTTTTCAAGTGTGGGT 1128
Db 826 TCACCTGGGCTCTCTGTGCAACTTAGATATATATGTPAAATGCTTTCAGTGTGGGT 767

Qy 1129 TTTCGCCCTGATTTGCAAAATACAAATTTCCACCTTCTGGAAGGTAGTGTTCGTGGAG 1188
Db 766 TTTCGCCCTGATTTGCAAAATACAAATTTCCACCTTCTGGAAGGTAGTGTTCGTGGAG 707

Qy 1189 GAATATATGCTAGATCATTTGTACAGAAAACCAACTATGATTATGTTGTTGTTTTC 1248
Db 706 GAATATATGCTAGATCATTTGTACAGAAAACCAACTATGATTATGTTGTTGTTTTC 647

Qy 1249 AGAATTCACATTTAAAGATTAATGTTTATTTAAAGCAACACATTCCTGCATTGAGGATGT 1308
Db 646 AGAATTCACATTTAAAGATTAATGTTTATTTAAAGCAACACATTCCTGCATTGAGGATGT 587

Qy 1309 GAGGCCATTTAATAAAAGGGCACAAGCCCTGTGAGAGTTTCAACGGTCTTACAGCTG 1368
Db 586 GAGGCCATTTAATAAAAGGGCACAAGCCCTGTGAGAGTTTCAACGGTCTTACAGCTG 527

Qy 1369 CCAGCTGGATTCBAACAGGTACCCCATTTGCTCTGAGCTAATGTTTATATTTTCCATT 1428
Db 526 CCAGCTGGATCCCAACAGCTACCCCATTTGCTCTGAGCTAATGTTTATATTTTCCACT 467

Qy 1429 CAGGCACCAATAGTTAATATTTAAATAAGTCTTCAAAAGAAAACAATAAGAGATTAT 1488
Db 466 CAGGCACCAATAGTTAATATTTAAATAAGTCTTCAAAAGAAAACAATAAGAGATTAT 407

Qy 1489 GAGTCTTTGGAGCTGGATCCTTTATTTTCATAGTTTCAGATCATCTTAATGAAATGCCA 1548
Db 406 GAGCTCTTGGAGCTGGATCCTTTATTTTCATAGTTTCAGATCATCTTAATGAAATGCCA 347

Qy 1549 TGATTATCTGCAGTTAAGTAGATGACACTATTCTACATCAGACTTGATTTTGTACGCT 1608
Db 346 TGATTANTCTGCAGTTAAGTAGATGACRCGTATTCTACATCAGACTTGATTTTGTACGCT 287

Qy 1609 AATTACATAATTGGTAAGNTAATAATTGAAACCTTATGGCTTAAATTCCTTAATCCTCTT 1668
Db 286 AATTACATAATTGGTAAGNTAATAATTGAAACCTTATGGCTTAAATTCCTTAATCCTCTT 227

Qy 1669 TTGATTCAATGTTGTAGTCATGTTGTCAACAGAGCAAAAGTTAAAGCTTTGATGATGTTTAA 1728
Db 226 TTGATTCAATGTTGTAGTCATGTTGTCAACAGAGCAAAAGTTAAAGCTTTGATGATGTTTAA 167

Qy 1729 AATCGGTTTGATAGCACCATGGGACATTTTTTTTAAACAAAATAATATGATGAAGAGACAT 1788
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Db 166 AATCGGTTTGATAGCACCATGGGACATTTTTCTAACAAAATAAATGATGAAGAGACAT 107
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Db 106 AGCCTTTTAGTGTGCTAAATTTGCAAAATGGAATGCTTTTACAGGAAGTAAATGCAAAATTA 47
Qy 1849 NTTTTAAGTGTGCTTTTAAAGAAAATATTTTCC 1881
Db 46 CTTTAAAGTGTGCTTTTAAAGAAAATATTTCCC 14

RESULT 16
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ILLUMIGEN MQC 32551 Katze MMR Macaca mulatta cDNA clone
IBIUM:12605 5' similar to Bases 1 to 965 highly similar to human
TTRAP (Hs.210628), mRNA sequence.
CN803230
CN803230.1 GI:47699206
EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 965)
AUTHORS Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
Proll,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
Iadonato,S.P.
TITLE Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
JOURNAL Genome Biol. 6 (7), R60 (2005)
PUBMED 15998449
COMMENT Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.04.02. 780 Q20 bases.
PCR Primers
FORWARD: CCCTCACTAAAGGGACACAAA
BACKWARD: CACTATAGGCGGAATTGGGTA
Insert Length: 965 Std Error: 0.00
Plate: CL000288 row: D column: 11
Seg primer: CCCTCACTAAAGGGACACAAA
POLYA=No.

FEATURES
source Location/Qualifiers
1..965
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBIUM:12605"
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/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze MMR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
kit (catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"

ORIGIN
Query Match          46.8%; Score 898.2; DB 7; Length 965;
Best Local Similarity 96.9%; Pred. No. 2e-211;
Matches 937; Conservative 0; Mismatches 28; Indels 2; Gaps 2;

Qy 253 CTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACACTGATTCACCACCTTC 312
Db 1 CTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACACTGATTCACCACCTTC 60
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QY	313	TAATAATCAGCCCATCTGAAGTACTCAGCAAGAAATGCGAGCATGTTCTCTCTCATTTAC	372
Db	61	TAATAATCAGCCCATCTGAAGTACTCAGCAAGAAATGCGAGCATGTTCTCTCTCATTTAC	120
QY	373	CTGGAATATTGATGATTAGATCTAAACAATCTGTGAGAGGGCTCGAGGGGTGTGTTTC	432
Db	121	CTGGAATATTGATGATTAGATCTAAACAATCTGTGAGAGGGCTCGAGGGGTGTGTTTC	180
QY	433	CTACTAGCTTTGTACAGCCAGATGTGATATTCTACAGGAAGTATTCCTCCCATATTA	492
Db	181	CTACTAGCTTTGTACAGCCAGATGTGATATTCTACAGGAAGTATTCCTCCCATATTA	240
QY	493	TAGTACCTTAAAGAGAGATCAAGTAATATGAGATTATTAACAGGTCTAGGAAGGATA	552
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QY	553	TTTTCAGCTATTAATGTTGAAGAAATCAAGAGTGAATTTAAAGGCCAAGAGATTATTC	612
Db	301	TTTTCAGCTATTAATGTTGAAGAAATCAAGAGTGAATTTAAAGGCCAAGAGATTATTC	360
QY	613	TTTTTCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGTCATGTAATGTCTCAGGAA	672
Db	361	TTTTTCAAGTACCAAAATGATGAGAAACCTTTTATGTGTGTCATGTAATGTCTCAGGAA	420
QY	673	TGAGCTTTTCCCTTATGACATCCCATTTGAGAGACACAGAGGCGATGCTGCGGAACGAAT	732
Db	421	TGAGCTTTTCCCTTATGACATCCCATTTGAGAGACACAGAGGCGATGCTGCGGAACGAAT	480
QY	733	GAATCAGTGTAAATGTTTTAAAGAAATGCAAGAGGCTCCAGAGTCAAGTACAGTTAT	792
Db	481	GAATCAGTGTAAATGTTTTAAAGAAATGCAAGAGGCTCCAGAGTCAAGTACAGTTAT	540
QY	793	ATTTGAGAGATACAAATCTAAGGATCAGAGGTTACAGATGTGTTGTTTACCCAA	852
Db	541	ATTTGAGAGATACAAATCTAAGGATCAGAGGTTACAGATGTGTTGTTTACCCAA	600
QY	853	CAACATTTGGATGCTCTGGAGTTTTTTGGGCAACCTTAAACATTTGCCAGTATACATGGGA	912
Db	601	CAACATTTGGATGCTCTGGAGTTTTTTGGGCAACCTTAAACATTTGCCAGTATACATGGGA	660
QY	913	TACACAAATGAACTTAATCTTGAATAAATGCTGCTTGTAACTTCCTGTTTATGATCGAAT	972
Db	661	TACACAAATGAACTTAATCTTGAATAAATGCTGCTTGTAACTTCCTGTTTATGATCGAAT	720
QY	973	ATTTTTCAGAGCAGCAGAGAGAGGACACATATTTCCTCCGAGTTTGGACCTTCTTGG	1032
Db	721	ATTTTTCAGAGCAGCAGAGAGAGGACACATATTTCCTCCGAGTTTGGACCTTCTTGG	780
QY	1033	ATTAGAAAACCTGAGCTGTGTTAGATTTCCTAGTGATCACTGGGGTCTTCTGTGCAACTT	1092
Db	781	ATTAGAAAACCTGAGCTGTGTTAGATTTCCTAGTGATCACTGGGGTCTTCTGTGCAACTT	840
QY	1093	AGATATAATATTGTAATAATGCTTTTCAAGTGTGGTTTTTGCCTGATTTGTCGAAATACA	1152
Db	841	AAATGTAATATTGTAATAATGCTTTTCAAGTGTGGTTTTTGCCTGATTTTGGCAATAAC	899
QY	1153	ATTTCCACCTTCTGGAAGGATAGGTTTGTCTGTGAGAGAAATATGATAGATCATGTC	1212
Db	900	AGTTCCCTTCTGGAAGGATAGGTTTGTCTGTGAGAGAAATATGATAGATCATGTC	958
QY	1213	ACAGAA 1219	
Db	959	ACAGAA 965	

RESULT 17
BX422491
LOCUS BX422491 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION CS0DM007YE11 5-PRIME, mRNA sequence.
ACCESSION BX422491
VERSION BX422491.2 GI:46955237
KEYWORDS EST.

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 904)
Li.W.B., Gruber.C., Jessee.J. and Polayes.D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30766188.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Crenieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DM007AC06QPI6c=3474.r.

FEATURES
source

Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM007YE11"
/tissue_type="FETAL LIVER"
/dev_stage="fetal"
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Query Match	46.6%	Score 894.8;	DB 5;	Length 904;
Best Local Similarity	98.8%	Pred. No. 1.4e-210;		
Matches 893;	Conservative 7;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	77	CCTGAGGTGAAAGCGGCGACTTCTGTGTGTGGAGTTTGCCTCGGTGCGAAGCTCGGAT	136	
Db	1	CCCGGGATGAAAGCGGCGACTTCTGTGTGTGGAGTTTGCCTCGGTGCGAAGCTCGGAT	60	
Qy	137	GCGCAGTGGCTCAGTGTCTTCTCGGCGGAGAACGACTCTGGGAGATGGAAGGGGCTCTGAAC	196	
Db	61	GCGCAGTGGCTCAGTGTCTTCTCGGCGGAGAACGACTCTGGGAGATGGAAGGGGCTCTGAAC	120	
Qy	197	TCCTACTTCGAGCCTCCGGTGGAGGAGAGCGCTTTGGAAACGCCGACTGAAACCATCTCT	256	
Db	121	TCCTACTTCGAGCCTCCGGTGGAGGAGAGCGCTTTGGAAACGCCGACTGAAACCATCTCT	180	
Qy	257	GAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACTGATTCACCACTTCTAAA	316	
Db	181	GAGCCCAARACCTATGTTGACCTAACCAATGAAGAAACAACTGATTCACCACTTCTAAA	240	
Qy	317	ATCAGCCCATCTGAAGATACTCAGCAAGAAATGGCAGCATGTTCTCTCTCATTAACCTGG	376	
Db	241	ATCAGCCCATCTGAAGATACTCAGCAARAANAAGGCAGCATGTTCTCTCTCATTAACCTGG	300	
Qy	377	AATATTGATGGATTAGATCTAAACAAATCTGTTCAGAGAGGGCTCGAGGGGTGTGTTCTCTAC	436	
Db	301	AATATTGATGGATTAGATCTAAACAAATCTGTTCAGAGAGGGCTCGAGGGGTGTGTTCTCTAC	360	
Qy	437	TTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTTCCCATATTTATAGC	496	
Db	361	TTAGCTTTGTACAGCCAGATGTGATATTTCTACAGGAAGTTATTTCCCATATTTATAGC	420	
Qy	497	TACCTAAAGAGAGATCAAGTAATTTATGAGATTTATTCAGGTCTATGAAGAGGATATTTTC	556	
Db	421	TACCTAAAGAGAGATCAAGTAATTTATGAGATTTATTCAGGTCTATGAAGAGGATATTTTC	480	

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QY 557 ACAGCTAATGTTGAGAAATCAAGAGTGAATTAAGAAAGCCAGAGATTATTCCTTTT 616
Db 481 ACAGCTAATGTTGAGAAATCAAGAGTGAATTAAGAAAGCCAGAGATTATTCCTTTT 540
QY 617 CCAAGTACCAAAATGATGAGAAACCTTTATGTTGTCATGTGAATGTGTGTCAGGAAATGAG 676
Db 541 CCAAGTACCAAAATGATGAGAAACCTTTATGTTGTCATGTGAATGTGTGTCAGGAAATGAG 600
QY 677 CTTTGCCCTTATGACATCCATTTGGAGAGCACCAGAGGCGATGTCGGGAACGAATGAAT 736
Db 601 CTTTGCCCTTATGACATCCATTTGGAGAGCACCAGAGGCGATGTCGGGAACGAATGAAT 660
QY 737 CAGTTAAATGCTTTTAAAGAAATGCAAGAGGCTCCAGAGTCAGCTACAGTTATATTT 796
Db 661 CAGTTAAATGCTTTTAAAGAAATGCAAGAGGCTCCAGAGTCAGCTACAGTTATATTT 720
QY 797 GCAGAGATCAAAATCTAAGGATCGAGAGGTTTACAGATGTTGTTTACCACCAAC 856
Db 721 GCAGAGATCAAAATCTAAGGATCGAGAGGTTTACAGATGTTGTTTACCACCAAC 780
QY 857 ATTGTGGATGTCGGAGTTTGGGCAACCTTAAACATTCGCCAGTATACATGGGATACA 916
Db 781 ATTGTGGATGTCGGAGTTTGGGCAACCTTAAACATTCGCCAGTATACATGGGATACA 840
QY 917 CAATGAATCTAATCTTGGATTAACCTGCTGTTGTAACCTGTTTGTGATCGAATATTT 976
Db 841 CAATGAATCTAATCTTGGATTAACCTGCTGTTGTAACCTGTTTGTGATCGAATATTT 900
QY 977 TTCA 980
Db 901 TTCA 904
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RESULT 18
BX433489/c
LOCUS
DEFINITION BX433489 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
CS0DN005YN02 3-PRIME, mRNA sequence.
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ACCESSION BX433489
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VERSION BX433489.2 GI:47002503
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KEYWORDS EST.
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SOURCE Homo sapiens (human)
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Hominidae; Homo.
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1 (bases 1 to 952)
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```
Li W.B., Gruber C., Jessee, J. and Polayes, D.
```

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Full-length cDNA libraries and normalization
```

```
Unpublished (2001)
```

```
On May 15, 2003 this sequence version replaced gi:30775195.
```

```
Contact: Genoscope
```

```
Genoscope - Centre National de Sequenage
```

```
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
```

```
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
```

```
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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This sequence belongs to sequence cluster 3474.r
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For more information about this cluster, see
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http://www.genoscope.cns.fr/cdna?#=CS0BA10562D12_CS05372_1&c=3474.r
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FEATURES
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source
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Location/Qualifiers
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1. 952
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/tissue_type="ADULT BRAIN"
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/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
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ORIGIN
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Query Match 46.3%; Score 888.6; DB 5; Length 952;
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Best Local Similarity 97.3%; Pred. No. 4.9e-209;
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Matches 925; Conservative 0; Mismatches 24; Indels 2; Gaps 2;
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QY 213 CGGTGGAGGAGAGCGCTTGGAAACGCGACCTGAACCATCTCTGAGCCCAAGACCTATG 272
Db 950 CCGTGGAGGAGAGCGCTTGGAAACGCGACCTGAACCATCTCTGAGCCCAAGACCTATG 891
QY 273 TTGACCTAAACCAATGAAGAAACCAACTG-ATTTCACCACTTCTTAAATCAGCCCATCTGAA 331
Db 890 -TGACCTAAACCAATGAAGAAACCAACTGNAITTCACACTTTCTTAAATCAGCCCATCTGAA 832
QY 332 GATACCTCAGCAAGAAATGGCAGCATGTTCTCTCTCAATACCTGGAATATTGATGGATTA 391
Db 831 GATACCTCAGCAAGAAATGGCAGCATGTTCTCTCTCAATACCTGGAATATTGATGGATTA 772
QY 392 GATCTAAACAATCTGTCTCAGAGAGGCTCGAGGGGTGTCTCTACTTAGCTTTCTACAGC 451
Db 771 GATCTAAACAATCTGTCTCAGAGAGGCTCGAGGGGTGTCTCTACTTAGCTTTCTACAGC 712
QY 452 CCAGATGTGATATTTCTACAGGAAGTTATTTCCCCCATATATAGCTACCTTAAAGAGAGA 511
Db 711 CCAGATGTGATATTTCTACAGGAAGTTATTTCCCCCATATATAGCTACCTTAAAGAGAGA 652
QY 512 TCAAGTAATTTATGAGATTATTAAGGTCATGAAGAGGATATTTTACAGCTATATATGTTG 571
Db 651 TCAAGTAATTTATGAGATTATTTACAGGTCATGAAGAGGATATTTTACAGCTATATATGTTG 592
QY 572 AAGAAATCAAGAGTGAATTAAGAAAGCAAGAGATTATTCCTTTTCCAAGTACCAAAATG 631
Db 591 AAGAAATCAAGAGTGAATTAAGAAAGCAAGAGATTATTCCTTTTCCAAGTACCAAAATG 532
QY 632 ATGAGAAACCTTTTATGTGTCATGTGAATGTGTGAGAAATGAGCTTTCCTTTATGACA 691
Db 531 ATGAGAAACCTTTTATGTGTCATGTGAATGTGTGAGAAATGAGCTTTCCTTTATGACA 472
QY 692 TCCCATTTGGAGAGACCAAGAGGCTCCAGAGTCAGCTACAGTTATATTTGAGGAGATACAAAT 811
Db 471 TCCCATTTGGAGAGACCAAGAGGCTCCAGAGTCAGCTACAGTTATATTTGAGGAGATACAAAT 412
QY 811 TTAAGAAATGCAAGAGGCTCCAGAGTCAGCTACAGTTATATTTGAGGAGATACAAAT 871
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QY 871 CTAAGGAGATCGAGAGGTTTACCAGATGTGTGGTTTACCCCAACCAATTTGCGATGCTGCG 871
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QY 931 GAGTTTTTGGGCAAACTTAAACATATGCGAGTATACATGGGATACACAAAATGAACTCTAAT 931
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QY 932 CTTGGAATAACTGCTGCTGTGTAACCTTTCGTTTTCATCGAATATTTTTCAGAGCAGCAGCA 991
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QY 991 GAAGAGGAGACACATTTATTTCCCGAAGTTTGGACCTTTCTTGATTTAGAAAACTCGACTGT 1051
Db 171 GAAGAGGAGACACATTTATTTCCCGAAGTTTGGACCTTTCTTGATTTAGAAAACTCGACTGT 112
QY 1052 GGTAGATTTCTAGTATCACTGGGGTCTTCTGTGCACTTAGATATATATTTCTAAAT 1111
Db 111 GGTAGATTTCTAGTATCACTGGGGTCTTCTGTGCACTTAGATATATATTTCTAAAT 52
QY 1112 GCTTTTCAAGTGTGGGTTTGGCCCTGATTTGTCGAAATACAAATTTCCACCT 1162
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Db 51 GCTTTTCAAGTGGGTTTTCCTGATTTGTCAGAAATACAAATTCACACT 1
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AGENCOURT_6445782 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5587154
5', mRNA sequence.
BM468826
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 972)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL2356 row: d column: 03
High quality sequence stop: 707.
Location/Qualifiers
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/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI. Cloned unidirectionally; oligo-dr primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

FEATURES
Source

ORIGIN

Query Match 45.8%; Score 878.8; DB 3; Length 972;
Best Local Similarity 97.1%; Pred. No. 1.3e-206;
Matches 938; Conservative 0; Mismatches 22; Indels 6; Gaps 4;

QY 127 AAGCTGGATGCGCAGTGGCTCAGTGTCTTCTTGGCGGAGAACGACTGGGAGATGGAAG 186
DB 3 AAGCTGGATGCGCAGTGGCTCAGTGTCTTCTTGGCGGAGAACGACTGGGAGATGGAAG 62

QY 187 GGCTCTGAATCTCTACTTCGAGCTCCGGTGGAGGAGCGCTTGGAAACGCCGACCTGA 246
DB 63 GGCTCTGAATCTCTACTTCGAGCTCCGGTGGAGGAGCGCTTGGAAACGCCGACCTGA 122

QY 247 AACCATCTCTGAGCCCAAGCCTATGTTGACCTAACCAATGAAGAACTGATTTCCAC 306
DB 123 AACCATCTCTGAGCCCAAGCCTATGTTGACCTAACCAATGAAGAACTGATTTCCAC 182

QY 307 CACTTCTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGCATGTTCTCT 366
DB 183 CACTTCTAAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGGCAGCATGTTCTCT 242

QY 367 CATTACCTGGAATATTGATGATATGATCTAAACAACTCTGTGAGAGGGCTCGAGGGGT 426
DB 243 CATTACCTGGAATATTGATGATATGATCTAAACAACTCTGTGAGAGGGCTCGAGGGGT 302

QY 427 GTGTTCTCTACTAGCTTTGTACGCCAGCATGTGATTTCTACAGGAAGTATTTCCTCCC 486

Db 303 GTGTTCTCTACTAGCTTTGTACGCCAGCATGTGATTTCTACAGGAAGTATTTCCTCCC 362
QY 487 ATATTATAGCTTACCTAAAGAGAGATCAAGTAATATTATGAGATTAATTACAGGTCAAGA 546
DB 363 ATATTATAGCTTACCTAAAGAGAGATCAAGTAATATTATGAGATTAATTACAGGTCAAGA 422
QY 547 AGGATATTTCACAGCTATAATTTGTAAGAAATCAAGAGTGAATTTAAAGCCCAAGAGAT 606
DB 423 AGGATATTTCACAGCTATAATTTGTAAGAAATCAAGAGTGAATTTAAAGCCCAAGAGAT 482
QY 607 TATTCTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAATGTGTC 666
DB 483 TATTCTCTTTTCCAAAGTACCAAAATGATGAGAAACCTTTTATGTGTGATGTGAATGTGTC 542
QY 726 AGGAAATCAGCTTTTGGCTTTATGACATCCATTTTGAGAGACCAAGAGGGCTCCAGAGTCA 726
DB 543 AGGAAATCAGCTTTTGGCTTTATGACATCCATTTTGAGAGACCAAGAGGGCTCCAGAGTCA 602
QY 727 ACGAATGAATCAGTTTAAATATGGTTTAAAGAAATGCAAGAGGCTCCAGAGTCAAGTAC 786
DB 603 ACGAATGAATCAGTTTAAATATGGTTTAAAGAAATGCAAGAGGCTCCAGAGTCAAGTAC 662
QY 787 AGTTATATTTCAGGAGATACAAATCTAAGGGATCGAGAGTTACAGATGTGGTGT 846
DB 663 AGTTATATTTCAGGAGATACAAATCTAAGGGATCGAGAGTTACAGATGTGGTGT 722
QY 847 ACCCAACACATTTGGAGTGTCTGGAGTTTGGGCAAACTTAAACATTTGCCAGTATAC 906
DB 723 ACCCAACACATTTGGAGTGTCTGGAGTTTGGGCAAACTTAAACATTTGCCAGTATAC 782
QY 907 ATGGGATACAAATGAACTCTAAATCTTGGAAATACCTGCTGTGTGTGT- AAATTCGTTTGG 965
DB 783 ATGGGATACAAATGAACTCTAAATCTTGGAAATACCTGCTGTGTGTGTGT- AAATTCGTTTGG 842
QY 966 ATCGAATATTTTCAGAGCAGCAGAG- AAGAGGACACATTTATCCCGAAGTTTGG- 1022
DB 843 ATCGAATATTTTCAGAGCAGCAGAG- AAGAGGACACATTTATTTCCCGAATTTTGGGA 902
QY 1023 ACCTTCTTGGATTAGAAAACCTGGACTGTGG- TAGATTTCTAGTGTACCTACCTGGGGTCT 1080
DB 903 CCCTTCTTGGATTAGAAAACCTGGACTGTGGTAGAATTTCTTAGGATCAGCTGGGGGTC 962
QY 1081 TCTGTG 1086
DB 963 TTTCTG 968

RESULT 20
BM926092
LOCUS
DEFINITION
5', mRNA sequence.
BM926092
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 1046)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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http://image.llnl.gov

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High quality sequence start: 4

High quality sequence stop: 632.

FEATURES

source

1. .1046

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/mol_type="mrna"

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/clone="IMAGE:5764440"

/lab_host="DH10B"

/clone_lib="NIH_MGC_114"

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 45.7%; Score 878.4; DB 3; Length 1046;
Best Local Similarity 94.3%; Pred. No. 1.7e-206;
Matches 965; Conservative 0; Mismatches 52; Indels 6; Gaps 5;

QY 156 TCCTGGCCGAGAACGACTGGGAGATGGAAAGGCTCTGAACCTCTTACCTTCGAGGCTCCGG 215
DB 10 TCCTCGTCCCTTGTGCTTTGTTTTCAGAGGGCTCTGAACCTCTTACCTTCGAGGCTCCGG 69

QY 216 TGGAGGAGCGCCTTGGAAAGCCGACCTGAACCTCTCTGAGCCCAAGACCTATGTTG 275
DB 70 TGGAGGAGCGCCTTGGAAAGCCGACCTGAACCTCTCTGAGCCCAAGACCTATGTTG 129

QY 276 ACCTAACCAATGAAGAAACAACTGATCCACCACTCTTAAATCAGCCCATCTCAAGATA 335
DB 130 ACCTAACCAATGAAGAAACAACTGATCCACCACTCTTAAATCAGCCCATCTCAAGATA 189

QY 336 CTCAGCAAGAAATGGCAGCATGTTCTCTCATCTACCTGGAATATTGATGATGATGATC 395
DB 190 CTCAGCAAGAAATGGCAGCATGTTCTCTCATCTACCTGGAATATTGATGATGATGATC 249

QY 396 TAAACATCTCTCAGAGAGGCTCGAGGGGTGTTCTCTACTAGCTTTGTTGACAGCCAG 455
DB 250 TAAACATCTCTCAGAGAGGCTCGAGGGGTGTTCTCTACTAGCTTTGTTGACAGCCAG 309

QY 456 ATGTGATATTTCTACAGGAAGTTATTCCTCCCATATTTATAGCTACTTAAAGAGAGATCAA 515
DB 310 ATGTGATATTTCTACAGGAAGTTATTCCTCCCATATTTATAGCTACTTAAAGAGAGATCAA 369

QY 516 GTAAATATGAGATATTACAGTCATGAAGAGGATATTTTACAGCTATAAATGTTGAAGA 575
DB 370 GTAAATATGAGATATTACAGTCATGAAGAGGATATTTTACAGCTATAAATGTTGAAGA 429

QY 576 AATCAAGATGAATTAAGAAACCAAGATATTTCTTTTCCAGTACCAAAATGATGA 635
DB 430 AATCAAGATGAATTAAGAAACCAAGATATTTCTTTTCCAGTACCAAAATGATGA 489

QY 636 GAAACCTTTTATGTGTCATGTGAATGTGTGAGGAATGAGCTTTGCTTATGACATCCC 695
DB 490 GAAACCTTTTATGTGTCATGTGAATGTGTGAGGAATGAGCTTTGCTTATGACATCCC 549

QY 696 ATTTGGAGACCAAGAGGCGATGTCGGGAACGAATGAATCAGTTAAAAATGTTTAA 755
DB 550 ATTTGGAGACCAAGAGGCGATGTCGGGAACGAATGAATCAGTTAAAAATGTTTAA 609

QY 756 AGAAATCAAGAGGCTCCAGATCAGCTACAGTTATATTTTCAGGAGATCAAACTTAA 815
DB 610 AGAAATCAAGAGGCTCCAGATCAGCTACAGTTATATTTTCAGGAGATCAAACTTAA 669

QY 816 GGGATCGAGAGGTTACCAAGATGTGGTGTGTGTACCCCAACAATTTGTGATGCTCTGGGAGT 875

DB 670 GGGATCGAGAGGTTACCAAGATGTGGTGTGTTCACCAACAACATTTGTGGATGCTCTGGGAG 729

QY 876 TTTTGGCAAAACCTAAACATTTGCCAGTATACATGGGATACACAATGAATCTTAATCTTG 935
DB 730 TTTTGGCAAAACCTAAACATTTGCCAGTATACATGGGATACACAATGAATCTTAATCTTG 789

QY 936 GAATAACTGCTGCTTGTAAACTTTCGTTTTCGATCGAATATTTTTCAGAGCAGCAGCAAG 995
DB 790 GAATAACTGCTGCTTGTAAACTTTCGTTTTCGATCGAATATTTTTCAGAGCAGCAGCAAG 849

QY 996 AGGACACATTTATTCCTCCGAGTTTGA - CTTCTTTGGATTAGAAAACTGGACTGTGGT 1054
DB 850 AGGACACATTTATTCCTCCGAGTTTGA - CTTCTTTGGATTAGAAAACTGGACTGTGGG 909

QY 1055 AGA - TTTCTTAGTATCATCTGGGCTTTCT - GTGCAACTTAGATATAATTTGTAAT 1111
DB 910 AAAATTTCTTAATGGATTCCTGGGGGCTTCTTGGGGCACTTTAAAAATAAATTTGTAAG 969

QY 1112 GC - TTTTCAAGTGTGGGTTTTCGCT - GATTGTTGCAATAACAATTTTCCACCTTCTCGAA 1169
DB 970 GCTTTTCAAGGGGGGTTTTCGCTCGATGTTGGCAATACAAATTTTCCACCTTTCGGA 1029

QY 1170 AGG 1172
DB 1030 AAG 1032

RESULT 21
AL555333
LOCUS
DEFINITION AL555333 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DK007YK05 5-PRIME, mRNA sequence.
ACCESSION AL555333
VERSION AL555333.3 GI:45860070
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 948)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31277141.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=CS0DK007AF03QP1&c=3474.r.

FEATURES
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/cell_type="HELA CELLS COT 25-NORMALIZED"
/clone_lib="HELA"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 45.3%; Score 870.4; DB 1; Length 948;

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Best Local Similarity 96.6%; Pred. No. 1.6e-204;
Matches 908; Conservative 12; Mismatches 14; Indels 6; Gaps 3;

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Db 1 TCGAGAGCGGCGAGGAGATGAGTTGGGAGTTGCTGGAGGCGGAGGAGCGGCG 60
QY 62 GAGGAGAGCGGAGGAGCTCAG-GTGAAAAAGCGGAGCTTCTGTGTGGAGTTGGCTC 120
Db 61 GAGGAGAGCGGAGGAGCTGAGTTGAAAAAGCGGAGCTTCTGTGTGGAGTTGGCTC 120
QY 121 GGTTCGAAGCTGCGATGCGCGAGTGCTCAGTCTCAGTCTTCTGGCGGAGAACGATGGAGAT 180
Db 121 GGTTCGAAGCTGCGATGCGCGAGTGCTCAGTCTCAGTCTTCTGGCGGAGAACGATGGAGAT 180
QY 181 GGAAGGGCTGGAACCTCTACTCTGAGCTCTCGAGCTCGGTGGAGGAGCGCTTGGAGCGCG 240
Db 181 GGAAGGGCTGGAACCTCTACTCTGAGCTCTCGAGCTCGGTGGAGGAGCGCTTGGAGCGCG 240
QY 241 ACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACTGA 300
Db 241 ACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAACTGA 300
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QY 361 CTCTCTCATCTACCTGGAATATGATGGATAGATCTAAACATCTGTCTCAGAGGCGCTCG 420
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QY 421 AGGGGTGTCTCTACTAGCTTTGTACAGCCAGATGATATTTCTACAGAACTTAT 480
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Db 896 CAGTATAABGGATMAAATGAACCTCTAATCTTGGAAATA 935
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RESULT 22
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LOCUS
DEFINITION BX337140 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI036YJ02 3-PRIME, mRNA sequence. EST 07-APR-2004

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ACCESSION BX337140
VERSION BX337140.2
KEYWORDS GI:46269284
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 954)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 2, 2003 this sequence version replaced gi:30335597.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CSODI036DE01NP1&c=3474.r.
Location/Qualifiers
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/organism="Homo sapiens"
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/clone="CSODI036YJ02"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 44.7%; Score 858.2; DB 5; Length 954;
Best Local Similarity 95.1%; Pred. No. 1.7e-201;
Matches 886; Conservative 9; Mismatches 35; Indels 2; Gaps 2;
QY 988 AGCAGAAGAGGAGACATTAATTCCTCCGAGAGTTTGGACCTTCTTGGATTAGAAAACTGA 1047
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QY 1048 CTGTGTAGATTTCTCTAGTGATCACTGGGCTCTCTGTGCAACTTAGATATAATATTGA 1107
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QY 1108 AAATGCTTTTCAAGTGTGGTTTGGCCCTGATTGTTGCAAAATACAAATTTCCACCTTCTGG 1167
Db 814 AAATGCTTTTCAAGTGTGGG-TTGGCCCTGATTGTTGCAAAATACAAATTTCCACCTTCTGG 756
QY 1168 AAAGGTAGTGTGCTGTGGAGAAATAATGTACTAGATCAATTTGTCTACAGAAAAACAAC 1227
Db 755 AAAGGTAGTGTGCTGTGGAGAAATAATGTACTAGATCAATTTGTCTACAGAAAAACAAC 696
QY 1228 ATGATTTATGGTGTGTTTTCAGAAATCAACATTAAGATTAAATGTTTATTTAAACGAAC 1287
Db 695 ATGATTTATGGTGTGTTTTCAGAAATCAACATTAAGATTAAATGTTTATTTAAACGAAC 636
QY 1288 ACATTCCTGCATTCAGGATGTAGGCGCATTTAATAAAGGGCACAAGCCTGTCAAGT 1347
Db 635 ACATTCCTGCATTCAGGATGTAGGCGCATTTAATAAAGGGCACAAGCCTGTCAAGT 576
QY 1348 TTTCAACGGTGTCTTACAGCTGCCAGCTGGATTCCAAACAGGTACCCCATTTGTCTGAGC 1407
Db 575 TTTCAACGGTGTCTTACAGCTGCCAGCTGGATTCCAAACAGGTACCCCATTTGTCTGAGC 516
QY 1408 TAATGTTTATATTTTTCATTCAGGCACCGAAATAGTTAATATTTAAATAAGTCTTCAA 1467
Db 1408 TAATGTTTATATTTTTCATTCAGGCACCGAAATAGTTAATATTTAAATAAGTCTTCAA 1467
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Db 515 TAATGCTTTATATTTTCCATTTCAGCCACCGAAATAGTTAATATTTAAATAAGTCTTCAA 456

Qy 1468 AAGAAAACATAAGAGATTATTGAGTCTTGGGACTGGATCCTTTATTTCATAAGTTGAGA 1527

Db 455 AAGAAAACATAAGAGATTATTGAGTCTTGGGACTGGATCCTTTATTTCATAAGTTGAGA 396

Qy 1528 TCATCTTAAATGAAATGCCATGATTATCTCGAGTTAAGTAGATGACAGCTATTCTACAT 1587

Db 395 TCACTTAAATGAAATGCCATGATTATCTCGAGTTAAGTAGATGACAGCTATTCTACAT 336

Qy 1588 CAGACTTGATTTTTGTTCAGCTAAATFACATAATTTGGTAAGNTATATTAATGAAACCTTATGGC 1647

Db 335 CAGACTTGATTTTTGTTCAGCTAAATFACATAATTTGGTAAGCTATAATTTGAACCTTATGGC 276

Qy 1648 TTAATAATCCCTTAATCTCTTTTGGATTCATGTTTGTAGTCAATGTTGTGTCACAGAGGCAAA 1707

Db 275 TTAATAATCCCTTAATCTCTTTTGGATTCATGTTTGTAGTCAATGTTGTGTCACAGAGGCAAA 216

Qy 1708 GTTAAGCTTGATGTTTAAATCGGTTTGTATAGCACCATGGGACATTTTTTTTAAACAAA 1767

Db 215 GTTAAGCTTGATGTTTAAATCGGTTTGTATAGCACCATGGGACATTTTTTTTAAACAAA 156

Qy 1768 AATAAATGCATCAAGACATAGAGCTTTTGTAGTTTGTCTAAATTTGCAATGCAAAATGCTTTT 1827

Db 155 AATAAATGCATCAAGACATAGAGCTTTTGTAGTTTGTCTAAATTTGCAATGCAAAATGCTTTT 96

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Db 95 ACAGAACTAAATGCAAAATTTTAAAGTGTGCTTTTAAAGAAATTTTCCCAACAA 36

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Db 35 GAGAAATTTAAATAAGAAATTTTATTTTGGTAA 4

RESULT 23

LOCUS BUI79107

DEFINITION AGENCOURT_7984768 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6174958

5', mRNA sequence.

ACCESSION BUI79107

VERSION BUI79107.1 GI:22693091

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 883)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

EMAIL: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

CDNA Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM13548 row: o column: 23

High quality sequence stop: 672.

Location/Qualifiers

FEATURES

source

1..883

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/mol_type="mRNA"

/db_xref="caxon:9606"

/clone="IMAGE:6174958"

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/clone_lib="NIH MGC 71"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2.1 kb. "

Query Match 44.3%; Score 850; DB 5; Length 883;

Best Local Similarity 99.2%; Pred. No. 1.8e-199;

Matches 875; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

ORIGIN

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Db 2 CGAGAACGACTGGGAGATGGAAGGGCTCTGAACCTCTACTCTCGAGCCTCGGTGGAGGA 61

Qy 223 GAGCGCTTCGAAACGCGCAGCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAAC 282

Db 62 GAGCGCTTCGAAACGCGCAGCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAAC 121

Qy 283 CAATGAAGAAACAACCTGATTTCCACCCTCTTAAATCAGCCCATCTCTGAAGATACCTAGCA 342

Db 122 CAATGAAGAAACAACCTGATTTCCACCCTCTTAAATCAGCCCATCTCTGAAGATACCTAGCA 181

Qy 343 AGAAATGGCAGCATGTTCTCTCTCATCTGCTGAATATTGATGGATTAGATCTAAACAA 402

Db 182 AGAAATGGCAGCATGTTCTCTCTCATCTGCTGAATATTGATGGATTAGATCTAAACAA 241

Qy 403 TCTGTACAGAGGCTCGAGGGGTGTTCTCTACTTAGCTTTGTCAGCCCGAGATGTGAT 462

Db 242 TCTGTACAGAGGCTCGAGGGGTGTTCTCTACTTAGCTTTGTCAGCCCGAGATGTGAT 301

Qy 463 ATTTCTACAGAGGATTTATTTCCCATATTATAGCTACTTAAAGAGAGATCAAGTAATTA 522

Db 302 ATTTCTACAGAGGATTTATTTCCCATATTATAGCTACTTAAAGAGAGATCAAGTAATTA 361

Qy 523 TGAGATTATTACAGGTCATGAAGAGATATTTTCAAGCTATTAATGTTGAAGAAATCAAG 582

Db 362 TGAGATTATTACAGGTCATGAAGAGATATTTTCAAGCTATTAATGTTGAAGAAATCAAG 421

Qy 583 AGTGAATTTAAAGCAAGAGATTTATTTCTTTTCCAAAGTACCAAAATGATGAGAAACCT 642

Db 422 AGTGAATTTAAAGCAAGAGATTTATTTCTTTTCCAAAGTACCAAAATGATGAGAAACCT 481

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Qy 823 AGAGTTTACAGATGTGTGTGTTTACCCCAACAAATTTGTGATGCTCTGGAGTTTTTGGG 882

Db 662 AGAGTTTACAGATGTGTGTGTTTACCCCAACAAATTTGTGATGCTCTGGAGTTTTTGGG 721

Qy 883 CAAACCTTAAACATTCGCGATATACATGGGATACAAATGAACCTCTAATCTTGAATTAAC 942

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Qy 1002 ACATTATT-CCCCGAAAGTTTGGACCTTCTTGGATTAGAAAAA 1042

Db 842 ACATTATTCCCCGAAAGTTTGGACCTTCTTGGATTAGAAAAA 883

RESULT 24

LOCUS BM553049

DEFINITION AGENCOURT_6542413 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742798

BM553049

1192 bp

mRNA

linear

EST 20-FEB-2002

IMAGE:5742798

5', mRNA sequence.
BM553049
BM553049.1 GI:18791437
EST.
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1192)
NIH-MGC <http://mgs.mci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12761 row: 1 column: 07
High quality sequence stop: 747.
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/note="Organ: brain; Vector: pCMV-SPORT6; Site:1: NotI;
Site:2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."
ORIGIN
Query Match 44.2%; Score 848.4; DB 3; Length 1192;
Best Local Similarity 97.1%; Pred. No. 4.9e-199;
Matches 886; Conservative 0; Mismatches 21; Indels 5; Gaps 2;
QY 1 GTGCAGAGCGGCGAGGATGAGTTGGGAGTTCCTGGAGGCGGAGGAGCGGC 60
DB 39 GTGTAGAGCGGCGAGGAGATGGAGTTGGGAGTTGCGTGGAGCGGAGGAGCGGC 98
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DB 99 GGAGGAAGAGCGGCGAGCTGAGGTGAAAAGCGCGGACTTCTGTGTGGAGTTGCCTC 158
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DB 159 GGTGCAAGCTGCGAGTCCGAGTGGCTAGTCTTCTGCGCGAGAACGACTGGAGAT 218
QY 181 GGAAGGGCTCTGAACCTCTTCTTCTGAGCTCCGCTGGAGGAGCGGCTTGGAAAGCGCG 240
DB 219 GGAAGGGCTCTGAACCTCTTCTTCTGAGCTCCGCTGGAGGAGCGGCTTGGAAAGCGCG 278
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QY 301 TTCACCACTTCTAAATACGCCCATCTGAAGATACCTCAGCAGAAATGGCAGCATGTT 360
DB 339 TTCACCACTTCTAAATACGCCCATCTGAAGATACCTCAGCAGAAATGGCAGCATGTT 398
QY 361 CTCTCTCATTTACCTGGATATTGATGATCTAAACAATCTGTCTCAGAGGCGGCTCG 420

Db 399 CTCTCTCATTTACCTGGATATTGATGATCTAAACAATCTGTCTCAGAGGCGGCTCG 458
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Db 939 TGCCAGTATACA 950

RESULT 25
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DEFINITION
ACCESSION BX432088
VERSION BX432088.2 GI:47020604
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 928)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30787122.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BAG074ZE04_CS07037_1&c=3474.r

FEATURES
source
1..928
Location/Qualifiers


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/clone="CS0DN05YN02"
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/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN
Query Match 44.1%; Score 847; DB 5; Length 928;
Best Local Similarity 97.6%; Pred. No. 1e-198;
Matches 900; Conservative 0; Mismatches 18; Indels 4; Gaps 4;

Qy 852 ACAACATTTGGATGCTCTGGGAGTTTGGGCAACCTTAAACATTCGCAGTATACATGGG 911
Db 1 ACAACATTTGGATGCTCTGGGAGTTTGGGCAACCTTAAACATTCGCAGTATACATGGG 60

Qy 912 ATACACAATGAACCTTAATCTTGAATAAAGTCTGCTTGTAAACCTTCGTTTTCATCGAA 971
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Qy 972 TATTTTTCAGAGCAGCAGACAGAGGACACATATTATCCCGAAGTTTGACCTTCTTG 1031
Db 121 TATTTTTCAGAGCAGCAGAGAGGACACATATTATCCCGAAGTTTGACCTTCTTG 180

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Db 181 GATTAGAAAACCTGGACTGCTGGTAGATTTCTAGTAGTCACTGGGGCTTCCTGTCGAAC 240

Qy 1092 TAGATATAATATTGTAAATGCTTTCAAGTGTGGGTTTTCGCCCTGATGTTGCAAAATAC 1151
Db 241 TAGATATAATATTGTAAATGCTTTCAAGTGTGGGTTTTCGCCCTGATGTTGCAAAATAC 300

Qy 1152 AATTTCCACCTTCGGAAGGTAGTTTGTGTGGAGGAATAATAGTACTAGATCATTTGT 1211
Db 301 AATTTCCACCTTCGGAAGGTAGTTTGTGTGGAGGAATAATAGTACTAGATCATTTGT 360

Qy 1212 CACAGAAAACCAACTATGATTATGTTGTTGTTTTCAGATTCAACATTAAGATTAAT 1271
Db 361 CACAGAAAACCAACTATGATTATGTTGTTGTTTTCAGATTCAACATTAAGATTAAT 420

Qy 1272 GTTTATTTAAACGACACATTCCTGCATTCAGGATGTGAGGCCATTTTAAATAAAGGGCA 1331
Db 421 GTTTATTTAAACGACACATTCCTGCATTCAGGATGTGAGGCCATTTTAAATAAAGGGCA 480

Qy 1332 CAAGCCTGTGAGAGTTTTCACCGTGTCTTACAGCTGCCAGCTGGATTCCTCAACAGGTAC 1391
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Qy 1392 CCCATTGCTCTGAGCTAATGTTTATATTTTTCATTCAGGACCGAATAGTAAATAT 1451
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Qy 1452 TAAATAAGTCTTCAAAAGAAAACAATAAGAGATTATTGAGTCTTGGGACTGGATCCCTTT 1511
Db 601 TAAATAAGTCTTCAAAAGAAAACAATAAGAGATTATTGAGTCTTGGGACTGGATCCCTTT 660

Qy 1512 ATTTTCATAGTTTCAGATCATCTTAAATGAAAATGCCATGATATCTCGAGTTAAGTAGAT 1571
Db 661 ATTTTCATAGTTTCAGATCATCTTAAATGAAAATGCCATGATATCTCGAGTTAAGTAGAT 720

Qy 1572 GACAGCTATTCTACATCAGCTTGATTTTTCAGCTAATTTACATAA--TTGGTAAAGTAT 1630
Db 721 GACAGCTATTCTACATCAGCTTGATTTTTCAGCTAATTTACATAA--TTGGTAAAGTAT 780

Qy 1631 AATTGAAACCTTATGGCTTAAAAATTCCTTAACTCTTTTTCATTCATGTTTGTAGTCA 1690
Db 781 AATTGAAACCTTATGGCTTAAAAATTCCTT--ACTCCCTTTTCATTCATGTTTGTAGTCA 839
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Qy 1691 TTGTCACACAG-AGCRAAGTTAAGCTTGATGATGGTTAAATCGGTTTGATGACCATG 1749
Db 840 GTGNACACAGAGCAAAATTTAGGCTTTGATGATGGTTTAAACACGGTTTGAAGCA-CATG 898

Qy 1750 GGACATTTTTTTTAAACAAAATA 1771
Db 899 GGACATTTTTTTTAAACAAAATAAA 920

RESULT 26
BX358707
LOCUS BX358707 942 bp mRNA linear EST 08-APR-2004
DEFINITION BX358707 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI042YL19 5-PRIME, mRNA sequence.
ACCESSION BX358707
VERSION BX358707.2 GI:46306560
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 942)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 5, 2003 this sequence version replaced gi:30378261.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DI042CF10QPl&c=3474.f.
FEATURES
Location/Qualifiers
1..942
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI042YL19"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 44.1%; Score 847; DB 5; Length 942;
Best Local Similarity 96.8%; Pred. No. 1e-198;
Matches 878; Conservative 7; Mismatches 18; Indels 4; Gaps 2;

Qy 170 GACTGGGAGATGGAAGGGCTCTGAACCTCTACTTCGAGCCTCGGGTGGAGAGAGCGCC 229
Db 20 GCCTTTGTTTTCAGAGGGCTCTGAACCTCTACTTCGAGCCTCGGGTGGAGAGAGCGCC 79

Qy 230 TTGGAACCGCAGCCTGAAACCATCTCTGAGCCCAAGACCTTATGTTGACCTTAACCAATGAA 289
Db 80 TTGGAACCGCAGCCTGAAACCATCTCTGAGCCCAAGACCTTATGTTGACCTTAACCAATGAA 139

Qy 290 GAAACAACCTGATTCACCACTTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAAAT 349
Db 140 GAAACAACCTGATTCACCACTTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAAAT 199

Qy 350 GGCAAGCATGTTCTCTCTCATTACCTGGAATATTGATGATTAGATCTTAAACAAATCTGTCA 409
Db 200 GGCAAGCATGTTCTCTCTCATTACCTGGAATATTGATGATTAGATCTTAAACAAATCTGTCA 259
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QY 410 GAGAGGGCTCGAGGGGTGTGTTCTTACTAGCTTTGTACAGCCAGATGTGATTTCTA 469
Db |||||
QY 470 CAGGAAGTTATTCCTCCCATATATATAGCTACCTTAAAGAGAGATCAAGTAATATGAGATT 529
Db |||||
QY 530 ATTACAGGTCATGAAGAAGATATTTACAGCTATTAATGTTGAAGAAATCAAGAGTGAAA 589
Db |||||
QY 590 TTAAGAGCCAGAGATTTCTTCCAGTACCAAAATGATGAGAAACCTTTTATGT 649
Db |||||
QY 650 GTGCATGTAATGTGTCAGGAATAGCTTTGCTTTATGACATCCATTTGGAGAGCACC 709
Db |||||
QY 710 AGAGGGCATGCTCGGGAACGAATGAATCAATTAATAAGTGTTTTAAAGAAATGCAAGAG 769
Db |||||
QY 770 GCTCCAGAGTCAGCTACAGTTATATTTGAGAGATACAAATCTAAGGGATCGAGAGTT 829
Db |||||
QY 830 ACCAGATGTGGTGTGTTTCCCAACAACTTTGAGATGCTGGAGTGTGTTGGCAACCT 889
Db |||||
QY 890 AAACATTTGCCAGTATACATGGGATACAAATGAATCTAAATCTTTGGAAATACTGCTGCT 949
Db |||||
QY 950 TGTAACTTCTGTTTCAATCGAATATTTTTCAGAGCAGCAGAGAGAGGAGACATATT 1009
Db |||||
QY 1010 CCCCGAAGTTTGACCTTCTTGATTAAGAAACTGGACTGTGTTAGATTTCTTAGTGAT 1069
Db |||||
QY 1070 CACTGGG 1076
Db |||||
QY 916 MATGGGG 922
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```
RESULT 27
BX444690/c
LOCUS
DEFINITION
BX444690 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
CS0DN005YN02 3-PRIME, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 988)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30778259.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Creteil, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
```

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 3474.r

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CS0DN005DGO1NP1&c=3474.r>.

FEATURES

source

1..988

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DN005YN02"

/tissue_type="ADULT BRAIN"

/dev_stage="adult"

/clone_lib="Homo sapiens ADULT BRAIN"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match	43.7%	Score	838.4	DB 5	Length	988			
Best Local Similarity	96.3%	Pred. No.	1.4e-196						
Matches	888	Conservative	9	Mismatches	20	Indels	5	Gaps	4

QY	961	TTTTGATCGAATATTTTTCAGAGCAGCAGCAGAGGAGGACACATTTATTTCCCGAAGTTT	1020
Db	917		860
QY	1021	GGACCTTCTTGATTAAGAAACTGGACTGTGTAGATTTCTCTAGTGATCACTGGGGTCT	1080
Db	859		802
QY	1081	TCGTGCAACTTGTAGATATAATTTGTAATGCTTTTCAAGTGTGGGTTTTCGCCCTGATT	1140
Db	801		742
QY	1141	GTTCGAATACAAATTTCCACCTTCTGGAAAGGTAGTGTTCGTGAGGAGAAATAATGTAC	1200
Db	741		682
QY	1201	TAGATCATTTGTCAAGAAACCAACTATGATTTATGTTGTTTTCAGAAATTCACAT	1260
Db	681		622
QY	1261	TAAAGATTAATCTTTATTTAAACGAACACATTCCTGCAATCAGGATGTGAGGCCATTAA	1320
Db	621		562
QY	1321	TAAAGAGGCACAAAGCCTGTCAGAGTTTTCACCGTGCTTACAGCTGCCAGCTGATTC	1380
Db	561		502
QY	1381	CAAAAGGTTACCCCATTTGCTCTGAGCTAATGTTTATATATTTTTCATTTCAGGCACCGAAA	1440
Db	501		443
QY	1441	TAGTTAATATTTAAATAAGTCTTCAAAAGAAACATAAGAGATTTATGAGTCTTTGGGA	1500
Db	442		383
QY	1501	CTGGATCTTTTATTTATTAAGTTTCAGATCATCTTAATGAATAATGCAATGATTTATCTGCA	1560
Db	382		323
QY	1561	GTTAAGTAGATGACAGCTATTCTACATCAGACTTGTGATTTTGTGACGCTAATACATAAT	1620
Db	322		263
QY	1621	GGTAAAGTAAATTTGAAACCTTATGGCTTAAATTCCTTAACTCTCTTTTGTGATTCATGTT	1680
Db			

Db 262 GGTAGCTATTAATGCAACCTTATGGCTTAAAAATTCCTTAACCTCCTTTTGAATCATGTT 203
Qy 1681 TGTAGTCATGTTGCAACAGAGGCAAAAGTTAAAGCTTGATGATGTTAAAAATCGGTTTGAT 1740
Db 202 TGTAGTCATGTTGTCACAGAGGCAAAAGTTAAAGCTTGATGATGTTAAAAATCGGTTTGAT 143
Qy 1741 AGCACCATTGGACATTTTTTTTAAACAAAATAAATGTCATGAAGACATAGCCTTTTAGTT 1800
Db 142 AGCACCATTGGACATTTTTTTTAAACAAAATAAATGTCATGAAGACATAGCCTTTTAGTT 83
Qy 1801 TTGCTAATTGGAATGGAATGCTTTACAGGAAGTAAATGCAATCAATTTTAAAGTGTG 1860
Db 82 TTGCTAATTGGAATGGAATGCTTTACAGGAAGTAAATGCAATCAATTTTAAAGTGTG 23
Qy 1861 CTTTAAAGAAAATATTTTCCC 1882
Db 22 ATTTAAAGAAAATATTTATCC 1

RESULT 28
CN641671 1090 bp mRNA linear EST 12-MAY-2004
LOCUS ILLUMIGEN MCQ 5159 Katze.MBR Macaca mulatta cDNA clone IB1UW:5970
DEFINITION 5' similar to Bases 11 to 990 highly similar to human TTRAP
(Hs.210628), mRNA sequence.
ACCESSION CN641671.1 GI:47152681
VERSION EST.
KEYWORDS Macaca mulatta
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 1090)
AUTHORS Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agv,M.B.,
Prohl,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
Iadonato,S.P.
TITLE Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
JOURNAL Genome Biol. 6 (7), R60 (2005)
PUBMED 15998449
COMMENT Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2003.12.04. 732 Q20 bases.
PCR Primers
FORWARD: CCCTCACTAAAGGGAACAAA
BACKWARD: CACTATAGGCGAATTGGGTA
Insert Length: 1090 Std Error: 0.00
Plate: CL000043 row: E column: 07
Seq primer: CCCTCACTAAAGGGAACAAA
POLYA=No.

FEATURES Location/Qualifiers
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/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IB1UW:5970"
/sex="female"
/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze MBR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site_1: EcoR I;
Site_2: Xho I; Created from Stratagene ZAP-CDNA Synthesis
kit (catalog #200400) and ZAP-CDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"

ORIGIN

Query Match

42.4%; Score 814.6; DB 7; Length 1090;

Best Local Similarity 96.3%; Pred. No. 1.2e-190;
Matches 856; Conservative 0; Mismatches 29; Indels 4; Gaps 2;
Qy 158 CTGCCCCAGAACGACCTGGGAGATGGAAAGGGCTCTGAACCTCTACTTTCGAGCCCTCCGGTG 217
Db 11 CTGCCCCAGAACGACCTGGGAGATGGAAAGGGCTCTCAAACTCCTACTTTCGAGCCCTCCGGTG 70
Qy 218 GAGGAGAGCCCTTGGAAACGCCGACCTGAAACCAATCTCTGAGCCCAAGACATATGTTGAC 277
Db 71 GAGGAGAGCCCTTGGAAACGCCCTGAAACCAATCTCTGAGCCCAAGACATATGTTGAC 130
Qy 278 CTAACCAATCAAGAAACAACTGATTCACCACTCTTAAATCAGCCCATCTGAAGATACT 337
Db 131 CTAACCAATCAAGAAACAACTGATTCACCACTCTTAAATCAGCCCATCTGAAGATACT 190
Qy 338 CAGCAAGAAAATGGCAGCATGTTCTCTCTCATTCACCTGGAAATTTGATGGATTAGACTTA 397
Db 191 CAGCAAGAAAATGACAGCATGTTCTCTCTCATTCACCTGGAAATTTGATGGATTAGACTTA 250
Qy 398 AACATCTCTCAGAGAGGGCTCGAGGGGTGTCTCTACTTGTATCAGCCCAAGAT 457
Db 251 AACATCTCTCAGAGAGGGCTCGAGGGGTGTCTCTACTTAGCGTGTGTACAGCCCAAGAT 310
Qy 458 GTGATATTTCTACAGGAAGTTATTTCCCCCATATTTATAGCTACCTTAAAGAAAGAGATCAAGT 517
Db 311 GTGATATTTCTACAGGAAGTTATTTCCCCCATATTTATAGCTACCTTAAAGAAAGAGAGCAAGT 370
Qy 518 AATTATGAGATTTATTCAGGTCATGAAGAAAGGATATTTTCACAGCTATAATGTTTGAAGAAA 577
Db 371 GATTATGAGATTTATTCAGGTCATGAAGAAAGGATATTTTCACAGCTATAATGTTTGAAGAAA 430
Qy 578 TCAAGAGTGAAATTTAAAGAGCCAGAGATTTATTCCTTTTCAAGTACCAAAATGATGAGA 637
Db 431 TCAAGAGTGAAATTTAAAGAGCCAGAGATTTATTCCTTTTCAAGTACCAAAATGATGAGA 490
Qy 638 AACCTTTTATGTGTCATGTGAATGTGTGAGGAAATGAGCTTTTGCCTTTATGACATCCCAT 697
Db 491 AACCTTTTATGTGTCATGTGAATGTGTGAGGAAATGAGCTTTTGCCTTTATGACATCCCAT 550
Qy 698 TTGAGAGACACCCAGAGGGCATGCTGCGAAACGAATGAATCAGTTTAAATAATGTTTAAAG 757
Db 551 TTGAGAGACACCCAGAGGGCATGCTGCGAAACGAATGAATCAGTTTAAATAATGTTTAAAG 610
Qy 758 AAAATGCAAGAGGCTCCAGAGTCAGCTACAGTTATATTTTCAGGAGATACAAATCTAAGG 817
Db 611 AAAATGCAAGAGGCTCCAGAGTCAGCTACAGTTATATTTTCAGGAGATACAAATCTAAGG 670
Qy 818 GATCGAGAGGTTACAGATGTGTGTGTTTACCCCAACAACTTTGCGATGTCTGGGAGTTT 877
Db 671 GATCAAGAGGTTACCAATGTGTGTGTTTACCCCAACAACTTTGCGATGTCTGGGAGTTT 730
Qy 878 TTGGGCAAACTAAACATTCGCAGTATACATGGGATACAAATGAACTCTTAATCTTTGGA 937
Db 731 TTGGGCAAACTAAACATTCGCAGTATACATGGGATACAAATGAACTCTTAATCTTTGGA 790
Qy 938 ATAACTGCTGCTTGTAAACCTCGTTTGTGATCGAATATTTTTCAGAGCAGCAGCAGAAG-A 996
Db 791 ATAACTGCTGCTTGTAAAGCTTCCTTTTGTGATCGAATATTTTTCAGAGCAGCAGCAGAAG 850
Qy 997 GGGACACATTTATCCCGAAAGTTTGG--ACCTTCTTTGGATTAGAAAA 1042
Db 851 GGGACACATTTATCCCGAAAGTTTGGAACTTCTTCTTGGATTGAAAAA 899

RESULT 29
CN801806
LOCUS ILLUMIGEN MCQ 37066 Katze.MBR Macaca mulatta cDNA clone
DEFINITION IB1UW:15450 5' similar to Bases 18 to 922 highly similar to human
TTRAP (Hs.210628), mRNA sequence.
ACCESSION CN801806
VERSION CN801806.1 GI:47697782
KEYWORDS EST.

SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 922)
AUTHORS Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B., and
Prohl, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
Iadonato, S.P.
TITLE Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
JOURNAL Genome Biol. 6 (7), R60 (2005)
PUBMED 15998449
COMMENT Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.05.13. 514 Q20 bases.
PCR Primers
FORWARD: CCTCACTAAAGGGAACAAA
BACKWARD: CACTATAGGCGAATGGGTA
Insert Length: 922 Std Error: 0.00
Plate: CL000291 Row: H Column: 09
Seq primer: CCTCACTAAAGGGAACAAA
POLYA=No.

Location/Qualifiers
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/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="TBIUW:15450"
/sex="female"
/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze_MBR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site: 1: EcoR I;
Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
kit (Catalog #200400) and ZAP-cDNA Gigapack III Gold
Cloning Kit (Catalog #200450)"

Query Match 42.4%; Score 813.2; DB 7; Length 922;
Best Local Similarity 94.1%; Pred. No. 2.5e-190;
Matches 845; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 145 GGCTCAGTCTTCTCGCGAGAACGACTGGGAGATGGAAGGCTCTGAACCTCTT 204
DB 8 GCCTCTCCGTTCTCGACGAGAGAGGAGTGACATGACACGAGGCTCTGATCTCTCGATT 67
QY 205 CGAGCTCCGGTGGAGAGAGCGCTTGGAAACCGGACCTGMAACCATCTCTGAGCCAA 264
DB 68 CGAGCTCCGGTGGAGAGAGCGCTTGGAAACCGGACCTGMAACCATCTCTGAGCCAA 127
QY 265 GACCTATGTTGACCTAACCAATGAAGAAACAACTGATTCACCACTCTTAAATCAGCCC 324
DB 128 GACCTATGTTGACCTAACCAATGAAGAAACAACTGATTCACCACTCTTAAATCAGCCC 187
QY 325 ATCTGAAGATACCTCAGCAAGAAATGGCAGCATGTTCTCTCTCATTCACCTGGAAATTTGA 384
DB 188 ATCTGAAGATACCTCAGCAAGAAATGGCAGCATGTTCTCTCTCATTCACCTGGAAATTTGA 247
QY 385 TGGATTAGATCTAAACAATCTGTCAGAGAGGCTCGAGGGGTGTGTTCTTACTTAGCTTT 444
DB 248 TGGATTAAATCTAAACAATCTGTCAGAGAGGCTCGAGGGGTGTGTTCTTACTTAGCTTT 307
QY 445 GTACAGCCCGAGATGTGATATTTCTACAGGAAGTTATTTCCCCCATATATATAGTACCTAAA 504
DB 308 GTACAGCCCGAGATGTGATATTTCTACAGGAAGTTATTTCCCCCATATATATAGTACCTAAA 367
QY 505 GAAGAGATCAAGTAATATGAGATTATATACAGGTCATGAAGAGGATATTTTCACAGCTAT 564

ORIGIN

BM555041 1103 bp mRNA linear EST 20-FEB-2002
AGENCOURT_6545705 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5737150
5', mRNA sequence.
BM555041
BM555041.1 GI:18795166
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 1103)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12746 Row: m Column: 23
High quality sequence stop: 678.
Location/Qualifiers
1..1103
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5737150"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_88"

FEATURES
source

Db 368 GAAGAGACGACGATGATTATGAGATTATTACAGGTCATGAAGAGGATATTTTCACAGCTAT 427
QY 565 AATGTTGAGAAATCAAGAGTGAATTAATAAAGCCAGAGATTTTCTCTTTTCCAAGTAC 624
Db 428 AATGTTGAGAAATCAAGAGTGAATTAATAAAGCCAGAGATTTTCTCTTTTCCAAGTAC 487
QY 625 CAAAATGATGAGAAACCTTTTATGTGTCATGTGAATGTGTGTCAGAAATAGCTTTGCT 684
Db 488 CAAAATGATGAGAAACCTTTTATGTGTCATGTGAATGTGTGTCAGAAATAGCTTTGCT 547
QY 685 TATGATATCCATTTGGAGAGACACAGAGGCGATCTCGGAAACGAATGAATCAGTTAAA 744
Db 548 TATGATATCCATTTGGAGAGACACAGAGGCGATCTCGGAAACGAATGAATCAGTTAAA 607
QY 745 AATGTTTAAAGAAATGCAAGAGGCTCCAGAGTCAGCTACAGTTATATTTTGCAGGAGA 804
Db 608 AATGTTTAAAGAGAAATGCAAGAGGCTCCAGAGTCAGCTACAGTTATATTTTGCAGGAGA 667
QY 805 TACAAATCTAAGGGATCGAGAGGTTTACAGATGTGGTGTGTTCACCAACAACATTTGTGA 864
Db 668 TACATATCTAAGGGATCAAGAGGTTTACCAATGTGTGTGTTCACCAACAACATTTGTGA 727
QY 865 TGCTGGAGATTTTGGGCAACCTTAAACATTCAGTATATCATCGGATACAAATGAA 924
Db 728 TGCTGGAGATTTTGGGCAACCTTAAACATTCAGTATATCATCGGATACAAATGAA 787
QY 925 CTCTAATCTTGAATAAATGCTGCTGTGTGAATCTGTTTGAATCAATATTTTTCAGAGC 984
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QY 985 AGCAGCAGAGAGGAGACACATTTATCCCGAAGTTTGGACCTTCTTGGATTAGAAAAA 1042
Db 848 ACCAACAGACGAGGACCAATTTATCCCGAAGCTTGTACTTCTTGGATTGAAAAA 905

RESULT 30
BM555041
LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES
source

/note="Organ: small intestine; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dr primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."		Query Match 42.0%; Score 807; DB 3; Length 1103; Best Local Similarity 95.1%; Pred. No. 8.9e-189; Matches 888; Conservative 0; Mismatches 36; Indels 10; Gaps 5;	
Qy	15	GGAAGATGGAGTTCGGGAGTTGCTTGGAGGCGGAGGCGGCGGAGGCGGAGGCGGCGGAGGCGGCGG	74
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Qy	75	AGCCTGAGGTGAAAAAGCGGCGACTTCTGTGTGTGGAGTTTGCCTCGGTGCGCAAGCTGCG	134
Db	85	AGCCTGAGGTGAAAAAGCGGCGACTTCTGTGTGTGGAGTTTGCCTCGGTGCGCAAGCTGCG	144
Qy	135	ATGCCGAGTGGCTCAGTGTCTTGGCCGAGAACGACTGGGAGATGGAAAGGCTCTGA	194
Db	145	ATGCCGAGTGGCTCAGTGTCTTGGCCGAGAACGACTGGGAGATGGAAAGGCTCTGA	204
Qy	195	ACTCCTACTTCGAGCTCCGGTGGAGGAGCGCTTGGACGCGGACCTGGAACCCATCT	254
Db	205	ACTCCTACTTCGAGCTCCGGTGGAGGAGCGCTTGGACGCGGACCTGGAACCCATCT	264
Qy	255	CTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAACTGATTCCACCACTTCTA	314
Db	265	CTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAACTGATTCCACCACTTCTA	324
Qy	315	AAATCAGCCCATCTGAAGATACCTCAGCAGAAAAATGGCAGCATGTTCTCTCATTTACCT	374
Db	325	AAATCAGCCCATCTGAAGATACCTCAGCAGAAAAATGGCAGCATGTTCTCTCATTTACCT	384
Qy	375	GGAATATTGTGGATTAGATCTAAACAACTCTCAGAGAGGCTCGAGGGGTGTTCTCT	434
Db	385	GGAATATTGTGGATTAGATCTAAACAACTCTCAGAGAGGCTCGAGGGGTGTTCTCT	444
Qy	435	ACTTAGCTTTGTACAGCCAGATGTATTTCTACAGGAGTTATTTCCCCCATATTATA	494
Db	445	ACTTAGCTTTGTACAGCCAGATGTATTTCTACAGGAGTTATTTCCCCCATATTATA	504
Qy	495	GCTACCTTAAGAGAGATCAAGTAATTATGAGATTATTAAGGTCATGAAGAGATATT	554
Db	505	GCTACCTTAAGAGAGATCAAGTAATTATGAGATTATTAAGGTCATGAAGAGATATT	564
Qy	555	TCACAGCTTATAATGTTGAAGAAATCAAGAGTGAATTTAAAGCCCAAGAGATTATTCCTT	614
Db	565	TCACAGCTTATAATGTTGAAGAAATCAAGAGTGAATTTAAAGCCCAAGAGATTATTCCTT	624
Qy	615	TTCCAAGTACCAGAAATGATGAGAAACCTTTTATGTGTCATGTGAATGTGTCAGGAAATG	674
Db	625	TTCCAAGTACCAGAAATGATGAGAAACCTTTTATGTGTCATGTGAATGTGTCAGGAAATG	684
Qy	675	AGCTTTGCTTATGACAT-CCCATTTGGAGAGCACAGAGGGCATGCTGCGGAAACGAATG	733
Db	685	AGCTTTGCTTATGACATCCCCATTTGGAGAGCACAGAGGGCATGCTGCGGAAACGAATG	744
Qy	734	AATCAGTTTAAAAATGGTTTTAAAGAAATCAAGAGGCTCCAGAGTCAGCTACAGTTATA	793
Db	745	AATCAGNTAAAAATGGTTTTAAAGAAATCAAGAGGCTCCAGAGTCACCTTACGTTATA	804
Qy	794	TTTGCAGGAGATACAAATCTAA--GGGATCGAGAGGTTACCAAG--TGTGTTGGTTTACCC	850
Db	805	TTTGCAGGAGATACAAATCTAAAGGGATCGAGAGGGTACCCGAATGTGTTGGTTTACCC	864
Qy	851	AACACATTGTGGA---TGTCTGGGATTTTGGGCAAAACCTAAACATTGCC---AGTAT	904
Db	865	ACAACCAATTGTGGAATGGCTGGGAAATTTTGGGCAAAACCTAAACCTTTGCCCAAGATAC	924
Qy	905	ACATGGGATACACAAATGAACCTCTAATCTTGGAA	938

Db 925 ATGGGGAAACCCCAATGGAACCCCTAATCTTTGGGA 958
Search completed: December 3, 2005, 23:18:15
Job time : 8074.87 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 09:15:11 ; Search time 9782.42 Seconds
(without alignments)
11156.694 Million cell updates/sec

Title: US-10-757-745-1
Perfect score: 1920
Sequence: 1 ggcagagcgccaggaaga.....aaagaattttatttggttaa 1920

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.in.*
- 3: gb.env.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pr.*
- 9: gb.ro.*
- 10: gb.ste.*
- 11: gb.sy.*
- 12: gb.un.*
- 13: gb.vi.*
- 14: gb.htg.*
- 15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1918	99.9	1920	6	BD205490
2	1918	99.9	1920	6	AR594294
3	1918	99.9	1920	6	AX011599
4	1910.6	99.5	1921	8	HA269473
5	1910	99.5	1952	8	BC017553
6	1897.6	98.6	1948	6	AR339398
7	1892.6	98.6	1936	8	AF223469
8	1880	97.9	1898	6	BD157138
9	1880	97.9	1898	6	AX878304
10	1880	97.9	1898	8	AK002168
11	1815.4	94.6	2499	6	E23195
12	1643.2	85.6	2151	8	HA240495
13	1253.4	65.3	1261	8	AF201687
14	1085	56.5	20938	8	AY613922
15	1085	56.5	167847	8	CR925830
16	1085	56.5	176819	8	CR942205
17	1081.8	56.3	102200	8	HS30M3
18	1086.4	55.5	1079	6	BD139846

c 92	51.6	2.7	762	10	BV346848	165	47	2.4	163812	14	CR854921	CR854921
c 93	51.6	2.7	199269	14	CR790364	c 166	46.8	2.4	271546	2	AE014843	AE014843 Plasmodi
c 94	51.2	2.7	15723	2	AY521251	c 167	46.6	2.4	47	6	AR291212	AR291212 Sequence
c 95	51.2	2.7	159593	8	AC004832	c 168	46.6	2.4	712	2	AF527397	AF527397 Cydia pom
c 96	51	2.6	254436	2	AE014827	c 169	46.6	2.4	113738	14	AC138298	AC138298 Mus muscu
c 97	50.6	2.6	1522	2	AY701231	c 170	46.6	2.4	161757	14	AC044901	AC044901 Homo sapi
c 98	50.4	2.6	169841	14	AC073888	c 171	46.6	2.4	167721	8	AL158841	AL158841 Human DNA
c 99	50.4	2.6	199200	8	AL359633	c 172	46.6	2.4	173019	5	BX321884	BX321884 Zebrafish
c 100	50.2	2.6	110000	14	AC127921_2	c 173	46.4	2.4	3078	6	AR551339	AR551339 Sequence
c 101	50.2	2.6	299186	14	AC120637	c 174	46.4	2.4	3606	2	DDI10934	DDI10934 Dictyosteli
c 102	50	2.6	111870	14	AC149995	c 175	46.4	2.4	18154	6	AX345157	AX345157 Sequence
c 103	49.8	2.6	110000	14	PFMAL13_01	c 176	46.4	2.4	136153	9	AC157925	AC157925 Mus muscu
c 104	49.8	2.6	137785	8	HS345P10_	c 177	46.4	2.4	146298	5	BX649439	BX649439 Zebrafish
c 105	49.8	2.6	147042	5	AL335296	c 178	46.4	2.4	168371	8	AC149237	AC149237 Pan trogl
c 106	49.8	2.6	165851	14	CR762438	c 179	46.4	2.4	175959	14	AL450429	AL450429 Homo sapi
c 107	49.8	2.6	180976	14	AC139726	c 180	46.4	2.4	243374	14	CR853299	CR853299 Danio rer
c 108	49.8	2.6	198181	14	CR855385	c 181	46.4	2.4	244536	14	AC099176	AC099176 Rattus no
c 109	49.6	2.6	6136	6	AX348429	c 182	46.4	2.4	253151	2	AE014842	AE014842 Plasmodi
c 110	49.4	2.6	47577	2	AF396436	c 183	46.4	2.4	349751	2	PFMAL4P3	PFMAL4P3 Plasmodi
c 111	49.2	2.6	104992	14	AC005504	c 184	46.2	2.4	1141	6	AR579680	AR579680 Sequence
c 112	49.2	2.6	108296	15	AC121162	c 185	46.2	2.4	1141	6	AX083744	AX083744 Sequence
c 113	49.2	2.6	169546	14	AC004157	c 186	46.2	2.4	3586	6	AX339195	AX339195 Sequence
c 114	49.2	2.6	250421	2	AE014849	c 187	46.2	2.4	75342	2	CEY47H9C	CEY47H9C
c 115	49	2.6	197665	14	CR450803	c 188	46.2	2.4	82797	14	AX890561_3	AX890561_3
c 116	48.8	2.5	7403	6	AX251562	c 189	46.2	2.4	110000	14	BX890561_0	BX890561_0
c 117	48.8	2.5	7403	6	AX347119	c 190	46.2	2.4	127349	14	CR753868	CR753868 Danio rer
c 118	48.8	2.5	124698	5	BX530406	c 191	46.2	2.4	128091	14	AC139626	AC139626 Takifugu
c 119	48.8	2.5	160491	14	CR387984	c 192	46.2	2.4	157090	14	AC144497	AC144497
c 120	48.8	2.5	186431	14	AC022281	c 193	46.2	2.4	170604	5	BX005481	BX005481 Zebrafish
c 121	48.6	2.5	174359	14	CR855123	c 194	46.2	2.4	172427	5	AL929392	AL929392 Zebrafish
c 122	48.4	2.5	595	6	CS083994	c 195	46.2	2.4	172445	5	BX664622	BX664622 Zebrafish
c 123	48.4	2.5	220183	8	AC011246	c 196	46.2	2.4	192581	14	PFMAL13P1	PFMAL13P1
c 124	48.4	2.5	347582	2	PFMAL4P1	c 197	46.2	2.4	215027	14	CR759958	CR759958
c 125	48.2	2.5	2000	6	AX655393	c 198	46.2	2.4	250078	2	AE014829	AE014829 Plasmodi
c 126	48.2	2.5	3801	2	PFNDACP	c 199	46.2	2.4	254050	2	PFPA293358	PFPA293358
c 127	48.2	2.5	200960	14	CR848802	c 200	46.2	2.4	331039	2	AC116979	AC116979 Dictyoste
c 128	48.2	2.5	214310	14	CR847982	c 201	46.2	2.4	333321	2	AC116986	AC116986 Dictyoste
c 129	48.2	2.5	348174	2	CR382399	c 202	46.2	2.4	347050	2	PFPA293351	PFPA293351
c 130	48	2.5	53932	14	AC023371	c 203	46	2.4	2036	2	AX113716	AX113716 Clona Int
c 131	48	2.5	110000	14	PFMAL13_05	c 204	46	2.4	8000	2	AF482387	AF482387 Dictyoste
c 132	48	2.5	253924	2	AE014822	c 205	46	2.4	87871	15	ATT4C12	ATT4C12 Arabidops
c 133	47.8	2.5	2000	6	AX655393	c 206	46	2.4	110000	14	PFMAL7P1_02	PFMAL7P1_02
c 134	47.8	2.5	66993	14	AC138074	c 207	46	2.4	124497	8	AC120053	AC120053 Homo sapi
c 135	47.8	2.5	152468	15	AC140023	c 208	46	2.4	168909	14	AC118862	AC118862 Rattus no
c 136	47.6	2.5	7218	6	I66494	c 209	46	2.4	175527	8	AC100863	AC100863 Homo sapi
c 137	47.6	2.5	18556	8	AY527817	c 210	46	2.4	185590	8	AC018529	AC018529 Homo sapi
c 138	47.6	2.5	18651	6	AR659551	c 211	46	2.4	199831	5	BX470099	BX470099 Zebrafish
c 139	47.6	2.5	18682	6	AR659745	c 212	46	2.4	232667	14	AC127058	AC127058 Rattus no
c 140	47.6	2.5	174741	8	AC040977	c 213	45.8	2.4	2580	6	AX347383	AX347383 Sequence
c 141	47.6	2.5	192929	14	AC005505	c 214	45.8	2.4	2580	6	AX349104	AX349104 Sequence
c 142	47.6	2.5	200579	5	BX663518	c 215	45.8	2.4	2580	6	AX657823	AX657823 Sequence
c 143	47.6	2.5	250713	2	AE014850	c 216	45.8	2.4	2580	6	AX659097	AX659097 Sequence
c 144	47.6	2.5	253151	2	AE014842	c 217	45.8	2.4	4601	2	DMU11584	DMU11584 Drosophila
c 145	47.6	2.5	349980	6	AX344563	c 218	45.8	2.4	5376	6	AX347052	AX347052 Sequence
c 146	47.6	2.5	349980	6	AX344564	c 219	45.8	2.4	19517	2	DMU37541	DMU37541 Drosophila
c 147	47.4	2.5	6092	6	AX251775	c 220	45.8	2.4	49306	2	AC115606	AC115606 Dictyoste
c 148	47.4	2.5	159930	9	AC118047	c 221	45.8	2.4	102585	15	AC007063	AC007063 Arabidops
c 149	47.4	2.5	175356	14	CR354555	c 222	45.8	2.4	110000	14	TANN3_01	TANN3_01
c 150	47.4	2.5	182427	5	CR361566	c 223	45.8	2.4	220331	14	AC159903	AC159903 Pan trogl
c 151	47.4	2.5	190156	9	AC124990	c 224	45.8	2.4	250029	2	AE014839	AE014839 Plasmodi
c 152	47.4	2.5	302156	2	AC116977	c 225	45.8	2.4	298406	2	CSY7588A	CSY7588A
c 153	47.4	2.5	340552	2	PFPA293354	c 226	45.6	2.4	1525	2	AY701198	AY701198 Orconecte
c 154	47.2	2.5	142687	14	CR388190	c 227	45.6	2.4	110000	14	PFMAL13_16	PFMAL13_16
c 155	47.2	2.5	166088	5	AL953304	c 228	45.6	2.4	110000	15	AP008215_083	AP008215_083
c 156	47.2	2.5	181284	14	CR855260	c 229	45.6	2.4	132254	2	AC116330	AC116330 Dictyoste
c 157	47.2	2.5	213323	5	BX510360	c 230	45.6	2.4	155906	15	AP005934	AP005934 Oryza sat
c 158	47	2.4	3845	2	AF487784	c 231	45.6	2.4	158432	9	AC161252	AC161252 Mus muscu
c 159	47	2.4	9901	1	U67530	c 232	45.6	2.4	159401	14	CR936468	CR936468 Danio rer
c 160	47	2.4	76568	2	MBREV	c 233	45.6	2.4	185906	14	CR678384	CR678384 Danio rer
c 161	47	2.4	110000	6	AC116984_1	c 234	45.6	2.4	196261	14	CR759840	CR759840 Rattus no
c 162	47	2.4	110000	6	AR271569_06	c 235	45.6	2.4	204954	14	AC128028	AC128028 Rattus no
c 163	47	2.4	110000	6	AR584244_06	c 236	45.6	2.4	225024	14	CR394539	CR394539 Danio rer
c 164	47	2.4	118959	15	AC135796	c 237	45.6	2.4	250195	2	AE014831	AE014831 Plasmodi

238	45.6	2.4	250563	2	AE014826	AE014826 Plasmodiu	C 311	44.6	2.3	114647	14	AC138291	AC138291 Mus muscu
239	45.4	2.4	615	15	AJ7834449	AJ7834449 Agrobiods	C 312	44.6	2.3	116344	14	CR962131	CR962131 Medicago
240	45.4	2.4	1984	2	AY496789	AY496789 Agrobiods	C 313	44.6	2.3	149184	14	AC159925	AC159925 Atelerix
241	45.4	2.4	2001	2	AY496798	AY496798 Agrobiods	C 314	44.6	2.3	150567	14	AC160584	AC160584 Atelerix
242	45.4	2.4	6036	6	AX344304	AX344304 Sequence	C 315	44.6	2.3	158605	14	CR936419	CR936419 Danio rer
243	45.4	2.4	8056	6	AX599046	AX599046 Sequence	C 316	44.6	2.3	181452	9	AC101723	AC101723 Mus muscu
244	45.4	2.4	20486	6	AX281500	AX281500 Sequence	C 317	44.6	2.3	196216	15	AF165818	AF165818 Guillard
245	45.4	2.4	86590	15	ATW7A7	AL161946 Arabidops	C 318	44.6	2.3	203829	14	CR936246	CR936246 Danio rer
246	45.4	2.4	88549	2	AC116924	AC116924 Dictyoste	C 319	44.6	2.3	204302	14	CR405716	CR405716 Zebrafish
247	45.4	2.4	110000	5	AB183488_0	AB183488 Oryzias	C 320	44.6	2.3	205587	5	CR936246	CR936246 Danio rer
248	45.4	2.4	110000	5	AB183488_1	Continuation (2 of	C 321	44.6	2.3	205807	14	CR388418	CR388418 Danio rer
249	45.4	2.4	110000	14	PFMAL13_10	Continuation (11 o	C 322	44.6	2.3	211161	14	AC098271	AC098271 Rattus no
250	45.4	2.4	144320	9	AC155241	AC155241 Mus muscu	C 323	44.6	2.3	222140	14	CR936443	CR936443 Danio rer
251	45.4	2.4	166236	8	AC022832	AC022832 Homo sapi	C 324	44.6	2.3	250029	2	AE014820	AE014820 Plasmodiu
252	45.4	2.4	176427	14	AC151671	AC151671 Gallus ga	C 325	44.6	2.3	254794	14	CR925716	CR925716 Danio rer
253	45.4	2.4	205568	5	BX470184	BX470184 Zebrafish	C 326	44.6	2.3	306037	1	AE014017	AE014017 Buchnera
254	45.4	2.4	208301	14	CR9333788	CR9333788 Plasmodiu	C 327	44.4	2.3	1992	2	AY496716	AY496716 Agrobiods
255	45.4	2.4	343050	2	PFA929353	AY653023 Tetrahyme	C 328	44.4	2.3	1999	2	AY496782	AY496782 Helianthu
256	45.2	2.4	925	2	AY653023	AP08090 Lotus cor	C 329	44.4	2.3	3672	15	AF472609	AF472609 Helianthu
257	45.2	2.4	87352	14	AP08090	AC011355 Homo sapi	C 330	44.4	2.3	3680	6	BD222045	BD222045 Pathogen-
258	45.2	2.4	114276	8	AC011355	AC011355 Homo sapi	C 331	44.4	2.3	3680	6	AX015679	AX015679 Sequence
259	45.2	2.4	125179	15	AC146371	AC146371 Medicago	C 332	44.4	2.3	3680	6	AX015679	AX015679 Sequence
260	45.2	2.4	154071	2	AC115598	AC115598 Dictyoste	C 333	44.4	2.3	6424	2	AC115608	AC115608 Dictyoste
261	45.2	2.4	174383	5	AL929216	AL929216 Zebrafish	C 334	44.4	2.3	26597	6	AX251506	AX251506 Sequence
262	45.2	2.4	189082	8	AL731537	AL731537 Human DNA	C 335	44.4	2.3	57892	8	AP001427	AP001427 Homo sapi
263	45	2.3	2355	6	CQ986648	CQ986648 Sequence	C 336	44.4	2.3	100000	8	AP000017	AP000017 Homo sapi
264	45	2.3	60604	14	AC023466	AC023466 Homo sapi	C 337	44.4	2.3	100000	8	AP000159	AP000159 Homo sapi
265	45	2.3	79782	5	CR522883	CR522883 Zebrafish	C 338	44.4	2.3	100000	14	PFMAL7P1_08	PFMAL7P1_08
266	45	2.3	99263	14	CNS01DX9	AL139177 Homo sapi	C 339	44.4	2.3	122392	15	AC137079	AC137079 Medicago
267	45	2.3	107765	15	AC159142	AC159142 Medicago	C 340	44.4	2.3	156404	14	CR626908	CR626908 Danio rer
268	45	2.3	110000	15	AP008218	Continuation (14 o	C 341	44.4	2.3	161907	14	AP001810	AP001810 Homo sapi
269	45	2.3	115944	14	AC152496	AC152496 Medicago	C 342	44.4	2.3	163089	14	AC090211	AC090211 Homo sapi
270	45	2.3	149452	14	AC124912	AC124912 Papio anu	C 343	44.4	2.3	171686	8	AC142284	AC142284 Pan trogl
271	45	2.3	151329	8	BS000541	BS000541 Pan trogl	C 344	44.4	2.3	193064	14	AC141312	AC141312 Homo sapi
272	45	2.3	157453	15	CNS080CDX	BS000507 Oryza sat	C 345	44.4	2.3	202249	8	AC147115	AC147115 Pan trogl
273	45	2.3	162626	9	AC118246	AC118246 Mus muscu	C 346	44.4	2.3	211536	14	AC163190	AC163190 Bos tauru
274	45	2.3	175157	14	AC138551	AC138551 Danio rer	C 347	44.4	2.3	219434	9	AC152168	AC152168 Mus muscu
275	45	2.3	181148	8	AC147668	AC147668 Pan trogl	C 348	44.4	2.3	228470	14	CR753875	CR753875 Danio rer
276	45	2.3	188603	8	AC147164	AC147164 Pan trogl	C 349	44.4	2.3	340000	8	AP001730	AP001730 Cydia pom
277	45	2.3	195039	14	AC159213	AC159213 Pan trogl	C 350	44.2	2.3	520	2	AF527401	AF527401 Rhizogoni
278	45	2.3	195234	14	CR735105	CR735105 Danio rer	C 351	44.2	2.3	912	15	AE413546	AE413546 Sequence
279	45	2.3	202366	14	BX927344	BX927344 Danio rer	C 352	44.2	2.3	5445	6	AX251349	AX251349 Sequence
280	45	2.3	204390	14	AC159014	AC159014 Pan trogl	C 353	44.2	2.3	6681	6	AX281262	AX281262 Sequence
281	45	2.3	206592	14	AC159016	AC159016 Pan trogl	C 354	44.2	2.3	6681	6	AX345057	AX345057 Sequence
282	45	2.3	212954	8	AC144376	AC144376 Pan trogl	C 355	44.2	2.3	7644	8	AL354533	AL354533 Sequence
283	45	2.3	245411	14	AC157173	AC157173 Bos tauru	C 356	44.2	2.3	24347	8	AL356964	AL356964 Human DNA
284	45	2.3	248191	14	AC105725	AC105725 Rattus no	C 357	44.2	2.3	49843	2	AF288092	AF288092 Naegleria
285	45	2.3	257757	2	AE014837	AE014837 Plasmodiu	C 358	44.2	2.3	88459	14	AC151343	AC151343 Xenopus t
286	45	2.3	272698	2	PFMAL4P4	AL035477 Plasmodiu	C 359	44.2	2.3	110000	14	AC096900_1	AC096900_1
287	45	2.3	334872	14	AC094810	AC094810 Rattus no	C 360	44.2	2.3	110000	14	PFMAL13_04	PFMAL13_04
288	44.8	2.3	340552	2	PFA929354	AL929354 Plasmodiu	C 361	44.2	2.3	110000	14	PFMAL13_05	PFMAL13_05
289	44.8	2.3	535	2	AF186853	AF186853 Tegosa an	C 362	44.2	2.3	152726	9	AC129195	AC129195 Mus muscu
290	44.8	2.3	1452	6	CS084036	CS084036 Sequence	C 363	44.2	2.3	152726	9	BSX11182	BSX11182 Zebrafish
291	44.8	2.3	101034	8	AC096550	AC096550 Homo sapi	C 364	44.2	2.3	155243	5	BSX11182	BSX11182 Zebrafish
292	44.8	2.3	125290	8	AC005048	AC005048 Homo sapi	C 365	44.2	2.3	155243	5	BSX11182	BSX11182 Zebrafish
293	44.8	2.3	126150	8	AC005152	AC005152 Homo sapi	C 366	44.2	2.3	158518	9	AC134334	AC134334 Mus muscu
294	44.8	2.3	136240	2	AC117070	AC117070 Dictyoste	C 367	44.2	2.3	159922	14	AC154280	AC154280 Mus muscu
295	44.8	2.3	148075	8	AC110014	AC110014 Homo sapi	C 368	44.2	2.3	163443	14	AC006280	AC006280 Plasmodiu
296	44.8	2.3	156164	14	CR352215	CR352215 Danio rer	C 369	44.2	2.3	174249	14	CR391973	CR391973 Danio rer
297	44.8	2.3	182871	2	AC117176	AC117176 Dictyoste	C 370	44.2	2.3	194809	8	BS000097	BS000097 Pan trogl
298	44.8	2.3	211489	14	AC156865	AC156865 Bos tauru	C 371	44.2	2.3	190709	14	CR925831	CR925831 Danio rer
299	44.8	2.3	236145	14	AC107515	AC107515 Rattus no	C 372	44.2	2.3	196149	14	AC004709	AC004709 Plasmodiu
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301	44.8	2.3	313050	2	PFA929352	AL929352 Plasmodiu	C 374	44.2	2.3	218807	14	AC009175	AC009175 Homo sapi
302	44.8	2.3	330050	2	PFA929355	AL929355 Plasmodiu	C 375	44.2	2.3	226607	14	CR847902	CR847902 Danio rer
303	44.6	2.3	1162	2	AF044851	AF044851 Colias cr	C 376	44.2	2.3	229336	14	AC153260	AC153260 Bos tauru
304	44.6	2.3	4529	2	DQ054838	DQ054838 Plasmodiu	C 377	44.2	2.3	250029	2	AE014838	AE014838 Plasmodiu
305	44.6	2.3	6106	6	AX251183	AX251183 Sequence	C 378	44.2	2.3	251551	2	AE014844	AE014844 Plasmodiu
306	44.6	2.3	6106	6	AX346374	AX346374 Sequence	C 379	44.2	2.3	252298	14	CR627491	CR627491 Danio rer
307	44.6	2.3	6106	6	AX348418	AX348418 Sequence	C 380	44.2	2.3	252650	2	AE014847	AE014847 Plasmodiu
308	44.6	2.3	23625	2	U29157	U29157 Caenorhabdi	C 381	44.2	2.3	256832	14	CR405709	CR405709 Danio rer
309	44.6	2.3	66317	14	AC099901	AC099901 Mus muscu	C 382	44.2	2.3	257020	14	AC155081	AC155081 Bos tauru
310	44.6	2.3	100882	5	AC099322	AC099322 Danio rer	C 383	44.2	2.3	266371	14	AC020619	AC020619 Mus muscu

c 384	44	2.3	422	2	AY004039	AY004039 Microchel	457	43.6	2.3	18218	6	AX346851	AX346851 Sequence
c 385	44	2.3	961	2	AY351412	AY351412 Arethuan	458	43.6	2.3	110000	1	CR925677_03	Continuation (4 of
c 386	44	2.3	20663	15	CG511533	AJ511533 Candida g	459	43.6	2.3	110000	15	AP008213_173	Continuation (174
c 387	44	2.3	38260	2	AC006642	AC006642 Caenorhab	460	43.6	2.3	146505	15	AP004299	AP004299 Oryza sat
c 388	44	2.3	73190	8	AC130416	AC130416 Homo sapi	461	43.6	2.3	148933	14	AC154428	AC154428 Mus muscu
c 389	44	2.3	85779	15	SC0111856	AJ011856 Saccharom	462	43.6	2.3	162737	14	CR788290	CR788290 Danio rer
c 390	44	2.3	92712	14	AP007719	AP007719 Lotu	463	43.6	2.3	167353	15	AP005261	AP005261 Zebrafish
c 391	44	2.3	95753	14	AP007636	AP007636 Lotu	464	43.6	2.3	170985	5	AX005220	AX005220 Oryza sat
c 392	44	2.3	101981	15	AC149295	AC149295 Populu	465	43.6	2.3	178086	8	AC145518	AC145518 Pan trogl
c 393	44	2.3	104265	15	AC155888	AC155888 Medicag	c 466	43.6	2.3	222025	14	CR749741	CR749741 Danio rer
c 394	44	2.3	105682	2	AC116957_3	Continuation (4 of	467	43.6	2.3	223585	9	AC154474	AC154474 Mus muscu
c 395	44	2.3	110000	14	PFMAL13_09	Continuation (11 o	468	43.6	2.3	232202	14	CR769785	CR769785 Danio rer
c 396	44	2.3	110000	14	PFMAL13_10	Continuation (10 o	469	43.6	2.3	234081	2	PFMAL4P2	AL035475 Plasmodi
c 397	44	2.3	110000	15	PFMAL8PI_11	Continuation (12 o	c 470	43.6	2.3	242559	14	AC098256	AC098256 Rattus no
c 398	44	2.3	122890	15	AF005672	AF005672 Physcomit	c 471	43.6	2.3	250053	2	AE014825	AE014825 Plasmodi
c 399	44	2.3	125020	8	AF429315	AF429315 Homo sapi	472	43.6	2.3	348174	2	CR382399	CR382399 Plasmodi
c 400	44	2.3	129327	15	AC146548	AC146548 Medicag	473	43.4	2.3	646	2	AF205393	AF205393 Ichthyoph
c 401	44	2.3	151144	5	BX3233575	BX3233575 Zebrafish	c 474	43.4	2.3	2001	2	AY496755	AY496755 Agrodiaet
c 402	44	2.3	152544	15	AC149424	AC149424 Populu	c 475	43.4	2.3	3037	2	AY691421	AY691421 Maconelli
c 403	44	2.3	154289	14	AC027714	AC027714 Homo sapi	c 476	43.4	2.3	35641	6	AX346299	AX346299 Sequence
c 404	44	2.3	161757	14	AC044901	AC044901 Homo sapi	477	43.4	2.3	6075	6	AX252016	AX252016 Sequence
c 405	44	2.3	164941	2	AC010052	AC010052 Drosophil	478	43.4	2.3	6075	6	AX349027	AX349027 Sequence
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c 407	44	2.3	184622	14	CR848702	CR848702 Danio rer	480	43.4	2.3	11812	6	AX251500	AX251500 Sequence
c 408	44	2.3	205013	14	AY269187	AY269187 Homo sapi	481	43.4	2.3	11812	6	AX278047	AX278047 Sequence
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c 412	44	2.3	252394	2	AE014833	AE014833 Plasmodi	485	43.4	2.3	14710	2	AF081829	AF081829 Rhipiceph
c 413	44	2.3	252704	14	CR792433	CR792433 Danio rer	c 486	43.4	2.3	15928	2	AB070263	AB070263 Bombyx ma
c 414	44	2.3	295143	2	AE003549	AE003549 Drosophil	487	43.4	2.3	17183	6	AX345388	AX345388 Sequence
c 415	44	2.3	318221	14	PFMAL13P3	AL049184 Plasmodi	488	43.4	2.3	76444	15	AP006099	AP006099 Lotu
c 416	44	2.3	346940	14	AC107420	AC107420 Homo sapi	c 489	43.4	2.3	110000	14	AC120578_2	Continuation (3 of
c 417	43.8	2.3	415	2	AF102763	AF102763 Apanteles	c 490	43.4	2.3	110000	14	AX324169_0	AX324169 Homo sapi
c 418	43.8	2.3	562	10	BV159376	BV159376 RPAMMBEQO	491	43.4	2.3	139747	14	AC148916	AC148916 Medicago
c 419	43.8	2.3	963	2	DGU132901	AJ132901 Drosophil	c 492	43.4	2.3	165577	8	CR545475	CR545475 Danio rer
c 420	43.8	2.3	1017	15	AB117696	AB117696 Cicer ret	493	43.4	2.3	167069	4	CNS06C88	AL391516 Human chr
c 421	43.8	2.3	1522	2	AY701231	AY701231 Orconecte	494	43.4	2.3	167953	14	AC010948	AC010948 Homo sapi
c 422	43.8	2.3	1591	2	AY496816	AY496816 Polymmat	495	43.4	2.3	18765	14	CR936844	CR936844 Danio rer
c 423	43.8	2.3	1997	2	AY496817	AY496817 Polymmat	496	43.4	2.3	187847	14	AC023155	AC023155 Homo sapi
c 424	43.8	2.3	2486	2	AF140273	AF140273 Ichthyoph	c 497	43.4	2.3	188569	9	AC115020	AC115020 Mus muscu
c 425	43.8	2.3	9483	6	AX251786	AX251786 Sequence	498	43.4	2.3	194875	14	AC148824	AC148824 Pan trogl
c 426	43.8	2.3	9483	6	AX345278	AX345278 Sequence	c 499	43.4	2.3	215234	14	CR855319	CR855319 Danio rer
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c 435	43.8	2.3	163034	9	AC153977	AC153977 Mus muscu							
c 436	43.8	2.3	168430	14	CR848803	CR848803 Danio rer							
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ALIGNMENTS

RESULT 1	BD205490	CD40-Interacting and TRAF-interacting protein.	1920 bp	DNA	linear	PAT 17-JUL-2003
BD205490	LOCUS					
DEFINITION	BD205490					
ACCESSION	BD205490.1	GI:33015260				
VERSION	JP 2002512796-A/1.					
KEYWORDS	Homo sapiens					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 1920)					
AUTHORS	Pype,S.M.C., Ghislaian,J.E.F.J., Remacle and Huylebroeck,D.F.E.					
TITLE	CD40-Interacting and TRAF-interacting protein					
JOURNAL	Patent: JP 2002512796-A 1 08-MAY-2002;					
COMMENT	VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE VZW					
	OS Homo sapiens (human)					
	PN JP 2002512796-A/1					
	PD 08-MAY-2002					
	PF 28-APR-1999	JP 2000546003				
	PP 29-APR-1998	EP 98201392.2				
	PI STEFAN MARIA CHRISTIAAN PYPE,					
	PI JACQUES EMILE FERNAND JOSIANE GHISLAIAN REMACLE, PI DANNY					

FRANCOIS EVELINE HUYLEBROECK									
PC	C12N15/09,A61K38/00,A61P9/10,A61P19/02,A61P25/00,A61P35/00,PC A61P37/02,								
PC	A61P37/06,A61P43/00,C07K14/47,C07K16/18,G01N33/15,G01N33/50,								
PC	G01N33/566,A61K37/02								
PC	C12N15/00,A61K37/02								
CC	C40-interacting and TRAF-interacting protein. FH Key								
	Location/Qualifiers								
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	Best Local Similarity 100.0%; Pred. No. 0;								
	Matches 1920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
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RESULT 2
LOCUS AR594294
DEFINITION Sequence 1 from patent US 6812203.
ACCESSION AR594294
VERSION AR594294.1 GI:56643900
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 1920)
AUTHORS Pyde,S.M.C., Remacle,J.E.F. and Huylebroeck,D.F.E.
TITLE CD40-Interacting and TRAF-Interacting proteins
JOURNAL Patent: US 6812203-A 1 02-NOV-2004;
Vlaams Interuniversitair Instituut voor Biotechnologie VZW;
Zwijnaarde;
WOX;

FEATURES
source Location/Qualifiers
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ORIGIN

Query Match 99.9%; Score 1918; DB 6; Length 1920;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Hominoidea; Homo.

REFERENCE 1
Remacle,J.E., Huylebroeck,D.F. and Pye,S.M.
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REFERENCE 1
AUTHORS Pye,S., Declercq,W., Ibrahim,A., Michiels,C., Van Rietschoten,J.G., Dewulf,N., de Boer,M., Vandenabeele,P., Huybrecock,D. and Remacle,J.E.
TITLE TTRAP, a novel protein that associates with CD40, tumor necrosis factor (TNF) receptor-75 and TNF receptor-associated factors (TRAFs), and that inhibits nuclear factor-kappa B activation
JOURNAL J. Biol. Chem. 275 (24), 18586-18593 (2000)
PUBMED 10764746
REFERENCE 2 (bases 1 to 1921)
AUTHORS Pye,S.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-1999) Pye S., VIB07, Dept. Cell Growth, Differentiation and Development, Flanders Interuniversity Institute for Biotechnology, CELGEN, K.U.Leuven, Gasthuisberg Campus, Herestraat 49, B-3000 Leuven, BELGIUM
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1 (bases 1 to 1952)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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2 (bases 1 to 1952)
Strausberg, R.
Direct Submission
Submitted (19-NOV-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Sep 16, 2003 this sequence version replaced gi:17028464.
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCT/BTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabh, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacque

Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23510347.

FEATURES

Location/Qualifiers
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ORIGIN

Query Match 99.5%; Score 1910; DB 8; Length 1952;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1913; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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DEFINITION	Sequence 889 from patent US 6569662.		
ACCESSION	AR339398		
VERSION	AR339398.1 GI:33726255		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1948)		
AUTHORS	Tang, Y.T., Zhou, P. and Dmanac, R.T.		
TITLE	Nucleic acids and polypeptides		
JOURNAL	Patent: US 6569662-A 889 27-MAY-2003;		
FEATURES	Hyseq, Inc.; Sunnyvale, CA		
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VERSION AF223469.1 GI:7578788
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1936)
AUTHORS Song,H., Gao,G., Peng,Y., Ren,S., Chen,Z. and Han,Z.
TITLE A novel gene expressed in human adrenal gland
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1936)
AUTHORS Song,H., Gao,G., Peng,Y., Ren,S., Chen,Z. and Han,Z.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-2000) Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, China

FEATURES
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ORIGIN
Query Match 98.6%; Score 1892.6; DB 8; Length 1936;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1898; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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Db	1081	ATATTGTAATGCTTTTCAAGTGTGGGTTTTGCGCTGATTTGCGCAATACAATTTCCA	1140	Homo sapiens (human)			
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QY	1400	CTCTGAGCTAATGTTTATATTTTCCATTCAGGACCGGAATAGTTAATTTAAATAA	1459	ISHII,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.			
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QY	1460	GTCTTCAAAAGAAAACATAAGAGATTATTGAGTTCTTGGGACTGGATCCTTTATTTTCATA	1519	Patent: EP 1074617-A 13209 07-FEB-2001;			
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RESULT 10

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LOCUS Homo sapiens cDNA FLJ11306 fis, clone PLACE1010031.

DEFINITION

AK002168

ACCESSION

AK002168.1 GI:7023882

VERSION

oligo capping; fis (full insert sequence).

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

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AUTHORS

Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahara, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, S., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hirakawa, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S.,

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RESULT 12

HSA420495

LOCUS

DEFINITION Homo sapiens mRNA 2151 bp mRNA linear PRI 23-NOV-2001

ACCESSION AJ420495

VERSION AJ420495.1 GI:17066359

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Auffray, C., Ansoerge, W., Ballabio, A., Estivill, X., Gibson, K., Lehrach, H., Poustka, A. and Lundeberg, J.

TITLE The European IMAGE consortium for integrated Molecular analysis of human gene transcripts

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2151)

AUTHORS Persson, A.

TITLE Direct Submission

JOURNAL Submitted (02-OCT-2001) Persson A., Center for Molecular Biotechnology, KTH, SCFAB, Institute of Biotechnology, Roslagssvagen 30B, 106 91 Stockholm, SWEDEN

COMMENT This clone is available royalty-free through IMAGE Consortium Distributors. IMPORTANT: This sequence represents the full insert of this IMAGE cDNA clone. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived.

FEATURES

Location/Qualifiers

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polyA_signal 2105..2110

ORIGIN

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ACCESSION AF201687
VERSION AF201687.1 GI:11493668
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SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 1261)
AUTHORS Pei, H., Yordy, J. S., Leng, Q., Zhao, Q., Watson, D. K. and Li, R.
TITLE EAP1 interacts with ETS1 and modulates its transcriptional
function
JOURNAL Oncogene 22 (18), 2699-2709 (2003)
PUBMED 12743594
REFERENCE 2 (bases 1 to 1261)
AUTHORS Li, R., Pei, H. and Papas, T. S.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-1999) Center for Molecular and Structural
Biology, Department of Medicine, and Hollings Cancer Center,
Medical University of South Carolina, 86 Jonathan Lucas St.,
Charleston, SC 29425, USA
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Hominidae; Homo.
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Almeida, J.
Direct Submission
Submitted (29-APR-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 30, 2005 this sequence version replaced gi:62551221.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
Rp11-948M1 is from the library RPCI-11.4 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACes.6. Location/Qualifiers
1. 176819
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FEATURES
source

ORIGIN

Query Match 56.5%; Score 1085; DB 8; Length 176819;
Best Local Similarity 99.4%; Pred. No. 2.6e-227; Indels 0; Gaps 0;
Matches 1088; Conservative 0; Mismatches 7;
Qy 825 AGTTTACCAGATCTGTGGTTTACCCAAACAATTTGGATGCTGGAGTTTGGGCA 884
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Qy 945 CTGCTTTGTAACACTCTGTTTGTGATCGAATATTTTTCAGAGCAGCAGCAGAGAGAGGACACA 1004
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Qy 1005 TTATTTCCCGAAGTTTGGACCTTTCTGGATTAGAAAACTGGACTGTGGTAGATTTTCCCTA 1064
Db 37365 TTATTTCCCGAAGTTTGGACCTTTCTGGATTAGAAAACTGGACTGTGGTAGATTTTCCCTA 37424
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QY 1185 GGAGGAATAATGTAAGTACTAGATCATTTGTGCACAGAAACCAACTATGATTTATGTTGGTTGTT 1244

Db 37545 GGAGGAATAATGTAAGTACTAGATCATTTGTGCACAGAAACCAACTATGATTTATGTTGGTTGTT 37604

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QY 1905 AATTTTATTTGGTAA 1919

Db 38265 AATTTTATTTGGTTTA 38279

RESULT 17

HS30M3

LOCUS

DEFINITION

Human DNA sequence from clone RP1-30M3 on chromosome 6p22.1-22.3

Contains the 5' end of gene KIAA0319, the gene for TRAF and TNF

receptor-associated protein (TRAP) (BAP2, AD022, MGC9099), gene

FLJ20501, the 3' end of gene FLJ12619 (DKFZP564G182) and two Cpg

islands, complete sequence.

AL031775

ACCESSION

AL031775.1

VERSION

GI:4071041

KEYWORDS

HTG; TRAF; Cpg island; DKFZP564G182; FLJ12619; FLJ20501; KIAA0319;

TNF; TRAF; TRAP.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 102200)
Phillips,S.
Direct Submission
Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
Clone request: clonerequest@sanger.ac.uk
On Dec 29, 1998 this sequence version replaced gi:4007165.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
RP1-30M3 is from the library RPCI-1 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vegas@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone; and the assembly was confirmed by restriction digest,
except on the rare occasion of the clone being a YAC.

FEATURES

source

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gene

mRNA

Db 63319 GGAGGAAATAATGTACTAGATCATTTGTACAGAAAAACCACTATGATTTATGGTTGTGT 63378
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Qy 1905 AATTTTATTTGGTAA 1919
Db 64039 AATTTTATTTGTTA 64053

RESULT 18
BD139846/c
LOCUS
DEFINITION BD139846 1079 bp DNA linear PAT 18-SEP-2002
Compounds for immunotherapy and diagnosis of breast cancer and
methods for their use.
ACCESSION BD139846
VERSION BD139846.1 GI:23234791
KEYWORDS JP 2002507387-A/63.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1079)
AUTHORS Reed,S.G. and Xu,J.
TITLE Compounds for immunotherapy and diagnosis of breast cancer and
methods for their use
JOURNAL Patent: JP 2002507387-A 63 12-MAR-2002;
CORIXA CORP
COMMENT OS Homo sapiens (human)
PN JP 2002507387-A/63
PD 12-MAR-2002

PF 22-DEC-1998 JP 2000526543
PR 24-DEC-1997 US 08/998253,24-DEC-1997 US 08/998255 PR
17-JUL-1998 US 09/118627,17-JUL-1998 US 09/118554 PI STEVEN
G REED,JIANGCHUN XU
PC C12N15/09,A61K38/00,A61K39/00,A61K39/39,A61K39/395,A61P35/00,
PC C07K14/47,
PC C07K16/18,C12N1/19,C12N1/21,C12N5/10,C12P21/08,C12Q1/68,G01N33/ PC
53,
PC G01N33/577,C12N15/00,A61K37/02,C12N5/00
CC Compounds for immunotherapy and diagnosis
of breast cancer and
CC methods for
CC their use
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Best Local Similarity 99.8%; Pred. No. 4.2e-223;
Matches 1078; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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Qy 723 CGGAACGAATGAATCAAGTTAAATGTTTAAAGAAATGCAAGAGGCTCCAGAGTCAG 782
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Qy 783 CTACAGTTTATTTTGCAGGAGATACAAATCTAAGGGATCGAGAGGTTTACCAGATGTGCTG 842
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[illegible]


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RESULT 22

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AC152027/c
LOCUS AC152027 150344 bp DNA linear HTG 11-NOV-2004
DEFINITION Dasytup novemcinctus clone VMRC5-12D21, WORKING DRAFT SEQUENCE, 5
ordered pieces.
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ACCESSION

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AC152027
VERSION AC152027.2 GI:55700150
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KEYWORDS

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HTG; HTGS PHASE2; HTGS DRAFT.
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SOURCE

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Dasytup novemcinctus (nine-banded armadillo)
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ORGANISM

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Dasytup novemcinctus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Antonellis,A., Ayele,K., Benjamin,B., Blakesley,R.W., Boakye,A.,
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Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,H.,
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Engle,J., Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N.,
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Ho,S.-L., Hu,P., Hurler,B., Idol,J.R., Jones,C., Kwong,P., Laric,P.,
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Larson,S., Lee-Lin,S.-O., Legaspi,R., Madden,M., Maduro,Q.B.,
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Maduro,V.B., Margulies,E.H., Masiello,C., Maekeri,B., McDowell,J.,
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Mullikin,J.C., Oestreicher,J.S., Park,M., Portnoy,M.E., Prasad,A.,
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Puri,O., Reddix-Dugue,N., Rosas,B., Schandler,K., Schueler,M.G.,
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Shah,K., Sison,C., Stantropop,S., Stephen,E., Thomas,J.W.,
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Thomas,P.J., Tsipouri,V., Vogt,J.L., Wetherby,K.D., Young,A. and
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Green,E.D.
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NISC Comparative Sequencing Initiative
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Unpublished
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2 (bases 1 to 150344)
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Green,E.D.
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Direct Submission
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Submitted (21-OCT-2004) NIH Intramural Sequencing Center, 8717
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Grovemont Circle, Gaithersburg, MD 20877, USA
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3 (bases 1 to 150344)
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Green,E.D.
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Direct Submission
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Submitted (11-NOV-2004) NIH Intramural Sequencing Center, 5625
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Fishers Lane, Rockville, MD 20852, USA
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On Nov 11, 2004 this sequence version replaced gi:54312159.
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----- Genome Center
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Center: NIH Intramural Sequencing Center
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Center code: NISC
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Web site: http://www.nisc.nih.gov
Contact: nisc.zoo@nhgri.nih.gov
----- Project Information
Center project name: ifi
Center clone name: 012D21
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8x average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 149480 bases at least Q40
Consensus quality: 149754 bases at least Q30
Consensus quality: 149909 bases at least Q20
Insert size: 155000; agarose-fp
Insert size: 149944; sum-of-contigs
Quality coverage: 9.52x in Q20 bases; agarose-fp
Quality coverage: 9.84x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 36273: contig of 36273 bp in length
* 36274 36373: gap of unknown length
* 36374 55049: contig of 18676 bp in length
* 55050 55149: gap of unknown length
* 55150 101939: contig of 46790 bp in length
* 101940 102039: gap of unknown length
* 102040 114806: contig of 12767 bp in length
* 114807 150344: gap of unknown length
* 114907 150344: contig of 35438 bp in length.

FEATURES

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/notes="clone overlaps with GenBank Accession Number AC152029 clone VMRC5-168B11 (center project name ifj)"

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101940..102039

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Matches 1435; Conservative 0; Mismatches 350; Indels 89; Gaps 14;				
QY	36	GCCTGGAGGCGGGAGGAGCGCGGAGGAAGAGGCGGAGCTCGATGCGCGAGTGGAGTGA	95	GAATAA
DB	53581	GGCCAGAGCCGAGGCGGCGAGAGCGAGCGGAGCGGGAGCCCGGGTGAAGAAGCGGC	53522	CTGCTGCTGTAAACTCTTGGATCGAATATTTTTCAGAGCAGCAGCAGCAGAG
QY	96	GACTTCTGTGTGGAGTTTGCCTCGGTGCGAAGCTGCGATGCGCGAGTGGCTCAGTGTCT	155	GAATACCTCGTCTACTGTGAAGCTTCGTTTGTGATGAATCTTTTTCAGAGCAGCAGCAGAG
DB	53521	GACTCTTGTGTGCGAGTTTGCCTCGGTGCGAATTTGCGACCGCGCGCTGGCCCAAGTGTCT	53462	AGGACACATTATTCCCGAAGTTTGGACCTTCTTGGATTAGAAAACTGGACTGTGTGA
QY	156	TCCTGGCCGAGAACTGCGGAGATGGAAAGGGCTCTGAACCTCTTCTGAGCCCGCTCCGG	215	AGGCCCATATCATTTCCCGAAGTATGGACCTTCTTGGTGGAAAACTGGACTGTGTGCA
DB	53461	TCCTGGCCGAGAACTGCGGAGATGGAAAGGGCTCTGAACCTCTTCTGAGCCCGCTCCGG	53402	GATTTCCTAGTGATCAGTGGGGTCTTCTGTGCAACTTAGATATATTTGTPAAAAATGCTT
QY	216	TGGAGGAGAGCGCCTTGGAAAGCGGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTG	275	GATTTCCTAGTGATCAGTGGGGTCTTCTGTGCGAGCTTAGATATATTTGTAACCTGCTA
DB	53401	TGGAGGAGAGCGCCCGGAGAGCGGCTCGGACCCCTCGGAGCCCGAGGCTGTGTGG	53342	TTCAAGTGTGGGTTTTT-----GCCCTGATTTGTCGAAATCAAAATTTCCACCT-TCTGGA
QY	276	ACCTAACCAATGAAGAACTGATTTCCACCATCTTCTAAATCAGCCCATCTGGAAGATA	335	TTCCAGATGTGAGTTTTTAAATCTTCTGCGTTTTTACCAATATATTTTACCTGTCTGGA
DB	53341	ACCTAACCAATGAAGATACGATGATCCCAATGTTCTTAAATCAGCCCATCTGGA	53282	AGGTAGGTTTCTGCGGAGGAAATAATGTACTAGATCAATCTCAGAAAAACCAACTA-
QY	336	CTCAGCAAGAAATGGCAGCATGTTCTCTCATTTACCTGGAATATGATGATTAGATC	395	AGATAGGTTTAAAAATTAAGGAATTAATATCTGGATCTCTGTAAGAGAAATTCCTTAC
DB	53281	TTACGCAAGAGATGGCAGTATGTTCTCTTTAAATTTACCTGGAATATGATGGAATGGATC	53222	TTCAAGTGTGGTGTGTTTTCAGAAATTCAGAACTTCAAGTGTGTTTATTTTAAACG
QY	396	TAAACAATCTGTCAGAGAGGCTCGAGGGGTGTGTCCTACTTGTACAGCCCGAG	455	TGTGACTTTTATTTTTCATGCTCCTCAGATTTTCAGAACTAAATGTTTATTTTAAACT
DB	53221	TAAACAATCTGTCAGAGAGGCTCGAGGGGTGTGTCCTACTTGTACAGCCCGAG	53162	AACHATTCCTGCAATTCAGGATGTAGGCCAATTTAATAAAGGGCACAAGCCCTGTCTAG
QY	456	ATGTGATATTTCTACAGGAAGTTATCCCCATATTTAGCTACCTTAAAGAGAGATCAA	515	AAAGCATGCTGTGTGTCAGAAATATGAGACCTCTTAGTGA---GGCCCAAGCCCTGTCT--
DB	53161	ATGTGATATTTCTACAGGAAGTTATCCCTCGTACTACAGTTACCTTAAAGAGAGCAA	53102	AGTTTTCACACGGTCTTACAGCTGCCAGCTGGATTTCCAAACAGGTACCC--CATTTGTCTC
QY	516	GTAATTTATGAGATTTATACAGGTATGAAGAGGATTTTACAGCTATATATTTGAAGA	575	AGCTTTTCHAGCAGTGTCTATAG-TGTGCTGGGTTCCAGCAGGGCGCAACAGTGTCTC
DB	53101	GTAATTTATGAGATTTATACAGGTCTGGAAGAGGATATTTACAGCTATATATTTGAAGA	53042	TGAGCTAATGTTTATATTTTTCATTCAGGCACCGAAATAGTTAATTTTAAAAATAAGTC
QY	576	AATCAAGAGTGAATTTAAAAAGCCAGAGATTTATCTTTTCCAAAGTACCAAAATGATGA	635	CAGGCTACTGATTTTGAATTTTCAATCAGAACTAGAAATGTTAATTTCCAAATAATTC
DB	53041	AATCAAGAGTGAATTTAAAAAGCCAGAGATTTATCTTTTCCAAAGTACCAAAATGATGA	52982	TTCAAAAGAGAAATGCTTACTAATGTATGAAGGTTTACTGAGTCTCTTCAGACTGGATC
QY	636	GAAACCTTTTATGTCGATGTGAATGTGTGAGGAATGAGCTTTGCTTATGACATCCC	695	CTTTTATTTTCAATGTCAGATCATCTTAAATGAAATGSCCATGATTATCTGCAGTTAAGT
DB	52981	GAAACCTTTATGTCGATGTGTGATGTGTGAGGAATGAACTTTACCTTATGACTTCCC	52922	AGATGACAGCTATTCTACATCAGACTTTGATTTTTTGTGCTAGCTTAATTTACATAATGGTAAGN
QY	696	ATTTTGGAGACACAGAGGCTGCTGGGAAAGGAATGAATCAGTTAAAAATGGTTTTTAA	755	AGAAGACAACATCTCTATATCAGACTT--CTTTTGTGCTAGCTAA-----TAGTG
DB	52921	ATTTTGGAGACACAGAGGATCTTAAGGAACGAATCAATCAGTTTAAAGTGTGTTTTAA	52862	TATTAATTGAAACCTTATGGCTTAAAAATTCCTTAATCTCTTTTGTATTCATGTTGTAGTC
QY	756	AGAAAATCAAGAGGCTCCAGAGTCAGTACAGTTTATATTTTGCAGGAGATACAAATCTAA	815	ATTTTCAAGAGACACAAAG-----GTTTGAATATGATTAAGTCAGGTAGACGAGCAT
DB	52861	AGAAAATCAAGAGGCTCCAGAGACAGCTACGTTTATATTTTGCAGGAGATACAAATTTAA	52802	TGGGACATTTTTTTTAAACAAAAATAAATGTCATGAAGAGACATAGCCTTTTAGTTTTGCTTAA
QY	816	GGGATCGAGAGGTTACCAGATGTGTGTTTACCCCAACAACTTGTGATGCTGGGAGT	875	TAGACTGTTTTTCTAAGAAAA-----AGTAAAGAGAAATAGGCTTTTAGTTTTTGTCTA
DB	52801	GGGATCAAGAGTTACCAGATGTGTGTTTACCCCAACAACTTGTGATGCTGGGAGT	52742	TTGTGAATGGAATGCTTTTACAGGAAGTAAATGCAAAATTAATTTTAACTGTGCTTTTAA
QY	876	TTTTGGGCAACCTTAAACATTCGCCAGTATACATGGGATACACAAATGAACCTTAATCTTG	935	CTTAAAAAAGTGAATTTTTCAGAGGTGACTAAAGGGCAGCTTTAAATGCTCTTTAAG
DB	52741	TTTTGGGCAAGCCTGAGCATTTGCCAGTTTACATGGGATACGCAATGAACCTTTAACCTTG	52682	GAAAAATATTTTTC 1881
RESULT 23				
MMU251328				
LOCUS				
MMU251328 1943 bp mRNA linear ROD 27-MAY-2000				

Db 1405 CCGCTGTGACAAAGTCATT---GTTGCATCAGAGTTTCAGTA-----ATGGCGG 1453

Qy 1402 CTGAGCTAATGTTTATATATTTTCCATTCCAGGCACCGAAATAGTTAATAATTTTAAATAAGT 1461

Db 1454 TATCTCAGGGCTAACTATTGTTTGAATTAGGCACCAATATA-----TTTAAATCAATTT 1507

Qy 1462 CTTCAAAAGAAACATNAGAGATTATTAGTTCCTTGGGACTGGATCCTTTATTTTCATTAAG 1521

Db 1508 TATTAAGAGAAAGTAAGCCATTGAACCTCTTTGAGACTGCATTTGCTTATATTTCTGTTAAG 1567

Qy 1522 TTCAGATCATCTTAATGAATAATGCGATGATTATCTGCAGTTAAGTAGATGACACTATT 1581

Db 1568 TTCAGA--AATGTAAGTGAAGAACCGTGACCAACCGTAGTAAGTAGATGACACTGTT 1625

Qy 1582 TPACATCAGACTTGATTTTTTGTGACGCTAATACATAATTGGTAAGNTATAATTGAAACCT 1641

Db 1626 GTATATCAGACTT-AATTTTGTGACGCTGATAGTATA-----TAGTGACTGATGAGTCAG 1678

Qy 1642 TATGGCTTAAATTCCTTAACTCCTTTTGTGATTCATGTTTGTAGTCATGTTGTCAACAGA 1701

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Qy 1762 AACAAAAATAATGCATGAAGAGACATAGCCCTTTTGTGTTTGTCTAATTGTGAAATGGAAA 1821

Db 1798 TTTTCTAAGAAGAAATTCAGAAGAAAGTAGTAAGTTTGTACTGTAAATGGAAA 1857

Qy 1822 TCGTTTACGGAGTA-----AATGCAATTTANTTTTAAAGTGTGCTTTTAAAGAAAAA 1873

Db 1858 TACTTTCACAGAGTGAATAAAGAATACTTTTTTTTGTAAATGTTCTGTAAAGAAAAA 1914

RESULT 24

BD150065

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

OS Homo sapiens (human)

PN JP 2002191363-A/4908

PD 09-JUL-2002

PF 28-JUL-2000 JP 2000280990

PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU SAITO,

PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,

PI KEIICHI NAGAI, TETSUJI OTSUKI

PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC 10,

PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC

Primer for synthesizing full-length cDNA and use thereof FH Key

Location/Qualifiers

FT source

FT Location/Qualifiers

1. .752

/organism='Homo sapiens (human)'

/organism='Homo sapiens'

ORIGIN

Query Match

Best Local Similarity

Matches

724; Conservative

0; Mismatches

18; Indels

2; Gaps

2;

Qy 20 ATGAGATTGGGAGATTGCTCGAGGGCGGAGAGGCGCGGAGGAGAAAGAGGGCGAGCCT 79

Db 1 ATGAGATTGGGAGATTGCTCGAGGGCGGAGAGGCGCGGAGGAGAAAGAGGGCGAGCCT 60

Qy 80 GAGGTGAAAACGCGGAGCTTCTGTGTGAGATTGCTCGGTGCGGAGCTGCGATGCC 139

Db 61 GAGGTGAAAACGCGGAGCTTCTGTGTGAGATTGCTCGGTGCGGAGCTGCGATGCC 120

Qy 140 GCAGTGGCTCAGTGTCTTCTCGCGGAGAAACGACTGGGAGATGGAAAGGGCTCTGAATCC 199

Db 121 CGGTGGCTCAGTGTCTTCTCGCGGAGAAACGACTGGGAGATGGAAAGGGCTCTGAATCC 180

Qy 200 TACTTCGAGCCTCCGGTGGAGAGAGCGCTTTGGAAACCGGAGCTGAAACCATCTCTGAG 259

Db 181 TGTTCGAGCCTCCGGTGGAGAGAGCGCTTTGGAAACCGGAGCTGAAACCATCTCTGAG 240

Qy 260 CCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAACTGATTCACCACTTCTAAAAATC 319

Db 241 CCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAACTGATTCACCACTTCTAAAAATC 300

Qy 320 AGCCATCTGAAGTACTCTCAGCAAGAAATGGCAGCATGTTCTCTCTCATTTACCTGGAAT 379

Db 301 AGCCATCTGAAGTACTCTCAGCAAGAAATGGCAGCATGTTCTCTCTCATTTACCTGGAAT 360

Qy 380 ATTGATGATTAGATCTAAACAATCTGTTCAGAGAGGCTCGAGGGGTGTGTTCTTACTTA 439

Db 361 ATTGATGATTAGATCTAAACAATCTGTTCAGAGAGGCTCGAGGGGTGTGTTCTTACTTA 420

Qy 440 GCTTTGTACAGCCAGATGTCATATTTCTACAGCAAGTTATTTCCCCCATATTTATAGCTAC 499

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Qy 500 CTAAGAAGAGATCAAGTAATTATGAGATTATTACAGGTCATGAGAGGATATTTCACA 559

Db 481 CTAAGAAGAGATCAAGTAATTATGAGATTATTACAGGTCATGAGAGGATATTTCACA 540

Qy 560 GCTATAATGTTGAAGAAATCAAGAGTGAATAATTAAGGAGGATATTATTCCTTTTCCA 619

Db 541 GCTATAATGTTGAAGAAATCAAGAGTGAATAATTAAGGAGGATATTATTCCTTTTCCA 600

Qy 620 AGTACCAAAATGATGAG-AAAACCTTTTATGTCATGTCATGTCAGGAAATGAGCT 678

Db 601 AGTACCAAAATGATGAGAAAAACCTTTTATGTCATGTCATGTCAGGAAATGAGCT 660

Qy 679 TTGCTTTATGACATCCCC-ATTTCGAGAGCACCAGAGGCGATGCTCGCGGAGGAAATGAATC 737

Db 661 TTGCTTTATGACATCCCCATTGCGGAGAACACANAGGCGATCTCGCGGAGGAAATGAATC 720

Qy 738 AGTTAAAAATCGTTTTTAAAGAAA 761

Db 721 AGTTAAAAATCGTTTTTAAAGAAA 744

RESULT 25

AX870003

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

752 bp

DNA

linear

Sequence 4908 from Patent EP1074617.

AX870003

AX870003.1

GI:40024866

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

Db	1242	CCCACTTGCAGCTTT	1256	
RESULT 28				
AX011601				
LOCUS	AX011601	1312 bp	DNA	linear
DEFINITION	Sequence 3 from Patent WO9955859.			PAT 06-SEP-2000
ACCESSION	AX011601			
VERSION	AX011601.1	GI:9998125		
KEYWORDS	Mus musculus (house mouse)			
SOURCE	Mus musculus			
ORGANISM	Mus musculus			
REFERENCE				
AUTHORS	Remacle J.E., Huybroeck D.F. and Pype,S.M.			
TITLE	Cd40-interacting and traf-interacting proteins			
JOURNAL	Patent: WO 9955859-A 3 04-NOV-1999;			
	REMACLE JACQUES EMILE FERNAND (BE); VLAAMS INTERUNIV INST BIOTECH			
	(BE); HUYLBROECK DANNY FRANCOIS EVE (BE); PYPE STEFAN MARIA			
	CHRISTIAAN (BE)			
FEATURES				
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	Location/Qualifiers			
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ORIGIN				
Query Match	34.8%;	Score 668.2;	DB 6;	Length 1312;
Best Local Similarity	77.0%;	Pred. No. 9.4e-136;		
Matches	843;	Conservative 0;	Mismatches 243;	Indels 9; Gaps 2;
Qy	36	GCCTGGAGGGCGGAGGAGCGCGGAGGAAGAGGCGGAGCTTGAGGTGAAAAGCGCG 95		
Db	171	GGCGGGCGCGTCGCGCGCCGAAGCAGCACAGCGGCGAGGAGACCGGCTGAAGAGCGCG 230		
Qy	96	GACTTCTGTGTGTGAGTTTGCTTCGGTTCGAAGCTCGGATGCGCAGTGGCTCAGTGCT 155		
Db	231	GGCTTCAGTGGCTCGGGCTTTCGTTGTGTGGGGGATGCGACCCACGATGGTCCCGACGC 290		
Qy	156	TCCTGGCGCGAAGCAGCTGGGAGATGAAAAGGGCTCTGAACTCCTACTTCGAGCCTCGG 215		
Db	291	TCCTGGCGGAGAACGACTGGCAGACGACGAGAAGCCCTGAGCGCCTACTTCGAGCTGCC 350		
Qy	216	TGGAGGAGAGCGCCTTGAAACGCGGACCTTGAAACCATCTCTGAGCCCAAGACCTATGTTG 275		
Db	351	AGAACGACCAAGGGTGGCGCGCCGACGCTCCACGTCCTTCAAGTCGAGGCGCTATGTTG 410		
Qy	276	ACCTAAACCAATGAAGAACAACTGATTCACACCTTCTTAAATCAGCCCATCTGAAGATA 335		
Db	411	ATCTAACCAACGAGATGCAATATGATACAACTTTTGAAGCCAGTCCATCTGGA---A 467		
Qy	336	CTCAGCAAGAAAATGGCAGCATGTTCTCTCTCATTTACCTGGAATATTTGATGGATTAGATC 395		
Db	468	CTCCTCTAGAAGATAGCAGCACTATTTCTTTTCATTACCTGGAATATTGATGGATTAGATG 527		
Qy	396	TAAACAATCTGTGACAGAGGCTCGAGGGGTGTGTTCTCTACTTAGCTTTGTACAGCCCG 455		
Db	528	GATGCAATCTGCCGAGAGGCTCGAGGGGTGTGTTCTGCTGCTAGCTTTGTATAGTCCAG 587		

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Tel: 403-690-5388

Fax: 503-690-5384

Email: spindelele@ohsu.edu

Primer A: acagaaaaaaccaactatgatt

Primer B: aaatttaactcatcatggac

STS size: 710

PCR Profile:

Hot Start: 95 degrees C for 2.00 min
Denaturation: 95 degrees C for 0.50 min
Annealing: 51 degrees C for 0.50 min
Polymerization: 72 degrees C for 1.00 min
PCR Cycles: 35
Extension: 72 degrees C for 7.0 min
Thermal Cycler: MJ Instruments PTC100

Protocol:

Template: 200 ng
Primer: each 1uM
dNTP's: each 200 uM
TaQ Polymerase: 0.05 units/ul (Fast Start High Fidelity, Roche)
Total Vol: 50 ul

Buffer: MgCl2: 1.8 mM
Fast Start polymerase reaction buffer (Roche)

Bases 3-686 are 96% homologous (Blast) to bases 1242-1925 of NM_016614.2. Primers were chosen to amplify genomic DNA in the 3' region of TTRAP. As human sequence was used to design the primers, the primer sequences are not included in the rhesus sequence provided below. To obtain additional information regarding primers or clones contact: Dr. Robert Norgren; Dept of Genetics, Cell Biology & Anatomy; University of Nebraska Medical Center; 986395 Nebraska Medical Center; Omaha, NE 68198. Email: rnorgren@unmc.edu

A database containing sequences associated with this project can be found at: <http://rhesusgenecchip.unomaha.edu/index.html>.

FEATURES

source
1. .710
/organism="Macaca mulatta"
/mol_type="genomic DNA"
/strain="Indian origin"
/db_xref="taxon:9544"
/clone="MMA5740"
/clone_lib="Rhesus macaque genomic DNA"
/dev_stage="Adult"
/note="Organ: Liver; Vector: pGEM-T Easy; V-type: Plasmid; STS was amplified from rhesus genomic DNA with the human forward and reverse primers listed above and subcloned into pGEM-T Easy"
1. .710
/gene="TTRAP"
/note="TRAF and TNF receptor associated protein"
<1. .>710
/gene="TTRAP"

ORIGIN

Query Match 33.0%; Score 632.8; DB 10; Length 710;
Best Local Similarity 95.0%; Pred. No. 5.6e-128;
Matches 652; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 1234 TATGGTTGTTTTCAGAAATTCACATTAAAGATTAATGTTTATTAACGACACATTC 1293
DB 1 TGTGGTTGTTTTCAGAAATTCACATTAAAGATTAATGTTTATTAACGACACATTC 60
QY 1294 CTGCATTACAGGATGTAGGCCATTTTAATAAAGGCGCACAAAGCCTGTTCAGAGTTTTCAA 1353
DB 61 CTGTGTTACAGGATGTAGGCCGTTTAATAAAGGCGCACAAAGCCTGTTCAGAGTTTTCAA 120
QY 1354 CGGTGTTACAGCTGCCAGCTGGATTCCAAACAGGTACCCCATTTGCTCTGAGCTAAATGT 1413
DB 121 CGGTGTTATAGCTGCCAGCTGGATTCCAAACAGGAATCACATTGCTCTGAGCTAAATGT 180

QY 1414 TTATATTTTTCATTTCAGGACCGAATAAGTAGTTAATATTTAAATAAGTCTTCAAAAGAAA 1473
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QY 1474 ACATAAGAGATTATTTAGTCTTTCGGACTGGATCCTTTATTTATAAGTTCAGATCATCT 1533
DB 241 ACATAAGAGATTATTTAGTCTTTCGGACTGGATCCTTTATTTATTCATGAGTTCAGATCATCT 300
QY 1534 TAAATGAAATGCCATGANTATTCGCAGTTAAGTAGTAGACAGCTATTTCTACATCAGACT 1593
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QY 1654 TTCCTTAACTCCTTTTGTGATTCATGTTTGTAGTCATGTTGTCAACAGAGGCAAAAGTTAAG 1713
DB 421 TTCCTTAACTCCTTTTGTGATTCATGTTTGTAGTCATGTTGTCAACAGAGGCAAAAGTTAAG 480
QY 1714 CTTGATGATGTTTAAATTCGGTTTGTAGTACCAATGGGACATTTTTTTTAAACAAAAATAAA 1773
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QY 1774 TGCATGAAGAGACATAGCCTTTTGTAGTCTTGTGTAATTTGTAATGGAATGGAATGCTTTTACAGGA 1833
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QY 1834 AGTAAATGCAAAATTTAAGTGTCTTTAAAGAAAAATATTTTCCCCACAGAGAGAAA 1893
DB 601 AGTAAATGCAAAATTTACTTGTAAAGTGTGCTTTAAAGAAAAATATTTTCCCCACAGAGAGAAA 660
QY 1894 TTTAAATAAGAAATTTTATTTGGTAA 1919
DB 661 TTTAAATAAGAAATTTTATTTGTTTA 686

RESULT 30
CQ726600
LOCUS CQ726600 858 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 12534 from Patent WO02068579.
ACCESSION CQ726600
VERSION CQ726600.1 GI:42290170
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 12534 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
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1. .858
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN
Query Match 32.1%; Score 617; DB 6; Length 858;
Best Local Similarity 78.8%; Pred. No. 1.6e-124;
Matches 858; Conservative 0; Mismatches 0; Indels 231; Gaps 1;
QY 20 ATGAGATTGGGAGTTGCTCGAGGCGGAGGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGCT 79
DB 1 ATGAGATTGGGAGTTGCTCGAGGCGGAGGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGCT 60
QY 80 GAGGTGAAAAAGCGCGAGCTTCTGTGTGTGAGTTTTCCTCGGTGCGCAAGTGCATGCC 139

Job time : 9845.42 secs

Db 61 GAGGTGAAAAAGCGGAGACTTCTGTGTGGAGTTTGCTCGGTGCGAAGCTGCGATGCC 120
Qy 140 GCAGTGGCTCAGTCTTCTGCGCGAGAACGACTGGAGATGGAAGGGCTCTGAACGCC 199
Db 121 GCAGTGGCTCAGTCTTCTGCGCGAGAACGACTGGAGATGGAAGGGCTCTGAACGCC 180
Qy 200 TACTTTCGAGCCTCGGTGGAGAGAGCGCTTGGAAACGCGACCTGGAACCACTCTCTGAG 259
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Db 361 ATTGATGGATTAGATCTAAACAACTCTCTCAGAGAGGGCTCGAGGG----- 405
Qy 440 GCTTTTGTACAGCCAGATGATATTTCTACAGGAAGTTATTCCCCCATATATTATAGCTAC 499
Db 406 ----- 405
Qy 500 CTAAGAAGAGATCAAGTAATTAATGAGATTTATTCAGGTCATGAAGAAGATATTTCAACA 559
Db 406 ----- 405
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Db 406 -----GTGATGTGTGAGGAATGAGCTT 429
Qy 680 TGCCTTATGACATCCCATTTGGAGAGCACCAGAGGGCATGCTCGGAAACGAATGAATCAG 739
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Qy 860 GTGGATGCTCGGAGTTTTTGGGCAACCTPAACATTGCGAGTATACATGGGATACACAA 919
Db 610 GTGGATGCTCGGAGTTTTTGGGCAACCTPAACATTGCGAGTATACATGGGATACACAA 669
Qy 920 ATGAACTCTAATCTTGGAATAAATGCTGCTGTGTAACCTTCTGTTTGTGATCGAATATTTTC 979
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Db 790 AAACCTGGACTGTGTAGATTTCTTAGTGATCACTGGGGTCTTCTGTGCAACTTAGATATA 849
Qy 1100 ATATTGTAA 1108
Db 850 ATATTGTAA 858

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